PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C12N 15/11, 15/10, C07K 14/47, C12P 21/00, C12Q 1/68, C07K 16/18, G06F 17/30, 17/50

A2

(11) International Publication Number: WO 99/53051

(43) International Publication Date: 21 October 1999 (21.10.99)

(21) International Application Number: PCT/IB99/00712

(22) International Filing Date: 9 April 1999 (09.04.99)

(30) Priority Data:

| | | |
|---|---|---|
| 09/057,719 | 9 April 1998 (09.04.98) | US |
| 09/069,047 | 28 April 1998 (28.04.98) | US |

(71) Applicant *(for all designated States except US)*: GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). GIORDANO, Jean-Yves [FR/FR]; 12, rue Duhesme, F-75018 Paris (FR).

(74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).

(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

**Published**
*Without international search report and to be republished upon receipt of that report.*

(54) Title: 5' ESTS AND ENCODED HUMAN PROTEINS

(57) Abstract

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be otained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

*FOR THE PURPOSES OF INFORMATION ONLY*

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| AL | Albania | ES | Spain | LS | Lesotho | SI | Slovenia |
| AM | Armenia | FI | Finland | LT | Lithuania | SK | Slovakia |
| AT | Austria | FR | France | LU | Luxembourg | SN | Senegal |
| AU | Australia | GA | Gabon | LV | Latvia | SZ | Swaziland |
| AZ | Azerbaijan | GB | United Kingdom | MC | Monaco | TD | Chad |
| BA | Bosnia and Herzegovina | GE | Georgia | MD | Republic of Moldova | TG | Togo |
| BB | Barbados | GH | Ghana | MG | Madagascar | TJ | Tajikistan |
| BE | Belgium | GN | Guinea | MK | The former Yugoslav Republic of Macedonia | TM | Turkmenistan |
| BF | Burkina Faso | GR | Greece | | | TR | Turkey |
| BG | Bulgaria | HU | Hungary | ML | Mali | TT | Trinidad and Tobago |
| BJ | Benin | IE | Ireland | MN | Mongolia | UA | Ukraine |
| BR | Brazil | IL | Israel | MR | Mauritania | UG | Uganda |
| BY | Belarus | IS | Iceland | MW | Malawi | US | United States of America |
| CA | Canada | IT | Italy | MX | Mexico | UZ | Uzbekistan |
| CF | Central African Republic | JP | Japan | NE | Niger | VN | Viet Nam |
| CG | Congo | KE | Kenya | NL | Netherlands | YU | Yugoslavia |
| CH | Switzerland | KG | Kyrgyzstan | NO | Norway | ZW | Zimbabwe |
| CI | Côte d'Ivoire | KP | Democratic People's Republic of Korea | NZ | New Zealand | | |
| CM | Cameroon | | | PL | Poland | | |
| CN | China | KR | Republic of Korea | PT | Portugal | | |
| CU | Cuba | KZ | Kazakstan | RO | Romania | | |
| CZ | Czech Republic | LC | Saint Lucia | RU | Russian Federation | | |
| DE | Germany | LI | Liechtenstein | SD | Sudan | | |
| DK | Denmark | LK | Sri Lanka | SE | Sweden | | |
| EE | Estonia | LR | Liberia | SG | Singapore | | |

# 5' ESTS AND ENCODED HUMAN PROTEINS

## Background of the Invention

The estimated 50,000-100,000 genes scattered along the human chromosomes offer tremendous promise for the understanding, diagnosis, and treatment of human diseases. In addition, probes capable of specifically hybridizing to loci distributed throughout the human genome find applications in the construction of high resolution chromosome maps and in the identification of individuals.

In the past, the characterization of even a single human gene was a painstaking process, requiring years of effort. Recent developments in the areas of cloning vectors, DNA sequencing, and computer technology have merged to greatly accelerate the rate at which human genes can be isolated, sequenced, mapped, and characterized.

Currently, two different approaches are being pursued for identifying and characterizing the genes distributed along the human genome. In one approach, large fragments of genomic DNA are isolated, cloned, and sequenced. Potential open reading frames in these genomic sequences are identified using bioinformatics software. However, this approach entails sequencing large stretches of human DNA which do not encode proteins in order to find the protein encoding sequences scattered throughout the genome. In addition to requiring extensive sequencing, the bioinformatics software may mischaracterize the genomic sequences obtained, *i.e.*, labeling non-coding DNA as coding DNA and vice versa.

An alternative approach takes a more direct route to identifying and characterizing human genes. In this approach, complementary DNAs (cDNAs) are synthesized from isolated messenger RNAs (mRNAs) which encode human proteins. Using this approach, sequencing is only performed on DNA which is derived from protein coding portions of the genome. Often, only short stretches of the cDNAs are sequenced to obtain sequences called expressed sequence tags (ESTs). The ESTs may then be used to isolate or purify extended cDNAs which include sequences adjacent to the EST sequences. The extended cDNAs may contain all of the sequence of the EST which was used to obtain them or only a portion of the sequence of the EST which was used to obtain them. In addition, the extended cDNAs may contain the full coding sequence of the gene from which the EST was derived or, alternatively, the extended cDNAs may include portions of the coding sequence of the gene from which the EST was derived. It will be appreciated that there may be several extended cDNAs which include the EST sequence as a result of alternate splicing or the activity of alternative promoters. Alternatively, ESTs having partially overlapping sequences may be identified and contigs comprising the consensus sequences of the overlapping ESTs may be identified.

In the past, these short EST sequences were often obtained from oligo-dT primed cDNA libraries. Accordingly, they mainly corresponded to the 3' untranslated region of the mRNA. In part, the prevalence of EST sequences derived from the 3' end of the mRNA is a result of the fact that typical

techniques for obtaining cDNAs, are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs (Adams *et al., Nature* 377:3-174, 1996, Hillier *et al., Genome Res.* 6:807-828, 1996).

In addition, in those reported instances where longer cDNA sequences have been obtained, the reported sequences typically correspond to coding sequences and do not include the full 5' untranslated region (5'UTR) of the mRNA from which the cDNA is derived. Indeed, 5'UTRs have been shown to affect either the stability or translation of mRNAs. Thus, regulation of gene expression may be achieved through the use of alternative 5'UTRs as shown, for instance, for the translation of the tissue inhibitor of metalloprotease mRNA in mitogenically activated cells (Waterhouse *et al, J Biol Chem.* 265:5585-9. 1990). Furthermore, modification of 5'UTR through mutation, insertion or translocation events may even be implied in pathogenesis. For instance, the fragile X syndrome, the most common cause of inherited mental retardation, is partly due to an insertion of multiple CGG trinucleotides in the 5'UTR of the fragile X mRNA resulting in the inhibition of protein synthesis via ribosome stalling (Feng *et al, Science* 268:731-4, 1995). An aberrant mutation in regions of the 5'UTR known to inhibit translation of the proto-oncogene *c-myc* was shown to result in upregulation of c-myc protein levels in cells derived from patients with multiple myelomas (Willis *et al, Curr Top Microbiol Immunol* 224:269-76, 1997). In addition, the use of oligo-dT primed cDNA libraries does not allow the isolation of complete 5'UTRs since such incomplete sequences obtained by this process may not include the first exon of the mRNA, particularly in situations where the first exon is short. Furthermore, they may not include some exons, often short ones, which are located upstream of splicing sites. Thus, there is a need to obtain sequences derived from the 5' ends of mRNAs.

While many sequences derived from human chromosomes have practical applications, approaches based on the identification and characterization of those chromosomal sequences which encode a protein product are particularly relevant to diagnostic and therapeutic uses. In some instances, the sequences used in such therapeutic or diagnostic techniques may be sequences which encode proteins which are secreted from the cell in which they are synthesized. Those sequences encoding secreted proteins as well as the secreted proteins themselves, are particularly valuable as potential therapeutic agents. Such proteins are often involved in cell to cell communication and may be responsible for producing a clinically relevant response in their target cells. In fact, several secretory proteins, including tissue plasminogen activator, G-CSF, GM-CSF, erythropoietin, human growth hormone, insulin, interferon-α, interferon-β, interferon-γ, and interleukin-2, are currently in clinical use. These proteins are used to treat a wide range of conditions, including acute myocardial infarction, acute ischemic stroke, anemia, diabetes, growth hormone deficiency, hepatitis, kidney carcinoma, chemotherapy-induced neutropenia and multiple sclerosis. For these reasons, extended cDNAs encoding secreted proteins or portions thereof represent a valuable source of therapeutic agents. Thus, there is a need for the identification and characterization of secreted proteins and the nucleic acids encoding them.

In addition to being therapeutically useful themselves, secretory proteins include short peptides, called signal peptides, at their amino termini which direct their secretion. These signal peptides are

encoded by the signal sequences located at the 5' ends of the coding sequences of genes encoding secreted proteins. These signal peptides can be used to direct the extracellular secretion of any protein to which they are operably linked. In addition, portions of the signal peptides called membrane-translocating sequences, may also be used to direct the intracellular import of a peptide or protein of interest. This may prove beneficial in gene therapy strategies in which it is desired to deliver a particular gene product to cells other than the cells in which it is produced. Signal sequences encoding signal peptides also find application in simplifying protein purification techniques. In such applications, the extracellular secretion of the desired protein greatly facilitates purification by reducing the number of undesired proteins from which the desired protein must be selected. Thus, there exists a need to identify and characterize the 5' portions of the genes for secretory proteins which encode signal peptides.

Sequences coding for non-secreted proteins may also find application as therapeutics or diagnostics. In particular, such sequences may be used to determine whether an individual is likely to express a detectable phenotype, such as a disease, as a consequence of a mutation in the coding sequence of a protein. In instances where the individual is at risk of suffering from a disease or other undesirable phenotype as a result of a mutation in such a coding sequence, the undesirable phenotype may be corrected by introducing a normal coding sequence using gene therapy. Alternatively, if the undesirable phenotype results from overexpression of the protein encoded by the coding sequence, expression of the protein may be reduced using antisense or triple helix based strategies.

The secreted or non-secreted human polypeptides encoded by the coding sequences may also be used as therapeutics by administering them directly to an individual having a condition, such as a disease, resulting from a mutation in the sequence encoding the polypeptide. In such an instance, the condition can be cured or ameliorated by administering the polypeptide to the individual.

In addition, the secreted or non-secreted human polypeptides or portions thereof may be used to generate antibodies useful in determining the tissue type or species of origin of a biological sample. The antibodies may also be used to determine the cellular localization of the secreted or non-secreted human polypeptides or the cellular localization of polypeptides which have been fused to the human polypeptides. In addition, the antibodies may also be used in immunoaffinity chromatography techniques to isolate, purify, or enrich the human polypeptide or a target polypeptide which has been fused to the human polypeptide.

Public information on the number of human genes for which the promoters and upstream regulatory regions have been identified and characterized is quite limited. In part, this may be due to the difficulty of isolating such regulatory sequences. Upstream regulatory sequences such as transcription factor binding sites are typically too short to be utilized as probes for isolating promoters from human genomic libraries. Recently, some approaches have been developed to isolate human promoters. One of them consists of making a CpG island library (Cross *et al.*, *Nature Genetics* 6: 236-244, 1994). The second consists of isolating human genomic DNA sequences containing SpeI binding sites by the use of SpeI binding protein. (Mortlock *et al., Genome Res.* 6:327-335, 1996). Both of these approaches have

their limits due to a lack of specificity and of comprehensiveness. Thus, there exists a need to identify and systematically characterize the 5' portions of the genes.

The present 5' ESTs may be used to efficiently identify and isolate 5'UTRs and upstream regulatory regions which control the location, developmental stage, rate, and quantity of protein synthesis, as well as the stability of the mRNA. Once identified and characterized, these regulatory regions may be utilized in gene therapy or protein purification schemes to obtain the desired amount and locations of protein synthesis or to inhibit, reduce, or prevent the synthesis of undesirable gene products.

In addition, ESTs containing the 5' ends of protein genes may include sequences useful as probes for chromosome mapping and the identification of individuals. Thus, there is a need to identify and characterize the sequences upstream of the 5' coding sequences of genes.

## Summary of the Invention

The present invention relates to purified, isolated, or enriched 5' ESTs which include sequences derived from the authentic 5' ends of their corresponding mRNAs. The term "corresponding mRNA" refers to the mRNA which was the template for the cDNA synthesis which produced the 5' EST. These sequences will be referred to hereinafter as "5' ESTs." The present invention also includes purified, isolated or enriched nucleic acids comprising contigs assembled by determining a consensus sequences from a plurality of ESTs containing overlapping sequences. These contigs will be referred to herein as "consensus contigated 5'ESTs."

As used herein, the term "purified" does not require absolute purity; rather, it is intended as a relative definition. Individual 5' EST clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. The sequences obtained from these clones could not be obtained directly either from the library or from total human DNA. The cDNA clones are not naturally occurring as such, but rather are obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The conversion of mRNA into a cDNA library involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection. Thus, creating a cDNA library from messenger RNA and subsequently isolating individual clones from that library results in an approximately $10^4$-$10^6$ fold purification of the native message. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

As used herein, the term "isolated" requires that the material be removed from its original environment (e.g., the natural environment if it is naturally occurring). For example, a naturally-occurring polynucleotide present in a living animal is not isolated, but the same polynucleotide, separated from some or all of the coexisting materials in the natural system, is isolated.

As used herein, the term "recombinant" means that the 5' EST is adjacent to "backbone" nucleic acid to which it is not adjacent in its natural environment. Additionally, to be "enriched" the 5' ESTs will

represent 5% or more of the number of nucleic acid inserts in a population of nucleic acid backbone molecules. Backbone molecules according to the present invention include nucleic acids such as expression vectors, self-replicating nucleic acids, viruses, integrating nucleic acids, and other vectors or nucleic acids used to maintain or manipulate a nucleic acid insert of interest. Preferably, the enriched 5' ESTs represent 15% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. More preferably, the enriched 5' ESTs represent 50% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules. In a highly preferred embodiment, the enriched 5' ESTs represent 90% or more of the number of nucleic acid inserts in the population of recombinant backbone molecules.

"Stringent," "moderate," and "low" hybridization conditions are as defined below.

The term "polypeptide" refers to a polymer of amino acids without regard to the length of the polymer; thus, peptides, oligopeptides, and proteins are included within the definition of polypeptide. This term also does not specify or exclude post-expression modifications of polypeptides, for example, polypeptides which include the covalent attachment of glycosyl groups, acetyl groups, phosphate groups, lipid groups and the like are expressly encompassed by the term polypeptide. Also included within the definition are polypeptides which contain one or more analogs of an amino acid (including, for example, non-naturally occurring amino acids, amino acids which only occur naturally in an unrelated biological system, modified amino acids from mammalian systems etc.), polypeptides with substituted linkages, as well as other modifications known in the art, both naturally occurring and non-naturally occurring.

As used interchangeably herein, the terms "nucleic acids," "oligonucleotides," and "polynucleotides" include RNA, DNA, or RNA/DNA hybrid sequences of more than one nucleotide in either single chain or duplex form. The term "nucleotide" as used herein as an adjective to describe molecules comprising RNA, DNA, or RNA/DNA hybrid sequences of any length in single-stranded or duplex form. The term "nucleotide" is also used herein as a noun to refer to individual nucleotides or varieties of nucleotides, meaning a molecule, or individual unit in a larger nucleic acid molecule, comprising a purine or pyrimidine, a ribose or deoxyribose sugar moiety, and a phosphate group, or phosphodiester linkage in the case of nucleotides within an oligonucleotide or polynucleotide. Although the term "nucleotide" is also used herein to encompass "modified nucleotides" which comprise at least one modifications (a) an alternative linking group, (b) an analogous form of purine, (c) an analogous form of pyrimidine, or (d) an analogous sugar, for examples of analogous linking groups, purine, pyrimidines, and sugars see for example PCT publication No. WO 95/04064. The polynucleotide sequences of the invention may be prepared by any known method, including synthetic, recombinant, *ex vivo* generation, or a combination thereof, as well as utilizing any purification methods known in the art.

The terms "base paired" and "Watson & Crick base paired" are used interchangeably herein to refer to nucleotides which can be hydrogen bonded to one another be virtue of their sequence

identities in a manner like that found in double-helical DNA with thymine or uracil residues linked to adenine residues by two hydrogen bonds and cytosine and guanine residues linked by three hydrogen bonds (See Stryer, L., *Biochemistry*, 4th edition, 1995).

The terms "complementary" or "complement thereof" are used herein to refer to the sequences of polynucleotides which are capable of forming Watson & Crick base pairing with another specified polynucleotide throughout the entirety of the complementary region. For the purpose of the present invention, a first polynucleotide is deemed to be complementary to a second polynucleotide when each base in the first polynucleotide is paired with its complementary base. Complementary bases are, generally, A and T (or A and U), or C and G. "Complement" is used herein as a synonym from "complementary polynucleotide," "complementary nucleic acid" and "complementary nucleotide sequence" . These terms are applied to pairs of polynucleotides based solely upon their sequences and not any particular set of conditions under which the two polynucleotides would actually bind. Preferably, a "complementary" sequence is a sequence which an A at each position where there is a T on the opposite strand, a T at each position where there is an A on the opposite strand, a G at each position where there is a C on the opposite strand and a C at each position where there is a G on the opposite strand.

Thus, 5' ESTs in cDNA libraries in which one or more 5' ESTs make up 5% or more of the number of nucleic acid inserts in the backbone molecules are "enriched recombinant 5' ESTs" as defined herein. Likewise, 5' ESTs in a population of plasmids in which one or more 5' ESTs of the present invention have been inserted such that they represent 5% or more of the number of inserts in the plasmid backbone are "enriched recombinant 5' ESTs" as defined herein. However, 5' ESTs in cDNA libraries in which 5' ESTs constitute less than 5% of the number of nucleic acid inserts in the population of backbone molecules, such as libraries in which backbone molecules having a 5' EST insert are extremely rare, are not "enriched recombinant 5' ESTs."

In some embodiments, the present invention relates to 5' ESTs which are derived from genes encoding secreted proteins. As used herein, a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal peptides in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g. soluble proteins), or partially (e.g. receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Such 5' ESTs include nucleic acid sequences, called signal sequences, which encode signal peptides which direct the extracellular secretion of the proteins encoded by the genes from which the 5' ESTs are derived. Generally, the signal peptides are located at the amino termini of secreted proteins.

Secreted proteins are translated by ribosomes associated with the "rough" endoplasmic reticulum. Generally, secreted proteins are co-translationally transferred to the membrane of the endoplasmic reticulum. Association of the ribosome with the endoplasmic reticulum during translation

of secreted proteins is mediated by the signal peptide. The signal peptide is typically cleaved following its co-translational entry into the endoplasmic reticulum. After delivery to the endoplasmic reticulum, secreted proteins may proceed through the Golgi apparatus. In the Golgi apparatus, the proteins may undergo post-translational modification before entering secretory vesicles which transport them across the cell membrane.

The 5' ESTs of the present invention have several important applications. For example, they may be used to obtain and express cDNA clones which include the full protein coding sequences of the corresponding gene products, including the authentic translation start sites derived from the 5' ends of the coding sequences of the mRNAs from which the 5' ESTs are derived. These cDNAs will be referred to hereinafter as "full-length cDNAs." These cDNAs may also include DNA derived from mRNA sequences upstream of the translation start site. The full-length cDNA sequences may be used to express the proteins corresponding to the 5' ESTs. As discussed above, secreted proteins and non-secreted proteins may be therapeutically important. Thus, the proteins expressed from the cDNAs may be useful in treating and controlling a variety of human conditions. The 5' ESTs may also be used to obtain the corresponding genomic DNA. The term "corresponding genomic DNA" refers to the genomic DNA which encodes the mRNA from which the 5' EST was derived.

Alternatively, the 5' ESTs may be used to obtain and express extended cDNAs encoding portions of the protein. In the case of secreted proteins, the portions may comprise the signal peptides of the secreted proteins or the mature proteins generated when the signal peptide is cleaved off.

The present invention includes isolated, purified, or enriched "EST-related nucleic acids." The terms "isolated," "purified" or "enriched" have the meanings provided above. As used herein, the term "EST-related nucleic acids" means the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622, extended cDNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622, full-length cDNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622 or genomic DNAs obtainable using the nucleic acids of SEQ ID NOs. 24-811 and 1600-1622. The present invention also includes the sequences complementary to the EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched "fragments of EST-related nucleic acids." The terms "isolated," "purified" and "enriched" have the meanings described above. As used herein the term "fragments of EST-related nucleic acids" means fragments comprising at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive nucleotides of the EST-related nucleic acids to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related nucleic acids being referenced. In particular, fragments of EST-related nucleic acids refer to "polynucleotides described in Table II," "polynucleotides described in Table III," and "polynucleotides described in Table IV." The present invention also includes the sequences complementary to the fragments of the EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched "positional segments of EST-related nucleic acids." As used herein, the term "positional segments of EST-related nucleic acids"

includes segments comprising nucleotides 1-25, 26-50, 51-75, 76-100, 101-125, 126-150, 151-175, 176-200, 201-225, 226-250, 251-300, 301-325, 326-350, 351-375, 376-400, 401-425, 426-450, 451-475, 476-500, 501-525, 526-550, 551-575, 576-600 and 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. The term "positional segments of EST-related nucleic acids also includes segments comprising nucleotides 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 450-500, 501-550, 551-600 or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. The term "positional segments of EST-related nucleic acids" also includes segments comprising nucleotides 1-100, 101-200, 201-300, 301-400, 501-500, 500-600, or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. In addition, the term "positional segments of EST-related nucleic acids" includes segments comprising nucleotides 1-200, 201-400, 400-600, or 601-the terminal nucleotide of the EST-related nucleic acids to the extent that such nucleotide positions are consistent with the lengths of the particular EST-related nucleic acids being referenced. The present invention also includes the sequences complementary to the positional segments of EST-related nucleic acids.

The present invention also includes isolated, purified, or enriched "fragments of positional segments of EST-related nucleic acids." As used herein, the term "fragments of positional segments of EST-related nucleic acids" refers to fragments comprising at least 10, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 150, or 200 consecutive nucleotides of the positional segments of EST-related nucleic acids. The present invention also includes the sequences complementary to the fragments of positional segments of EST-related nucleic acids.

The present invention also includes isolated or purified "EST-related polypeptides." As used herein, the term "EST-related polypeptides" means the polypeptides encoded by the EST-related nucleic acids, including the polypeptides of SEQ ID NOs. 812-1599.

The present invention also includes isolated or purified "fragments of EST-related polypeptides." As used herein, the term "fragments of EST-related polypeptides" means fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of an EST-related polypeptide to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related polypeptides being referenced. In particular, fragments of EST-related polypepides refer to polypeptides encoded by "polynucleotides described in Table II," "polynucleotides described in Table III," and "polynucleotides described in Table IV."

The present invention also includes isolated or purified "positional segments of EST-related polypeptides." As used herein, the term "positional segments of EST-related polypeptides" includes polypeptides comprising amino acid residues 1-25, 26-50, 51-75, 76-100, 101-125, 126-150, 151-175, 176-200, or 201-the C-terminal amino acid of the EST-related polypeptides to the extent that such amino

acid residues are consistent with the lengths of the particular EST-related polypeptides being referenced. The term "positional segments of EST-related polypeptides also includes segments comprising amino acid residues 1-50, 51-100, 101-150, 151-200 or 201-the C-terminal amino acid of the EST-related polypeptides to the extent that such amino acid residues are consistent with the lengths of the particular EST-related polypeptides being referenced. The term "positional segments of EST-related polypeptides" also includes segments comprising amino acids 1-100 or 101-200 of the EST-related polypeptides to the extent that such amino acid residues are consistent with the lengths of particular EST-related polypeptides being referenced. In addition, the term "positional segments of EST-related polypeptides" includes segments comprising amino acid residues 1-200 or 201-the C-terminal amino acid of the EST-related polypeptides to the extent that amino acid residues are consistent with the lengths of the particular EST-related polypeptides being referenced.

The present invention also includes isolated or purified "fragments of positional segments of EST-related polypeptides." As used herein, the term "fragments of positional segments of EST-related polypeptides" means fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of positional segments of EST-related polypeptides to the extent that fragments of these lengths are consistent with the lengths of the particular EST-related polypeptides being referenced.

The present invention also includes antibodies which specifically recognize the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In the case of secreted proteins, such as those of SEQ ID NOs. 1554-1580 antibodies which specifically recognize the mature protein generated when the signal peptide is cleaved may also be obtained as described below. Similarly, antibodies which specifically recognize the signal peptides of SEQ ID NOs. 812-1516 or 1554-1580 may also be obtained.

In some embodiments and in the case of secreted proteins, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids include a signal sequence. In other embodiments, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may include the full coding sequence for the protein or, in the case of secreted proteins, the full coding sequence of the mature protein (*i.e.* the protein generated when the signal polypeptide is cleaved off). In addition, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may include regulatory regions upstream of the translation start site or downstream of the stop codon which control the amount, location, or developmental stage of gene expression.

As discussed above, both secreted and non-secreted human proteins may be therapeutically important. Thus, the proteins expressed from the EST-related nucleic acids, fragments of EST-related

nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may be useful in treating or controlling a variety of human conditions.

The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal gene expression. In addition, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids are useful for constructing a high resolution map of the human chromosomes.

The present invention also relates to secretion vectors capable of directing the secretion of a protein of interest. Such vectors may be used in gene therapy strategies in which it is desired to produce a gene product in one cell which is to be delivered to another location in the body. Secretion vectors may also facilitate the purification of desired proteins.

The present invention also relates to expression vectors capable of directing the expression of an inserted gene in a desired spatial or temporal manner or at a desired level. Such vectors may include sequences upstream of the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids, such as promoters or upstream regulatory sequences.

The present invention also comprises fusion vectors for making chimeric polypeptides comprising a first polypeptide and a second polypeptide. Such vectors are useful for determining the cellular localization of the chimeric polypeptides or for isolating, purifying or enriching the chimeric polypeptides.

The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids may also be used for gene therapy to control or treat genetic diseases. In the case of secreted proteins, signal peptides may be fused to heterologous proteins to direct their extracellular secretion.

Bacterial clones containing Bluescript plasmids having inserts containing the sequence of the non-aligned 5'ESTs, also referred to as singletons, and sequences of the 5'ESTs which were aligned to yield consensus contigated 5' ESTs are presently stored at 80°C in 4% (v/v) glycerol in the inventor's laboratories under internal designations. The non-aligned 5'ESTs are those which comprise a single EST from a single tissue in the listing of Table V. The inserts may be recovered from the stored materials by growing the appropriate clones on a suitable medium. The Bluescript DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR

can be performed with primers designed at both ends of the inserted EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids. The PCR product which corresponds to the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of nucleic acids can then be manipulated using standard cloning techniques familiar to those skilled in the art.

One embodiment of the present invention is a purified nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is a purified nucleic acid comprising at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive nucleotides, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

A further embodiment of the present invention is a purified nucleic acid comprising the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 24-811.

Yet another embodiment of the present invention is a purified nucleic acid comprising the full coding sequences of a sequence selected from the group consisting of SEQ ID NOs. 766-792 wherein the full coding sequence comprises the sequence encoding the signal peptide and the sequence encoding the mature protein.

Still another embodiment of the present invention is a purified nucleic acid comprising a contiguous span of a sequence selected from the group consisting of SEQ ID NOs. 766-792 which encodes the mature protein.

Another embodiment of the present invention is a purified nucleic acid comprising a contiguous span of a sequence selected from the group consisting of SEQ ID NOs. 24-728 and 766-792 which encodes the signal peptide.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising a sequence selected from the group consisting of the sequences of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising a mature protein included in a sequence selected from the group consisting of the sequences of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified nucleic acid encoding a polypeptide comprising a signal peptide included in a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1516 and 1554-1580.

Another embodiment of the present invention is a purified nucleic acid at least 30, 35, 40, 50, 75, 100, 200, 300, 500 or 1000 nucleotides in length which hybridizes under stringent conditions to a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a mature protein of a polypeptide selected from the group consisting of SEQ ID NOs. 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising a signal peptide of a sequence selected from the group consisting of the polypeptides of SEQ ID NOs. 812-1516 and 1554-1580.

Another embodiment of the present invention is a purified or isolated polypeptide comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, 75, 100, 200, 300, 500, or 1000 consecutive amino acids, to the extent that fragments of these lengths are consistent with the specific sequence, of a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of contacting a collection of mRNA molecules from human cells with a primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, hybridizing said primer to an mRNA in said collection that encodes said protein reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA, making a second cDNA strand complementary to said first cDNA strand and isolating the resulting cDNA encoding said protein comprising said first cDNA strand and said second cDNA strand.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

In one aspect of this embodiment, the cDNA encodes at least a portion of a human polypeptide.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of obtaining a cDNA comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, contacting said cDNA with a detectable probe comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence

selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 under conditions which permit said probe to hybridize to said cDNA, identifying a cDNA which hybridizes to said detectable probe, and isolating said cDNA which hybridizes to said probe.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

In one aspect of this embodiment, the cDNA encodes at least a portion of a human polypeptide.

Another embodiment of the present invention is a method of making a cDNA comprising the steps of contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA, hybridizing said first primer to said polyA tail, reverse transcribing said mRNA to make a first cDNA strand, making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

Another embodiment of the present invention is a purified cDNA obtainable by the method of the preceding paragraph.

In one aspect of this embodiment, said cDNA encodes at least a portion of a human polypeptide.

In another aspect of the preceding method the second cDNA strand is made by contacting said first cDNA strand with a first pair of primers, said first pair of primers comprising a second primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and a third primer having a sequence therein which is included within the sequence of said first primer, performing a first polymerase chain reaction with said first pair of primers to generate a first PCR product, contacting said first PCR product with a second pair of primers, said second pair of primers comprising a fourth primer, said fourth primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of said sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and a fifth primer, wherein said fourth and fifth hybridize to sequences within said first PCR product, and performing a second polymerase chain reaction, thereby generating a second PCR product.

One aspect of this embodiment is a purified cDNA obtainable by the method of the preceding paragraph.

In another aspect of this embodiment, said cDNA encodes at least a portion of a human polypeptide.

Alternatively, the second cDNA strand may be made by contacting said first cDNA strand with a second primer comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, hybridizing said second primer to said first strand cDNA, and extending said hybridized second primer to generate said second cDNA strand.

One aspect of the above embodiment is a purified cDNA obtainable by the method of the preceding paragraph.

In a further aspect of this embodiment said cDNA encodes at least a portion of a human polypeptide.

Another embodiment of the present invention is a method of making a polypeptide comprising the steps of obtaining a cDNA which encodes a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 or a cDNA which encodes a polypeptide comprising at least 6, 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive amino acids of a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NOs. 24-811, inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter, introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA, and isolating said protein.

Another aspect of this embodiment is an isolated protein obtainable by the method of the preceding paragraph.

Another embodiment of the present invention is a method of obtaining a promoter DNA comprising the steps of obtaining genomic DNA located upstream of a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, screening said genomic DNA to identify a promoter capable of directing transcription initiation, and isolating said DNA comprising said identified promoter.

In one aspect of this embodiment, said obtaining step comprises walking from genomic DNA comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622. In another aspect of this embodiment, said screening step comprises inserting genomic DNA located upstream of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 into a promoter reporter vector. For example, said screening step may comprise identifying motifs in genomic DNA located upstream of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 which are transcription factor binding sites or transcription start sites.

Another embodiment of the present invention is a isolated promoter obtainable by the method of the paragraph above.

Another embodiment of the present invention is the inclusion of at least one sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of said sequence in an array of discrete ESTs or fragments thereof of at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 nucleotides in length. In some aspects of this embodiment, the array includes at least two sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of said sequences. In another aspect of this embodiment., the array includes at least one, three, five, ten, fifteen, or twenty sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, 50, or 100 consecutive nucleotides of said sequences.

Another embodiment of the present invention is an enriched population of recombinant nucleic acids, said recombinant nucleic acids comprising an insert nucleic acid and a backbone nucleic acid, wherein at least 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 5%, 10%, or 20% of said insert nucleic acids in said population comprise a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a polypeptide comprising a sequence selected from the group consisting of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a purified or isolated antibody capable of specifically binding to a polypeptide comprising at least 6, 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 consecutive amino acids of a sequence selected from the group consisting of SEQ ID NOs. 812-1599.

Yet, another embodiment of the present invention is an antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide comprising a contiguous span of at least 8, 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 amino acids of any of SEQ ID NOs. 812-1599, wherein said antibody is polyclonal or monoclonal.

Another embodiment of the present invention is a computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

Another embodiment of the present invention is a computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599. In one aspect of this embodiment the computer system further comprises a sequence comparer and a data storage device having reference sequences stored thereon. For example, the sequence comparer may comprise a computer program which indicates polymorphisms. In another aspect of this embodiment, the computer system further comprises an identifier which identifies features in said sequence.

Another embodiment of the present invention is a method for comparing a first sequence to a reference sequence wherein said first sequence is selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of reading said first sequence and said reference sequence through use of a computer program which compares sequences and determining differences between said first sequence and said reference sequence with said computer program. In some aspects of this embodiment, said step of determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

Another embodiment of the present invention is a method for identifying a feature in a sequence selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of reading said sequence through the use of a computer program which identifies features in sequences and identifying features in said sequence with said computer program.

Another embodiment of the present invention is a vector comprising a nucleic acid according to any one of the nucleic acids described above.

Another embodiment of the present invention is a host cell containing the above vector.

Another embodiment of the present invention is a method of making any of the nucleic acids described above comprising the steps of introducing said nucleic acid into a host cell such that said nucleic acid is present in multiple copies in each host cell and isolating said nucleic acid from said host cell.

Another embodiment of the present invention is a method of making a nucleic acid of any of the nucleic acids described above comprising the step of sequentially linking together the nucleotides in said nucleic acids.

Another embodiment of the present invention is a method of making any of the polypeptides described above wherein said polypeptides is 150 amino acids in length or less comprising the step of sequentially linking together the amino acids in said polypeptide.

Another embodiment of the present invention is a method of making any of the polypeptides described above wherein said polypeptides is 120 amino acids in length or less comprising the step of sequentially linking together the amino acids in said polypeptides.

## Brief Description of the Drawings

Figure 1 is a summary of a procedure for obtaining cDNAs which have been selected to include the 5′ ends of the mRNAs from which they derived. In the first step (1), the cap of intact mRNAs is oxidized to be chemically ligated to an oligonucleotide tag. In the second step (2), a reverse transcription is performed using random primers to generate a first cDNA strand. In the third step (3), mRNAs are eliminated and the second strand synthesis is carried out using a primer contained in the oligonucleotide tag.

Figure 2 is an analysis of the 43 amino terminal amino acids of all human SwissProt proteins to determine the frequency of false positives and false negatives using the techniques for signal peptide identification described herein.

Figure 3 summarizes a general method used to clone and sequence extended cDNAs containing sequences adjacent to 5'ESTs.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags.

Figure 5 describes the transcription factor binding sites present in each of the promoters of Figure 4.

Figure 6 is a block diagram of an exemplary computer system.

Figure 7 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database.

Figure 8 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous.

Figure 9 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence.

Figure 10 is a table with all of the parameters that can be used for each step of extended cDNA analysis.

## Detailed Description of the Preferred Embodiment

### I. Obtaining 5'ESTs from cDNA libraries including the 5'Ends of their Corresponding mRNAs

The 5' ESTs of the present invention were obtained from cDNA libraries including cDNAs which include the 5'end of their corresponding mRNAs. The general method used to obtain such cDNA libraries is described in Examples 1 to 5.

**EXAMPLE 1**

Preparation of mRNA

Total human RNAs or polyA$^{+}$ RNAs derived from 29 different tissues were respectively purchased from LABIMO and CLONTECH and used to generate 44 cDNA libraries as described below.

The purchased RNA had been isolated from cells or tissues using acid guanidium thiocyanate-phenol-chloroform extraction (Chomczyniski and Sacchi, *Analytical Biochemistry* 162:156-159, 1987). $PolyA^+$ RNA was isolated from total RNA (LABIMO) by two passes of oligo dT chromatography, as described by Aviv and Leder, *Proc. Natl. Acad. Sci. USA* 69:1408-1412, 1972) in order to eliminate ribosomal RNA.

The quality and the integrity of the polyA+ RNAs were checked. Northern blots hybridized with a globin probe were used to confirm that the mRNAs were not degraded. Contamination of the $polyA^+$ mRNAs by ribosomal sequences was checked using Northern blots and a probe derived from the sequence of the 28S rRNA. Preparations of mRNAs with less than 5% of rRNAs were used in library construction. To avoid constructing libraries with RNAs contaminated by exogenous sequences (prokaryotic or fungal), the presence of bacterial 16S ribosomal sequences or of two highly expressed fungal mRNAs was examined using PCR.

## EXAMPLE 2

### Methods for Obtaining mRNAs having Intact 5' Ends

Following preparation of the mRNAs from various tissues as described above, selection of mRNA with intact 5' ends and specific attachment of an oligonucleotide tag to the 5' end of such mRNA was performed using either a chemical or enzymatic approach. Both techniques takes advantage of the presence of the "cap" structure, which characterizes the 5'end of intact mRNAs and which comprises a guanosine generally methylated once, at the 7 position. The chemical approach is illustrated in Figure 1.

The chemical modification approach involves the optional elimination of the 2′, 3′-cis diol of the 3′ terminal ribose, the oxidation of the 2', 3', -cis diol of the ribose linked to the cap of the 5' ends of the mRNAs into a dialdehyde, and the coupling of the such obtained dialdehyde to a derivatized oligonucleotide tag. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in International Application No. WO96/34981, published November 7, 1996.

The enzymatic approach for ligating the oligonucleotide tag to the 5' ends of mRNAs with intact 5' ends involves the removal of the phosphate groups present on the 5' ends of uncapped incomplete mRNAs, the subsequent decapping of mRNAs with intact 5' ends and the ligation of the phosphate present at the 5' end of the decapped mRNA to an oligonucleotide tag. Further detail regarding the enzymatic approaches for obtaining mRNAs having intact 5' ends are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato *et al., Gene* 150:243-250 (1994).

In either the chemical or the enzymatic approach, the oligonucleotide tag has a restriction enzyme site (e.g. EcoRI sites) therein to facilitate later cloning procedures. Following attachment of the oligonucleotide tag to the mRNA, the integrity of the mRNA was then examined by performing a Northern blot using a probe complementary to the oligonucleotide tag.

## EXAMPLE 3

cDNA Synthesis Using mRNA Templates Having Intact 5' Ends

For the mRNAs joined to oligonucleotide tags, first strand cDNA synthesis was performed using a reverse transcriptase with random nonamers as primers. In order to protect internal EcoRI sites in the cDNA from digestion at later steps in the procedure, methylated dCTP was used for first strand synthesis. After removal of mRNA by an alkaline hydrolysis, the first strand of cDNA was precipitated using isopropanol in order to eliminate residual primers.

The second strand of the cDNA was synthesized with a Klenow fragment using a primer corresponding to the 5'end of the ligated oligonucleotide. Methylated dCTP was also used for second strand synthesis in order to protect internal EcoRI sites in the cDNA from digestion during the cloning process.

## EXAMPLE 4

Cloning of cDNAs derived from mRNA with intact 5' ends into BlueScript

Following second strand synthesis, the ends of the cDNA were blunted with T4 DNA polymerase (Biolabs) and the cDNA was digested with EcoRI. Since methylated dCTP was used during cDNA synthesis, the EcoRI site present in the tag was the only hemi-methylated site, hence the only site susceptible to EcoRI digestion. The cDNA was then size fractionated using exclusion chromatography (AcA, Biosepra) and fractions corresponding to cDNAs of more than 150 bp were pooled and ethanol precipitated. The cDNA was directionally cloned into the SmaI and EcoRI ends of the phagemid pBlueScript vector (Stratagene). The ligation mixture was electroporated into bacteria and propagated under appropriate antibiotic selection.

## EXAMPLE 5

Selection of Clones Having the Oligonucleotide Tag Attached Thereto

Clones containing the oligonucleotide tag attached were then selected as follows. The plasmid DNAs containing 5' EST libraries made as described above were purified (Qiagen). A positive selection of the tagged clones was performed as follows. Briefly, in this selection procedure, the plasmid DNA was converted to single stranded DNA using gene II endonuclease of the phage F1 in combination with an exonuclease (Chang *et al.*, **Gene 127**:95-8, 1993) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA was then purified using paramagnetic beads as described by Fry *et al.*, *Biotechniques*, 13: 124-131, 1992. In this procedure, the single stranded DNA was hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide tag. Clones including a sequence complementary to the biotinylated oligonucleotide were captured by incubation with streptavidin coated magnetic beads followed by magnetic selection. After capture of the positive clones, the plasmid DNA was released from the magnetic beads and converted into double

stranded DNA using a DNA polymerase such as the Thermosequenase obtained from Amersham Pharmacia Biotech. The double stranded DNA was then electroporated into bacteria. The percentage of positive clones having the 5' tag oligonucleotide was estimated using dot blot analysis to typically be between 90 and 98%.

Following electroporation, the libraries were ordered in 384-microtiter plates (MTP). A copy of the MTP was stored for future needs. Then the libraries were transferred into 96 MTP and sequenced as described below.

**EXAMPLE 6**

Sequencing of Inserts in Selected Clones

Plasmid inserts were first amplified by PCR on PE-9600 thermocyclers (Perkin-Elmer, Applied Biosystems Division, Foster City, CA), using standard SETA-A and SETA-B primers (Genset SA), AmpliTaqGold (Perkin-Elmer), dNTPs (Boehringer), buffer and cycling conditions as recommended by the Perkin-Elmer Corporation.

PCR products were then sequenced using automatic ABI Prism 377 sequencers (Perkin Elmer). Sequencing reactions were performed using PE 9600 thermocyclers with standard dye-primer chemistry and ThermoSequenase (Amersham Pharmacia Biotech). The primers used were either T7 or 21M13 (available from Genset SA) as appropriate. The primers were labeled with the JOE, FAM, ROX and TAMRA dyes. The dNTPs and ddNTPs used in the sequencing reactions were purchased from Boehringer. Sequencing buffer, reagent concentrations and cycling conditions were as recommended by Amersham.

Following the sequencing reaction, the samples were precipitated with ethanol, resuspended in formamide loading buffer, and loaded on a standard 4% acrylamide gel. Electrophoresis was performed for 2.5 hours at 3000V on an ABI 377 sequencer, and the sequence data were collected and analyzed using the ABI Prism DNA Sequencing Analysis Software, version 2.1.2.

**EXAMPLE 7**

Obtaining 5' ESTs from Extended cDNA libraries

Obtained from mRNA with Intact 5' Ends

Alternatively, 5'ESTs may be isolated from other cDNA or genomic DNA libraries. Such cDNA or genomic DNA libraries may be obtained from a commercial source or made using other techniques familiar to those skilled in the art. One example of such cDNA library construction, a full-length cDNA library, is as follows.

PolyA+ RNAs are prepared and their quality checked as described in Example 1. Then, the caps at the 5' ends of the polyA+ RNAs are specifically joined to an oligonucleotide tag as described in Example 2. The oligonucleotide tag may contain a restriction site such as Eco RI to facilitate further

subcloning procedures. Northern blotting is then performed to check the size of mRNAs having the oligonucleotide tag attached thereto and to ensure that the mRNAs are actually tagged.

First strand synthesis is subsequently carried out for mRNAs joined to the oligonucleotide tag as described in Example 3 above except that the random nonamers are replaced by an oligo-dT primer. For instance, this oligo-dT primer may contain an internal tag of 4 nucleotides which is different from one tissue to the other. Following second strand synthesis using a primer contained in the oligonucleotide tag attached to the 5' end of mRNA, the blunt ends of the obtained double stranded full-length DNAs are modified into cohesive ends to facilitate subcloning. For example, the extremities of full-length cDNAs may be modified to allow subcloning into the Eco RI and Hind III sites of a Bluescript vector using the Eco RI site of the oligonucleotide tag and the addition of a Hind III adaptor to the 3' end of full-length cDNAs.

The full-length cDNAs are then separated into several fractions according to their sizes using techniques familiar to those skilled in the art. For example, electrophoretic separation may be applied in order to yield 3 or 6 different fractions. Following gel extraction and purification, the cDNA fractions are subcloned into appropriate vectors, such as Bluescript vectors, transformed into competent bacteria and propagated under appropriate antibiotic conditions. Subsequently, plasmids containing tagged full-length cDNAs are positively selected as described in Example 5.

The 5' end of full-length cDNAs isolated from such cDNA libraries may then be sequenced as described in Example 6 to yield 5'ESTs.

## II. Computer Analysis of the Isolated 5' ESTs: Construction of the SignalTag™ Database

The sequence data from the cDNA libraries made as described above were transferred to a database, where quality control and validation steps were performed. A base-caller, working using a Unix system, automatically flagged suspect peaks, taking into account the shape of the peaks, the inter-peak resolution, and the noise level. The base-caller also performed an automatic trimming. Any stretch of 25 or fewer bases having more than 4 suspect peaks was considered unreliable and was discarded. Sequences corresponding to cloning vector or ligation oligonucleotides were automatically removed from the EST sequences. However, the resulting EST sequences may contain 1 to 5 bases belonging to the above mentioned sequences at their 5' end. If needed, these can easily be removed on a case to case basis.

Following sequencing as described above, the sequences of the 5' ESTs were entered in a database for storage and manipulation as described below. Before searching the ESTs in the database for sequences of interest, ESTs derived from mRNAs which were not of interest were identified. Briefly, such undesired sequences may be of three types. First, contaminants of either endogenous (ribosomal RNAs, transfert RNAs, mitochondrial RNAs) or exogenous (prokaryotic RNAs and fungal RNAs) origins were identified. Second, uninformative sequences, namely redundant sequences, small sequences and highly degenerate sequences were identified. Third, repeated sequences (Alu, L1, THE

and MER repeats, SSTR sequences or satellite, micro-satellite, or telomeric repeats) were identified and masked in further processing.

In order to determine the accuracy of the sequencing procedure as well as the efficiency of the 5' selection described above, the analyses described in Examples 8 and 9 respectively were performed on 5'ESTs obtained from the database following the elimination of endogenous and exogenous contaminants and following the masking of repeats.

### EXAMPLE 8

Measurement of Sequencing Accuracy by Comparison to Known Sequences

To further determine the accuracy of the sequencing procedure described in Example 6, the sequences of 5' ESTs derived from known sequences were identified and compared to the original known sequences. First, a FASTA analysis with overhangs shorter than 5 bp on both ends was conducted on the 5' ESTs to identify those matching an entry in the public human mRNA database available at the time of filing the priority applications. The 5' ESTs which matched a known human mRNA were then realigned with their cognate mRNA and dynamic programming was used to include substitutions, insertions, and deletions in the list of "errors" which would be recognized. Errors occurring in the last 10 bases of the 5' EST sequences were ignored to avoid the inclusion of spurious cloning sites in the analysis of sequencing accuracy. This analysis revealed that the sequences incorporated in the database had an accuracy of more than 99.5%.

### EXAMPLE 9

Determination of Efficiency of 5' EST Selection

To determine the efficiency at which the above selection procedures isolated 5' ESTs which included sequences close to the 5' end of the mRNAs from which they derived, the sequences of the ends of the 5' ESTs derived from the elongation factor 1 subunit $\alpha$ and ferritin heavy chain genes were compared to the known cDNA sequences of these genes. Since the transcription start sites of both genes are well characterized, they may be used to determine the percentage of derived 5' ESTs which included the authentic transcription start sites. For both genes, more than 95% of the obtained 5' ESTs actually included sequences close to or upstream of the 5' end of the corresponding mRNAs.

To extend the analysis of the reliability of the procedures for isolating 5' ESTs from ESTs in the database, a similar analysis was conducted using a database composed of human mRNA sequences extracted from GenBank database release 97 for comparison. The 5' ends of more than 85% of 5' ESTs derived from mRNAs included in the GenBank database were located close to the 5' ends of the known sequence. As some of the mRNA sequences available in the GenBank database are deduced from genomic sequences, a 5' end matching with these sequences will be counted as an internal match. Thus, the method used here underestimates the yield of ESTs including the authentic 5' ends of their corresponding mRNAs.

## EXAMPLE 10

Calculation of Novelty Indices for 5'EST Libraries

In order to evaluate the novelty of 5'EST libraries, the following analysis was performed. For each sequenced 5'EST library, the sequences were clustered by the 5' end. Each sequence in the library was compared to the others and the longest sequence found in the cluster was used as representative of the group. A novelty rate (NR) was then defined as: NR= 100 X (Number of new unique sequences found in the library/Total number of sequences from the library). Typically, novelty rating ranged between 10% and 41% depending on the tissue from which the 5'EST library was obtained. For most of the libraries, the random sequencing of 5' EST libraries was pursued until the novelty rate reached 20%.

## EXAMPLE 11

Generation of Consensus Contigated 5' ESTs

Since the cDNA libraries made above include multiple 5' ESTs derived from the same mRNA, overlapping 5'ESTs may be assembled into continuous sequences. The following method describes how to efficiently align multiple 5'ESTs in order to yield not only consensus contigated 5'EST sequences for mRNAs derived from different genes but also consensus contigated 5'EST sequences for different mRNAs, so called variants, transcribed from the same gene such as alternatively spliced mRNAs.

The whole set of sequences was first partitioned into small clusters containing sequences which exhibited perfect matches with each other on a given length and which derived from a small number of different genes. Some 5'EST sequences, so called singletons, were not aligned using this approach because they were not homologous to any other sequence.

Thereafter, all variants of a given gene were identified in each cluster using a proprietary software. 5'EST sequences belonging to the same variant were then contigated and consensus contigated 5'EST sequences generated for each variant. All consensus contigated 5' EST sequences were subsequently compared to the whole set of individual 5'EST sequences used to obtained them.

If desired, the consensus contigated 5'EST sequences may be verified by identifying clones in nucleic acid samples derived from biological tissues, such as cDNA libraries, which hybridize to the probes based on the sequences of the consensus contigated 5'ESTs using any methods described herein and sequencing those clones.

Application of this alignment method to a selected set of 5'ESTs free from endogenous contaminants and uninformative sequences, and following the masking of repeats, yielded consensus contigated 5'EST sequences or variants of clustered genes encompassing many individual 5'ESTs. Both non aligned 5'ESTs, *i.e.* singletons, and consensus contigated 5'ESTs were then compared to already known sequences and those sequences matching human mRNA sequences were eliminated from further analysis.

## EXAMPLE 12

Identification of Open Reading Frames in 5' ESTs

Subsequently, consensus contigated 5'ESTs and 5'ESTs were screened to identify those having an open reading frame (ORF).

Such open reading frames were simply defined as uninterrupted nucleic acid sequences longer than 45 nucleotides and beginning with an ATG codon.

Alternatively, the nucleic acid sequence was first divided into several subsequences which coding propensity was evaluated separately using one or several different methods known to those skilled in the art such as the evaluation of N-mer frequency and its variants (Fickett and Tung, *Nucleic Acids Res*;20:6441-50 (1992)) or the Average Mutual Information method (Grosse *et al*, International Conference on Intelligent Systems for Molecular Biology, Montreal, Canada. June 28-July 1, 1998). Each of the scores obtained by the techniques described above were then normalized by their distribution extremities and then fused using a neural network into a unique score that represents the coding probability of a given subsequence. The coding probability scores obtained for each subsequence, thus the probability score profiles obtained for each reading frame, was then linked to the initiation codons present on the sequence. For each open reading frame, defined as a nucleic acid sequence beginning with an ATG codon, an ORF score was determined. Preferably, this score is the sum of the probability scores computed for each subsequence corresponding to the considered ORF in the correct reading frame corrected by a function that negatively accounts for locally high score values and positively accounts for sustained high score values. The most probable ORF with the highest score was selected.

In some embodiments, nucleic acid sequences encoding an "incomplete ORF", as referred therein, namely an open reading frame in which a start codon has been identified but no stop codon has been identified, were obtained.

In other embodiments, nucleic acid sequences encoding a "complete ORF", as used therein, namely an open reading frame in which a start codon and a stop codon have been identified, are obtained.

In a preferred embodiment, open reading frames encoding polypeptides of at least 50 amino acids were obtained.

To confirm that the chosen ORF actually encodes a polypeptide, the consensus contigated 5'EST or 5'EST may be used to obtain an extended cDNA using any of the techniques described therein, and especially those described in Examples 19 and 20. Then, such obtained extended cDNAs may be screened for the most probable open reading frame using any of the techniques described therein. The amino acid sequence of the ORF encoded by the consensus contigated 5'EST or 5'EST may then be compared to the amino acid sequence of the ORF encoded by the extended cDNA using any of the algorithms and parameters described therein in order to determine whether the ORF encoded by the extended cDNA is basically the same as the one encoded by the consensus contigated 5'EST or 5'EST.

Alternatively, to confirm that the chosen ORF actually encodes a polypeptide, the consensus contigated 5'EST or 5'EST may be used to obtain an extended cDNA using any of the techniques described therein, and especially those described in Examples 19 and 20. Such an extended cDNA may then be inserted into an appropriate expression vector and used to express the polypeptide encoded by the extended cDNA as described therein. The expressed polypeptide may be isolated, purified, or enriched as described therein. Several methods known to those skilled in the art may then be used to determine whether the expressed polypeptide is the one actually encoded by the chosen ORF, therein referred to an the expected polypeptide. Such methods are based on the determination of predictable features of the expressed polypeptide, including but not limited to its amino acid sequence, its size or its charge, and the comparison of these features to those predicted for the expected polypeptide. The following paragraphs present examples of such methods.

One of these methods consists in the determination of at least a portion of the amino acid sequence of the expressed polypeptide using any technique known to those skilled in the art. For example, the amino-terminal residues may be determined using techniques either based on Sanger's technique of acid hydrolysis of a polypeptide which N-terminal residue has been covalently labeled or using techniques based on Edman degradation of polypeptides which N-terminal residues are sequentially labeled and cleaved from the polypeptide of interest. The amino acid sequence of the expressed polypeptide may then be compared to the one predicted for the expected polypeptide using any algorithm and parameters described therein.

Alternatively, the size of the expressed polypeptides may be determined using techniques familiar to those skilled in the art such as Coomassie blue or silver staining and subsequently compared to the size predicted for the expected polypeptide. Generally, the band corresponding to the expressed polypeptide will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, specific antibodies or antipeptides may be generated against the expected polypeptide as described in Example 34 and used to perform immunoblotting or immunoprecipitation studies against the expressed polypeptide. The presence of a band in samples from cells containing the expression vector with the extended cDNA which is absent in samples from cells containing the expression vector encoding an irrelevant polypeptide indicates that the expected polypeptide or portion thereof is being expressed. Generally, the band corresponding to the expressed polypeptide will have a mobility near that expected based on the number of amino acids in the open reading frame of the extended cDNA. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage

## EXAMPLE 13

Identification of Potential Signal Sequences in 5' ESTs

The 5'ESTs or consensus contigated 5'ESTs found to encode an ORF were then searched to identify potential signal motifs using slight modifications of the procedures disclosed in Von Heijne, *Nucleic Acids Res. 14*:4683-4690, 1986. Those sequences encoding a 15 amino acid long stretch with a score of at least 3.5 in the Von Heijne signal peptide identification matrix were considered to possess a signal sequence. Those nucleic acid sequences which match a known human mRNA or EST sequence and have a 5′ end located downstream of the known 5′ end, preferably by more than 20 nucleotides, were excluded from further analysis. The remaining nucleic acids having signal sequences therein were included in a database called SignalTag™.

## EXAMPLE 14

Confirmation of Accuracy of Identification of Potential Signal Sequences in 5' ESTs

The accuracy of the above procedure for identifying signal sequences encoding signal peptides was evaluated by applying the method to the 43 amino acids located at the N terminus of all human SwissProt proteins. The computed Von Heijne score for each protein was compared with the known characterization of the protein as being a secreted protein or a non-secreted protein. In this manner, the number of non-secreted proteins having a score higher than 3.5 (false positives) and the number of secreted proteins having a score lower than 3.5 (false negatives) could be calculated.

Using the results of the above analysis, the probability that a peptide encoded by the 5' region of the mRNA is in fact a genuine signal peptide based on its Von Heijne's score was calculated based on either the assumption that 10% of human proteins are secreted or the assumption that 20% of human proteins are secreted. The results of this analysis are shown in Figure 2.

Using the above method of identification of secretory proteins, 5' ESTs of the following polypeptides known to be secreted were obtained: human glucagon, gamma interferon induced monokine precursor, secreted cyclophilin-like protein, human pleiotropin, and human biotinidase precursor. Thus, the above method successfully identified those 5' ESTs which encode a signal peptide.

To confirm that the signal peptide encoded by the 5' ESTs or consensus contigated 5' ESTs actually functions as a signal peptide, the signal sequences from the 5' ESTs or consensus contigated 5' ESTs may be cloned into a vector designed for the identification of signal peptides. Such vectors are designed to confer the ability to grow in selective medium only to host cells containing a vector with an operably linked signal sequence. For example, to confirm that a 5' EST or consensus contigated 5' EST encodes a genuine signal peptide, the signal sequence of the 5' EST or consensus contigated 5' EST may be inserted upstream and in frame with a non-secreted form of the yeast invertase gene in signal peptide selection vectors such as those described in U.S. Patent No. 5,536,637. Growth of host cells containing signal sequence selection vectors with the correctly inserted 5' EST or consensus contigated 5' EST signal sequence confirms that the 5' EST or consensus contigated 5' ESTs encodes a genuine signal peptide.

Alternatively, the presence of a signal peptide may be confirmed by cloning the extended cDNAs obtained using the ESTs or consensus contigated 5' ESTs into expression vectors such as pXT1 as described below, or by constructing promoter-signal sequence-reporter gene vectors which encode fusion proteins between the signal peptide and an assayable reporter protein. After introduction of these vectors into a suitable host cell, such as COS cells or NIH 3T3 cells, the growth medium may be harvested and analyzed for the presence of the secreted protein. The medium from these cells is compared to the medium from control cells containing vectors lacking the signal sequence or extended cDNA insert to identify vectors which encode a functional signal peptide or an authentic secreted protein.

## EXAMPLE 15

Analysis of the Sequences of the Invention

The set of the nucleic acid sequences of the invention (SEQ ID NOs.24-811 and 1600-1622) was obtained as described in Example 11. Subsequently, the most probable open reading frame was determined and signal sequences were searched, as described in Examples 12 and 13, for all sequences of the invention.

The nucleotide sequences of the SEQ ID NOs. 24-811 and 1600-1622 and the polypeptides sequences encoded by SEQ ID NOs. 24-811 (*i.e.* polypeptide sequences of SEQ ID NOs. 812-1599) are provided in the appended sequence listing which structure is as follows.

SEQ ID NOs. 24-728 are nucleic acids having an incomplete ORF which encodes a signal peptide. The locations of the incomplete ORFs and sequences encoding signal peptides are listed in the accompanying Sequence Listing. In addition, the von Heijne score of the signal peptide computed as described in Example 13 is listed as the "score" in the accompanying Sequence Listing. The sequence of the signal-peptide is listed as "seq" in the accompanying Sequence Listing. The "/" in the signal peptide sequence indicates the location where proteolytic cleavage of the signal peptide occurs to generate a mature protein.

SEQ ID NOs. 729-765 are nucleic acids having an incomplete ORF in which no sequence encoding a signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a sequence encoding a signal peptide in these nucleic acids. The locations of the incomplete ORFs are listed in the accompanying Sequence Listing.

SEQ ID NOs. 766-792 are nucleic acids having a complete ORF which encodes a signal peptide. The locations of the complete ORFs and of the signal peptides, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the proteolytic cleavage site are indicated as described above.

SEQ ID NOs. 793-811 are nucleic acids having a complete ORF in which no sequence encoding a signal peptide has been identified to date. However, it remains possible that subsequent analysis will

identify a sequence encoding a signal peptide in these nucleic acids. The locations of the complete ORFs are listed in the accompanying Sequence Listing.

SEQ ID NOs. 812-1516 are "incomplete polypeptide sequences" which include a signal peptide. "Incomplete polypeptide sequences" are polypeptide sequences encoded by nucleic acids in which a start codon has been identified but no stop codon has been identified. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 24-728. The location of the signal peptide, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the proteolytic cleavage site are indicated as described above.

SEQ ID NOs. 1517-1553 are incomplete polypeptide sequences in which no signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a signal peptide in these polypeptides. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 729-765.

SEQ ID NOs. 1554-1580 are "complete polypeptide sequences" which include a signal peptide. "Complete polypeptide sequences" are polypeptide sequences encoded by nucleic acids in which a start codon and a stop codon have been identified. These polypeptides are encoded by the nucleic acids of SEQ ID NOs. 766-792. The location of the signal peptide, the von Heijne score of the signal peptide, the sequence of the signal-peptide and the proteolytic cleavage site are indicated as described above..

SEQ ID NOs. 1581-1599 are complete polypeptide sequences in which no signal peptide has been identified to date. However, it remains possible that subsequent analysis will identify a signal peptide in these polypeptides. These polypeptides are encoded by the nucleic acids of SEQ ID NOs.793-811.

SEQ ID NOs. 1600-1622 are nucleic acid sequences in which no open reading frame has been conclusively identified to date. However, it remains possible subsequent analysis will identify an open reading frame in these nucleic acids.

In the accompanying Sequence Listing, all instances of the symbol "n" in the nucleic acid sequences mean that the nucleotide can be adenine, guanine, cytosine or thymine. In some instances the polypeptide sequences in the Sequence Listing contain the symbol "Xaa." These "Xaa" symbols indicate either (1) a residue which cannot be identified because of nucleotide sequence ambiguity or (2) a stop codon in the determined sequence where applicants believe one should not exist (if the sequence were determined more accurately). In some instances, several possible identities of the unknown amino acids may be suggested by the genetic code.

In the case of secreted proteins, it should be noted that, in accordance with the regulations governing Sequence Listings, in the appended Sequence Listing, the full protein (*i.e.* the protein containing the signal peptide and the mature protein) extends from an amino acid residue having a negative number through a positively numbered C-terminal amino acid residue. Thus, the first amino acid of the mature protein resulting from cleavage of the signal peptide is designated as amino acid

number 1, and the first amino acid of the signal peptide is designated with the appropriate negative number.

If one of the nucleic acid sequences of SEQ ID NOs. 24-811 and 1600-1622 are suspected of containing one or more incorrect or ambiguous nucleotides, the ambiguities can readily be resolved by resequencing a fragment containing the nucleotides to be evaluated. If one or more incorrect or ambiguous nucleotides are detected, the corrected sequences should be included in the clusters from which the sequences were isolated, and used to compute other consensus contigated sequences on which other ORFs would be identified. Nucleic acid fragments for resolving sequencing errors or ambiguities may be obtained from deposited clones or can be isolated using the techniques described herein. Resolution of any such ambiguities or errors may be facilitated by using primers which hybridize to sequences located close to the ambiguous or erroneous sequences. For example, the primers may hybridize to sequences within 50-75 bases of the ambiguity or error. Upon resolution of an error or ambiguity, the corresponding corrections can be made in the protein sequences encoded by the DNA containing the error or ambiguity. The amino acid sequence of the protein encoded by a particular clone can also be determined by expression of the clone in a suitable host cell, collecting the protein, and determining its sequence.

In addition, if one of the sequences of SEQ ID NOs. 812-1599 is suspected of containing a truncated ORF as the result of a frameshift in the sequence, such frameshifting errors may be corrected by combining the following two approaches. The first one involves thorough examination of all double predictions, *i.e.* all cases where the probability scores for two ORFs located on different reading frames are high and close, preferably different by less than 0.4. The fine examination of the region where the two possible ORFs overlap may help to detect the frameshift. In the second approach, homologies with known proteins are used to correct suspected frameshifts.

Of the identified clusters, some were shown to be multivariant, *i.e.* to contain several variants of the same gene. Table I gives for each of the multivariant clusters named by its internal reference (first column), the list of all variant consensus contigated 5'ESTs (second column), each being represented by a different sequence identification number.

**TABLE I**

| Cluster Internal Reference | SEQ ID NOs of Variants |
|---|---|
| C1 | 687, 791 |
| C2 | 744, 798 |
| C3 | 640, 811 |
| C4 | 59, 66 |
| C5 | 84, 97 |

| | |
|---|---|
| C6 | 287, 289 |
| C7 | 286, 775, 777 |
| C8 | 762, 768 |
| C9 | 783, 784 |
| C10 | 80, 1603 |
| C11 | 655, 736 |
| C12 | 805, 806 |

Table II provides a list preferred polynucleotide fragments which are derivatives of the consensus contigated 5'ESTs. As used herein the term "polynucleotide described in Table II" refers to the all of the preferred polynucleotide fragments defined in Table II in the following manner. The fragments are referred to by their SEQ ID numbers in the first column. The preferred polynucleotide fragments are then defined by a range of nucleotide positions from the SEQ IDs of the consensus contigated 5'ESTs as indicated in the second column entitled "positions of preferred fragments." The preferred polynucleotide fragments correspond to the individual 5'ESTs aligned to obtain the consensus contigated 5'EST and to those filed in the priority documents. The third column entitled "variant nucleotides" describes the nucleotide sequence variations observed between the consensus contigated 5'EST and preferred nucleic acid fragments as follows:

A) Substitutions in the sequence of a consensus contigated 5'EST to derive a preferred polynucleotide fragment are denoted by an "S", followed by a number indicating the first nucleotide position in a specific SEQ ID to be substituted in a string of substituted nucleotides or the position of the substituted nucleotide in the case of a single substituted nucleotide. Then there is a coma followed by one or more lower case letters indicating the identity of the nucleotide(s) occurring in the substituted position(s). For example, SEQ ID NO: 3401; Position of preferred fragments: 1-250; Variant nucleotides S45,atc would indicate that a preferred polynucleotide fragment had the sequence of positions 1 to 250 of SEQ ID NO. 3401, except that the nucleotides at positions 45, 46, and 47 were substituted with A, T, and C, respectively, in the preferred polynucleotide as compared with the sequence of SEQ ID No. 3401.

B) Insertions in the sequence of a consensus contigated 5'EST to derive a preferred polynucleotide fragment are denoted by an "I", followed by a number indicating the nucleotide position in a specific SEQ ID after which a string of nucleotides is inserted or the position after which the nucleotide is inserted in the case of a single inserted nucleotide. Then there is a coma followed by one or more lower case letters indicating the identity of the nucleotide(s) occurring in the inserted position(s). For example, SEQ ID NO: 7934; Position of preferred fragments: 1-500; Variant nucleotides: I36,gataca would indicate that a preferred polynucleotide fragment had the sequence of positions 1 to 500 of SEQ ID NO. 7934, except that after the nucleotides at position 36 a GATACA string of nucleotides is inserted in the preferred polynucleotide as compared with the sequence of SEQ ID No. 7934.

C) Deletions in the sequence of a consensus contigated 5'EST to derive a preferred nucleic acid fragment are denoted by an "D", followed by a number indicating the first nucleotide position in a specific SEQ ID to be deleted in a string of deleted nucleotides or the position of the deleted nucleotide in the case of a single deleted nucleotide. Then there is a coma followed by number indicating the number of nucleotide(s) deleted from the sequence provided in the sequence ID. For example, SEQ ID NO: 5398; Position of preferred fragments: 56-780; Variant nucleotides D114,5 would indicate that a preferred polynucleotide fragment had the sequence of positions 56 to 780 of SEQ ID NO. 5398, except that the nucleotides in positions 114 to 118 had been deleted in the preferred polynucleotide as compared with the sequence of SEQ ID No. 5398.

The present invention encompasses isolated, purified, or recombinant nucleic acids which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, or 500 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular polynucleotide, of a polynucleotide described in Table II, or a sequence complementary thereto, wherein said polynucleotide described in Table II is selected individually or in any combination from the polynucleotides described in Table II. The present invention also encompasses isolated, purified, or recombinant nucleic acids which consist of or consist essentially of a polynucleotide described in Table II, or a sequence complementary thereto, wherein said polynucleotide is selected individually or in any combination from the polynucleotides described in Table II. The present invention further encompasses isolated or purified polypeptides which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, or 100 amino acids encoded by a polynucleotide described in Table II.

**Table II**

| SEQ ID NO. | Positions of Preferred Fragments | Variant nucleotides |
|---|---|---|
| 35 | 1-423 | S124, s; I135, a; S293, w; I363, a; S377, r; D424, 15 |
| 41 | 1-427 | I117, m; S120, r; S124, g; D373, 1; S376, b; S378, b; I427, gggg; D428, 109 |
| 43 | 1-276 | S114, m; S118, rg; S123, r; S139, nr; I142, t; D148, 1; D152, 1; I228, t; I276, gg; D277, 136 |
| 45 | 126-420 | D1, 125; I420, ggg; D421, 100 |
| 46 | 1-255 | S139, r; I145, r; S146, mm; S150, ar; S254, g; D256, 128 |
| 48 | 4-437 | D1, 3; S49, a; S55, g; S79, a; S90, a; I437, tctctg |
| 59 | 1-471 | S26, a; S44, t; S48, t; S109, a; S191, t; S200, gc; S203, a; S210, g; S237, a; S240, g; S255, a; S272, a; S277, a; S279, a; S284, t; S297, g; S305, g; S316, a; I471, ggtca |
| 66 | 1-428 | I428, tactgggg |

| | | |
|---|---|---|
| 82 | 1-399 | S251, t; S277, d; I399, aagccggg |
| 84 | 5-488 | D1, 4; S210, g; S293, a; S325, g; S339, a; S348, g; S353, g; S395, g; I488, cacca |
| 93 | 1-508 | I508, gattt |
| 96 | 26-315 | D1, 25; S28, a; S62, c; I315, cagatgg |
| 97 | 4-460 | D1, 3; S19, g; S31, g; S114, gt; S118, a; S123, tc; S127, c; S132, a; S186, g; S190, c; S203, t; S210, g; S232, c; I460, acgtt |
| 105 | 1-281 | S273, a; I281, g; D282, 211 |
| 114 | 10-315 | I0, t; D1, 9; S91, m; S267, n; S276, w; S292, h; S295, m; I315, tggg; D316, 19 |
| 118 | 1-145 | S57, d; S126, d; I145, ccctc |
| 120 | 2-348 | D1, 1; S104, t; I348, g; D349, 38 |
| 121 | 1-190 | I121, c; I190, ccctt |
| 123 | 1-353 | I117, m; I186, w; S187, y; I353, caccgggg |
| 124 | 1-249 | I249, ggrvgggg |
| 125 | 114-375 | D1, 113; S206, wn; I231, a; I375, ccctagg |
| 126 | 1-437 | S297, cc; S307, tg; S312, a; S318, g; S341, a; S351, t; S353, g; S383, c; S387, a; D404, 1 |
| 136 | 82-428 | D1, 81; I428, aaagtg |
| 139 | 1-268 | I268, gggaaggg |
| 148 | 6-405 | D1, 5; I405, ggtgt |
| 159 | 1-230 | S227, ta; I230, ccctggg |
| 165 | 3-256 | I0, tat; D1, 2; I17, c; S18, t; S111, d; I115, t; S123, r; I256, aaggcggg |
| 170 | 1-280 | I103, t; S104, c; I111, t; I280, cgttcggg |
| 194 | 1-215 | S50, s; S186, sn; S199, k; I215, gcagcggg |
| 213 | 1-158 | S128, m; I132, w; S143, d; I158, tgcccggg |
| 223 | 3-431 | D1, 2; S28, s; S79, c; S82, s; S308, nr; S328, nb; I431, ccggc |
| 247 | 1-359 | I76, gttt; I359, tccctgg |
| 258 | 1-236 | S72, r; S81, g; S197, s; I205, ss; S232, k; I236, acttcggg |
| 264 | 5-283 | D1, 4; S64, g; S122, m; S134, yy; I137, c; I151, t; I283, gttgc |
| 269 | 1-143 | S111, s; I143, ggggcggg |
| 286 | 5-207 | D1, 4; S204, a; S206, c; I207, gg; D208, 567 |
| 287 | 1-277 | S114, r; I125, t; S131, ag; S256, tg; S259, tt; S262, at; S267, t; S269, c; S273, c; I277, ccggg; D278, 337 |
| 289 | 69-416 | D1, 68; I416, agccaggg |
| 289 | 1-278 | S114, r; I125, t; S131, ag; S277, c; I278, cggg; D279, 138 |
| 292 | 20-254 | D1, 19; I254, aaagagg |
| 293 | 1-414 | I414, tagcag |
| 300 | 1-285 | S16, m; S67, y; I285, baccacggg; D286, 1 |
| 349 | 23-431 | D1, 22; I118, a; S214, y; I431, caactgg |
| 350 | 3-386 | D1, 2; S42, w; I263, c; I386, gggat |
| 368 | 3-446 | D1, 2; I446, tctct |
| 385 | 1-193 | I35, t; I108, t; I134, r; S135, a; S137, r; S143, w; I178, c; I193, gagcgggg |
| 411 | 6-391 | D1, 5; S17, r; S27, t; S334, y; D392, 244 |
| 412 | 1-185 | S49, s; S127, s; I185, gctggg; D186, 150 |

| | | |
|---|---|---|
| 415 | 2-229 | D1, 1; S3, a; I229, caaatggg |
| 435 | 1-386 | S4, s; I386, ccggg |
| 436 | 4-472 | D1, 3; S61, sa; D238, 1; S239, s; I472, agtgtgg |
| 437 | 1-340 | I340, ggg; D341, 129 |
| 441 | 1-409 | S109, smag; I409, cgcacggg |
| 454 | 1-492 | S72, nn; S115, t; S121, bwy; S181, yn; I492, gagtc |
| 455 | 1-177 | I14, w; I16, a; I177, gagctggg |
| 459 | 1-311 | S39, n; S74, rg; I311, accatggg |
| 460 | 1-425 | I425, agtac |
| 461 | 5-420 | D1, 4; I420, tcgtc |
| 481 | 1-429 | I10, w; S262, d; S333, n; I429, ctccaggg |
| 489 | 1-414 | D72, 1; S117, n; S396, d; I414, ggaca |
| 496 | 1-215 | I215, ttttcggg |
| 501 | 1-430 | S275, n; I430, aggat |
| 502 | 91-413 | D1, 90; I413, aaacgggg |
| 504 | 21-420 | D1, 20; S47, w; S83, n; I280, n; S281, na; S292, v; S314, sm; S368, ww; S373, w; I420, cccca |
| 505 | 18-457 | D1, 17; D36, 1; S182, g; S273, n; S283, a; S416, bh; I457, ctcga |
| 514 | 1-303 | I303, accca |
| 515 | 1-455 | S11, t; I12, n; S30, r; S256, wr; I333, t; I455, cataa |
| 517 | 24-453 | D1, 23; I453, agagcggg |
| 519 | 1-275 | I119, gt; S125, w; I129, w; S133, k; S137, k; S167, k; I275, gcccc |
| 522 | 1-313 | I313, agcgtggg |
| 526 | 4-366 | I0, t; D1, 3; I366, ggcccggg |
| 530 | 1-434 | S328, g; I434, aagat |
| 535 | 1-379 | S128, g; S162, m; D380, 5 |
| 561 | 2-341 | D1, 1; I341, raagagg |
| 568 | 1-246 | I118, g; S137, g; I246, aaaccggg |
| 570 | 1-207 | I207, ttttt |
| 576 | 1-288 | I34, c; I288, cccgtgg |
| 588 | 1-390 | S218, a; S224, k; S314, dh; S358, s; D376, 1; I390, atg; D391, 23 |
| 597 | 31-274 | D1, 30; S49, n; I274, tccatgg |
| 606 | 1-354 | I141, g; D174, 1; S229, rr; D355, 72 |
| 627 | 1-415 | S7, a; I415, cattt |
| 634 | 1-178 | D179, 212 |
| 640 | 6-428 | D1, 5; D429, 79 |
| 641 | 64-483 | D1, 63; I165, d; D183, 1; S185, y; S253, t; D279, 2; S416, a; I483, atata |
| 655 | 1-280 | S58, c; I84, g; S88, k; S204, ac; S244, g; S247, g; I280, ggg; D281, 90 |
| 672 | 34-489 | D1, 33; S316, k; S331, k; S333, w; S486, g; S488, c; D490, 4 |
| 687 | 116-473 | D1, 115; S142, n; I473, cctcgggg |
| 697 | 1-202 | S142, s; S144, sr; S148, d; S152, d; I155, a; I164, a; S174, k; I202, gcc; D203, 291 |
| 708 | 8-384 | D1, 7; S104, b; I384, gaaaa |
| 710 | 1-167 | S40, k; S49, db; I167, tatct |

| | | |
|---|---|---|
| 722 | 1-191 | I125, c; I191, ttttt |
| 723 | 1-316 | I316, aggg; D317, 157 |
| 729 | 15-373 | D1, 14; S139, t; I373, cgcag; D374, 99 |
| 730 | 29-372 | D1, 28; I155, g; S192, ka; S333, d; I372, m; D373, 93 |
| 731 | 1-290 | S10, kk; S30, b; S32, t; S92, t; S197, dy; S278, g; I290, aggg; D291, 55 |
| 732 | 8-277 | D1, 7; I113, a; S127, w; I131, s; S132, r; S156, w; S160, r; S211, n; S215, w; I247, a; D278, 121 |
| 733 | 20-375 | D1, 19; S306, sbs; I325, h; S326, nr; S338, ywd; S344, v; I375, aggg; D376, 68 |
| 734 | 1-359 | D66, 1; D360, 14 |
| 735 | 25-322 | D1, 24; S30, r; I193, a; I322, ccaaggg |
| 736 | 9-181 | D1, 8; S58, g; I181, aactaggg |
| 737 | 1-160 | S97, ta; I160, aggtc |
| 738 | 1-227 | D228, 7 |
| 739 | 45-514 | D1, 44; S178, s; I182, c; S436, dmn; S461, v; S476, c; S506, t; D515, 75 |
| 740 | 11-388 | D1, 10; I388, cgacaggg |
| 741 | 1-478 | S118, s; S125, a; I126, s; S134, k; S421, vn; I478, aatsc |
| 742 | 217-553 | I0, tt; D1, 216; S286, r; S294, m; S311, r; S317, s; S338, r; S442, dm; S469, h; S476, r; S485, s; S491, w; I495, ht; S496, v; S513, r; D521, 1; S536, m; D554, 199 |
| 743 | 1-459 | I11, s; S258, m; I270, m; I304, c; I308, amta; S313, c; S438, v; I459, agggag |
| 744 | 25-316 | D1, 24; S315, g; D317, 95 |
| 745 | 21-283 | D1, 20; I40, g; S41, c; D123, 1; S181, sr; S227, r; I283, ccgcg; D284, 121 |
| 746 | 1-256 | D257, 173 |
| 747 | 1-179 | S134, w; S138, w; S140, kt; I179, cacca |
| 748 | 1-235 | S46, t; I72, t; S189, cc; S222, c; D236, 148 |
| 749 | 2-370 | D1, 1; S32, cg; D144, 1; S341, g; D371, 76 |
| 750 | 18-410 | I0, aag; D1, 17; I410, aatcc |
| 751 | 22-355 | D1, 21; D148, 1; S150, c; S152, a; S313, n; D356, 181 |
| 752 | 1-139 | S50, t; I118, g; I139, ccct |
| 753 | 1-189 | S26, r; S115, s; I121, r; S122, r; S128, s; S143, r; I146, w; S156, r; D190, 4 |
| 754 | 1-395 | S212, wd; I395, cggca |
| 755 | 19-460 | D1, 18; S26, c; S156, a; S253, n; I460, tagaagg |
| 756 | 2-142 | D1, 1; I106, gc; S107, t; S110, c; I142, ccaccggg |
| 757 | 28-296 | D1, 27; I119, s; I122, t; S128, s; S255, t; S267, m; D297, 66 |
| 758 | 11-368 | D1, 10; I200, g; S201, c; S281, d; S317, c; I368, ccatcggg |
| 759 | 19-452 | D1, 18; S421, w; I452, a |
| 760 | 25-175 | D1, 24; S34, yk; I175, ccggg; D176, 120 |
| 761 | 1-212 | I212, cactcggg |
| 762 | 1-374 | S320, s; S349, a; D375, 249 |
| 763 | 8-152 | D1, 7; I152, acggg; D153, 109 |

| | | |
|---|---|---|
| 764 | 1-160 | I127, g; I145, g; I160, cgcccggg |
| 765 | 137-313 | D1, 136; S272, m; I279, s; S310, t; I313, ggg; D314, 203 |
| 766 | 1-320 | S278, ag; S281, cagacc; S288, ta; S291, caag; S296, c; S317, m; I320, cggg; D321, 306 |
| 767 | 6-336 | I0, aa; D1, 5; S149, w; S245, y; D337, 137 |
| 768 | 1-374 | S320, s; D375, 299 |
| 769 | 53-435 | D1, 52; S59, b; S344, nnkw; D436, 104 |
| 770 | 24-448 | D1, 23; S25, g; S411, w; S416, m; D449, 31 |
| 771 | 1-370 | S3, c; S180, m; S275, r; D371, 122 |
| 772 | 1-388 | I299, c; S326, c; D389, 8 |
| 773 | 1-143 | S18, c; S66, a; I143, ggg; D144, 274 |
| 774 | 1-347 | S194, a; S205, c; I347, ggg; D348, 107 |
| 775 | 5-207 | D1, 4; S111, tg; S158, g; S171, c; S191, a; S204, a; S206, c; I207, gg; D208, 324 |
| 776 | 1-368 | I200, c; S201, a; S291, ta; I332, c |
| 777 | 5-207 | D1, 4; S204, a; S206, c; I207, gg; D208, 262 |
| 778 | 39-342 | D1, 38; S184, r; D343, 126 |
| 779 | 4-360 | D1, 3; S13, m; S15, c; S22, s; S24, m; S48, r; S56, s; S335, c; S345, rs; I360, ggg; D361, 119 |
| 780 | 1-472 | I347, c; D473, 32 |
| 781 | 116-426 | D1, 115; S219, m; S424, g; D427, 118 |
| 782 | 1-391 | S386, k; D392, 64 |
| 783 | 1-453 | D109, 1; S110, y; S125, y; I128, g; S132, k; I453, ctctc |
| 784 | 29-494 | D1, 28; S72, r; D495, 93 |
| 785 | 99-461 | D1, 98; S218, r; I461, gaccgggg |
| 786 | 2-465 | D1, 1; S8, y; S388, s; I398, g; S400, t; S403, at; S417, g; D466, 24 |
| 787 | 28-271 | D1, 27; S99, t; S230, c; S266, ga; S269, c; I271, g; D272, 126 |
| 788 | 1-285 | D280, 1; I285, g; D286, 310 |
| 789 | 1-209 | S205, c; D210, 150 |
| 790 | 51-297 | D1, 50; I297, ggggg; D298, 539 |
| 791 | 113-327 | D1, 112; S218, g; I226, g; D280, 1; I327, cgcaggg; D328, 224 |
| 792 | 17-218 | D1, 16; S58, t; S217, t; I218, gggg; D219, 219 |
| 793 | 11-92 | D1, 10; S91, c; I92, a; D93, 258 |
| 794 | 9-431 | D1, 8; I431, taagt |
| 795 | 30-341 | D1, 29; I341, a; D342, 175 |
| 796 | 1-442 | S17, w; S19, wr; D35, 1; S134, t; S264, n; S322, nr; S369, s; S420, s; S422, y; I442, tcctcggg |
| 797 | 1-420 | S136, c; S150, c; I245, ccc; I420, ggagtg |
| 798 | 25-316 | D1, 24; S315, g; D317, 97 |
| 799 | 1-344 | D345, 57 |
| 800 | 7-465 | D1, 6; S59, k; S146, a; S186, krn; I465, gttca |
| 801 | 121-422 | D1, 120; I269, c; S419, cc; I422, gg; D423, 207 |
| 802 | 46-477 | D1, 45; S132, bn; I477, actac |
| 803 | 15-467 | D1, 14; S45, k; S65, t; S418, ys; D452, 1; D468, 119 |
| 804 | 1-341 | S42, t; S97, d; S326, gtg; S331, tgt; S336, a; |

| | | |
|---|---|---|
| | | S338, c; I341, cccccggg; D342, 218 |
| 805 | 2-409 | D1, 1; S334, d; I409, aggg; D410, 161 |
| 806 | 5-384 | D1, 4; I384, actaa |
| 807 | 1-301 | S113, a; S117, c; S123, t; D128, 1; D134, 1; S282, g; S284, a; I301, gacggagggg; D302, 70 |
| 808 | 2-314 | D1, 1; S306, g; I314, ggg; D315, 121 |
| 809 | 1-394 | S53, g; S228, n; S272, vk; I301, g; I358, m; S368, nb; S375, w; I383, mm; I388, yt; I394, nhaccggg |
| 810 | 6-205 | I0, a; D1, 5; I141, t; I205, ggg; D206, 630 |
| 811 | 6-270 | D1, 5; I270, gggg; D271, 115 |
| 1600 | 1-247 | S45, m; S114, k; I122, m; S123, yc; S158, rr; S221, k; I247, ccccaggg |
| 1601 | 1-225 | S109, bm; S195, m; I225, tgcacggg |
| 1602 | 23-245 | D1, 22; D138, 1; S139, s; S242, t; S244, g; I245, g; D246, 13 |
| 1603 | 1-303 | S71, c; D277, 1; I303, ggagggg; D304, 38 |
| 1604 | 1-242 | S47, w; S50, c; S81, h; S85, d; S91, k; S106, r; I242, tgtggg; D243, 50 |
| 1605 | 2-225 | D1, 1; S20, k; S91, c; I225, ggg; D226, 132 |
| 1606 | 15-293 | D1, 14; S156, g; S193, g; I200, t; I293, acaaaggg |
| 1607 | 1-361 | S323, c; I361, cccca |
| 1608 | 1-151 | I151, taagggg; D152, 154 |
| 1609 | 1-242 | S55, s; I135, a; S152, h; I242, cagtaggg |
| 1610 | 1-196 | I151, w; S190, k; I196, cctgtgg |
| 1611 | 1-228 | S115, k; S174, rk; I228, cgtttggg |
| 1612 | 1-221 | S108, v; I221, tgatcggg |
| 1613 | 1-281 | I66, w; I137, a; D282, 79 |
| 1614 | 1-171 | S53, k; S76, k; I80, k; S81, kw; S86, r; S92, k; S126, k; I171, gccgagg |
| 1615 | 2-193 | D1, 1; S67, c; I121, s; S122, mm; S126, g; S130, r; S146, r; S156, gm; I193, cctca |
| 1616 | 1-349 | S251, ww; S259, rs; S275, k; I279, w; S285, y; S292, y; I320, m; I331, m; I338, w; I341, s; I349, accccggg |
| 1617 | 1-129 | I118, t; D130, 26 |
| 1618 | 1-184 | D9, 1; D185, 1 |
| 1619 | 1-169 | I122, t; I169, gcccaggg |
| 1620 | 1-187 | S106, k; S118, m; S122, cg; S132, k; D188, 59 |
| 1621 | 1-153 | D125, 1; I131, ttt; S152, t; I153, gg; D154, 127 |
| 1622 | 1-400 | S43, s; I126, g; I129, y; S353, d; I400, tatat |

## EXAMPLE 16

Categorization of 5' ESTs and Consensus Contigated 5'ESTs

The nucleic acid sequences of the present invention (SEQ ID NOs. 24-811 and 1600-1622) were grouped based on their homology to known sequences as follows. All sequences were compared to EMBL release 57 and daily releases available at the time of filing using BLASTN. All matches with a minimum of 25 nucleotides with 90% homology were retrieved and used to compute Tables IV and V.

In some embodiments, 5'ESTs or consensus contigated 5'ESTs nucleic acid sequence do not match any known vertebrate sequence nor any publicly available EST sequence, thus being completely new.

In other embodiments, 5'ESTs or consensus contigated 5'ESTs match a known sequence. Tables III and IV gives for each sequence of the invention in this category referred to by its sequence identification number in the first column, the positions of their preferred fragments in the second column entitled "Positions of preferred fragments." As used herein the term "polynucleotide described in Table III" refers to the all of the preferred polynucleotide fragments defined in Table III in this manner, and the term "polynucleotide described in Table IV" refers to the all of the preferred polynucleotides fragments defined in Table IV in this manner. The present invention encompasses isolated, purified, or recombinant nucleic acids which consist of, consist essentially of, or comprise a contiguous span of at least 8, 10, 12, 15, 18, 20, 25, 35, 40, 50, 70, 80, 100, 250, or 500 nucleotides in length, to the extent that a contiguous span of these lengths is consistent with the lengths of the particular polynucleotide, of a polynucleotide described in Table III or Table IV, or a sequence complementary thereto, wherein said polynucleotide described in Table III or Talbe IV is selected individually or in any combination from the polynucleotides described in Table III or Talbe IV. The present invention also encompasses isolated, purified, or recombinant nucleic acids which consist of or consist essentially of a polynucleotide described in Table III or Table IV, or a sequence complementary thereto, wherein said polynucleotide is selected individually or in any combination from the polynucleotides described in Table III or Table IV.

**Table III**

| SEQ ID NO | Positions of preferred fragments |
|---|---|
| 24 | 1-251 |
| 25 | 1-83 |
| 28 | 227-276 |
| 29 | 1-27 |
| 30 | 130-242, 283-315, 365-461 |
| 32 | 314-399 |
| 33 | 89-321 |
| 34 | 1-38 |
| 35 | 1-52, 171-222 |
| 36 | 1-30, 408-441 |
| 37 | 1-138 |
| 39 | 115-140 |
| 40 | 1-97 |
| 41 | 1-112 |
| 42 | 1-177 |
| 46 | 1-38 |
| 48 | 376-400 |
| 51 | 400-466 |
| 54 | 1-259 |
| 55 | 189-320 |

| | |
|---|---|
| 56 | 265-457 |
| 58 | 246-469 |
| 59 | 81-123, 418-444 |
| 60 | 1-348 |
| 61 | 78-123, 418-457 |
| 62 | 386-439 |
| 63 | 1-214 |
| 64 | 109-297 |
| 65 | 1-370 |
| 66 | 92-428 |
| 68 | 1-180 |
| 69 | 165-259 |
| 70 | 1-178 |
| 71 | 1-27 |
| 72 | 1-179 |
| 73 | 1-65, 107-192 |
| 75 | 1-314 |
| 77 | 263-388 |
| 78 | 1-64 |
| 79 | 1-149 |
| 80 | 101-142, 302-380 |
| 82 | 1-192 |
| 83 | 1-398 |
| 85 | 1-290 |
| 86 | 1-118, 149-336 |
| 87 | 1-262 |
| 88 | 1-149 |
| 89 | 1-315 |
| 90 | 1-74 |
| 91 | 1-335, 364-423 |
| 92 | 1-316 |
| 93 | 338-508 |
| 94 | 179-321 |
| 95 | 219-402 |
| 96 | 26-315 |
| 97 | 348-460 |
| 98 | 1-230 |
| 99 | 391-467 |
| 101 | 214-336 |
| 102 | 1-289 |
| 103 | 1-383 |
| 104 | 1-211 |
| 105 | 1-36 |
| 106 | 1-126 |
| 107 | 1-49 |
| 108 | 294-336 |
| 109 | 1-128 |
| 111 | 1-154 |
| 112 | 407-441 |
| 113 | 1-80, 139-184 |
| 114 | 10-79 |
| 116 | 1-292 |
| 117 | 1-304 |

| | |
|---|---|
| 119 | 1-288 |
| 120 | 2-348 |
| 121 | 1-122 |
| 123 | 188-353 |
| 124 | 1-249 |
| 125 | 295-375 |
| 128 | 1-244 |
| 129 | 1-232 |
| 130 | 196-312 |
| 131 | 178-276 |
| 132 | 37-174 |
| 133 | 1-344 |
| 134 | 1-244 |
| 135 | 1-217 |
| 136 | 82-428 |
| 137 | 1-29, 103-155, 274-434 |
| 138 | 1-395 |
| 139 | 1-268 |
| 140 | 1-170 |
| 141 | 1-396 |
| 142 | 1-73, 227-357 |
| 143 | 1-159 |
| 144 | 1-433 |
| 145 | 61-116 |
| 146 | 1-71, 179-205 |
| 147 | 177-300 |
| 149 | 1-146 |
| 151 | 1-166 |
| 152 | 1-382 |
| 153 | 1-208 |
| 154 | 121-251 |
| 155 | 1-147 |
| 157 | 1-115 |
| 158 | 1-175 |
| 159 | 1-44, 80-230 |
| 160 | 1-346 |
| 161 | 1-277 |
| 162 | 1-235 |
| 163 | 1-34 |
| 164 | 1-195 |
| 165 | 19-78, 175-217 |
| 166 | 1-209 |
| 167 | 1-65 |
| 168 | 128-218 |
| 169 | 49-245 |
| 170 | 179-280 |
| 171 | 1-103 |
| 172 | 1-218 |
| 173 | 1-380 |
| 174 | 1-139 |
| 175 | 1-122 |
| 176 | 1-300 |
| 177 | 1-466 |

| | |
|---|---|
| 179 | 1-86 |
| 180 | 1-245 |
| 181 | 1-241 |
| 182 | 1-263 |
| 183 | 1-170 |
| 184 | 58-106, 399-443 |
| 185 | 1-427 |
| 186 | 1-365 |
| 187 | 1-260 |
| 188 | 1-172 |
| 189 | 1-150 |
| 190 | 161-271, 301-339 |
| 191 | 1-91 |
| 192 | 1-264 |
| 193 | 1-246 |
| 194 | 1-150 |
| 195 | 1-209 |
| 196 | 1-363 |
| 197 | 1-155 |
| 198 | 1-135 |
| 200 | 1-125 |
| 201 | 1-210 |
| 202 | 1-338 |
| 203 | 1-188 |
| 204 | 228-347 |
| 205 | 1-440 |
| 206 | 56-221 |
| 208 | 1-422 |
| 209 | 169-195 |
| 210 | 1-363 |
| 211 | 1-368 |
| 212 | 1-448 |
| 213 | 1-134 |
| 214 | 1-193 |
| 215 | 1-214 |
| 216 | 1-134 |
| 218 | 1-189 |
| 219 | 1-248 |
| 220 | 1-115 |
| 221 | 1-113 |
| 222 | 1-370 |
| 224 | 1-251 |
| 225 | 1-198 |
| 226 | 45-141 |
| 227 | 1-206 |
| 228 | 1-480 |
| 229 | 1-144 |
| 230 | 1-42, 281-351, 432-457 |
| 231 | 1-112 |
| 233 | 1-301 |
| 234 | 1-109 |
| 235 | 1-393 |
| 236 | 1-222 |

| | |
|---|---|
| 237 | 1-154 |
| 238 | 1-439 |
| 239 | 112-137 |
| 240 | 1-194 |
| 241 | 1-44 |
| 242 | 1-242 |
| 244 | 1-324 |
| 245 | 1-38, 217-280 |
| 246 | 1-60 |
| 247 | 77-359 |
| 248 | 1-236 |
| 249 | 1-342 |
| 250 | 80-382 |
| 251 | 1-303 |
| 252 | 62-259 |
| 253 | 1-165 |
| 254 | 1-328 |
| 255 | 1-320 |
| 256 | 1-305 |
| 257 | 1-181 |
| 258 | 116-174 |
| 259 | 1-265 |
| 260 | 1-272 |
| 261 | 1-62 |
| 263 | 1-371 |
| 266 | 1-274 |
| 267 | 1-342 |
| 268 | 364-427 |
| 269 | 31-143 |
| 270 | 1-79 |
| 271 | 1-121 |
| 272 | 229-292 |
| 273 | 1-158 |
| 274 | 1-113 |
| 275 | 1-254 |
| 276 | 1-333 |
| 277 | 1-130 |
| 278 | 1-184 |
| 279 | 1-265 |
| 280 | 1-188 |
| 281 | 1-177 |
| 282 | 1-336 |
| 283 | 1-294 |
| 284 | 1-171 |
| 285 | 1-297 |
| 288 | 1-42 |
| 290 | 1-170 |
| 292 | 20-155 |
| 294 | 1-334 |
| 295 | 1-375 |
| 296 | 1-226 |
| 297 | 1-232 |
| 299 | 40-139 |

| | |
|---|---|
| 300 | 1-285 |
| 301 | 1-242 |
| 302 | 1-136 |
| 303 | 1-175 |
| 304 | 1-493 |
| 305 | 1-214 |
| 306 | 89-458 |
| 307 | 1-328 |
| 308 | 1-380 |
| 309 | 1-236 |
| 310 | 1-357 |
| 311 | 1-470 |
| 312 | 1-187 |
| 313 | 1-159 |
| 315 | 1-162 |
| 316 | 1-404 |
| 317 | 1-450 |
| 318 | 1-395 |
| 319 | 1-257 |
| 320 | 56-325 |
| 321 | 1-201 |
| 322 | 1-159 |
| 323 | 1-420 |
| 324 | 1-210 |
| 325 | 1-192 |
| 326 | 88-181 |
| 327 | 1-185 |
| 328 | 128-210 |
| 330 | 1-223 |
| 331 | 1-362 |
| 332 | 1-89 |
| 334 | 1-188 |
| 335 | 1-115 |
| 336 | 1-300 |
| 337 | 1-307 |
| 338 | 1-123 |
| 339 | 1-297 |
| 340 | 1-34 |
| 341 | 1-44 |
| 342 | 1-37 |
| 343 | 141-169 |
| 344 | 1-112 |
| 345 | 1-235, 266-349 |
| 346 | 1-191 |
| 347 | 1-229 |
| 348 | 1-210 |
| 350 | 139-266 |
| 351 | 1-307 |
| 352 | 1-170 |
| 353 | 1-293 |
| 354 | 30-161, 192-331 |
| 355 | 1-93 |
| 356 | 1-178 |

| | |
|---|---|
| 357 | 1-107 |
| 358 | 1-29, 168-209 |
| 359 | 1-298 |
| 360 | 1-193 |
| 362 | 1-360 |
| 363 | 1-45, 100-212 |
| 364 | 39-170, 202-242 |
| 365 | 1-248 |
| 366 | 1-351 |
| 367 | 1-208 |
| 368 | 228-446 |
| 369 | 1-62 |
| 370 | 1-132 |
| 371 | 1-127 |
| 372 | 1-196 |
| 373 | 1-148 |
| 374 | 1-126 |
| 375 | 1-112 |
| 376 | 1-146 |
| 378 | 1-143 |
| 379 | 1-261 |
| 380 | 202-228 |
| 382 | 1-151 |
| 383 | 1-45 |
| 384 | 1-190, 250-456 |
| 385 | 1-55, 141-181 |
| 386 | 1-281 |
| 387 | 1-111 |
| 388 | 1-374 |
| 389 | 1-192 |
| 390 | 1-371 |
| 392 | 1-303 |
| 394 | 1-126 |
| 395 | 1-329 |
| 396 | 1-99 |
| 397 | 1-316 |
| 398 | 1-251 |
| 399 | 1-120 |
| 401 | 1-206 |
| 402 | 1-330 |
| 403 | 1-311 |
| 405 | 1-153 |
| 406 | 1-206 |
| 407 | 1-479 |
| 408 | 1-289 |
| 410 | 229-321 |
| 413 | 1-158 |
| 415 | 95-229 |
| 416 | 1-265 |
| 417 | 1-228 |
| 418 | 1-225 |
| 419 | 207-293 |
| 420 | 1-194 |

| | |
|---|---|
| 421 | 1-90 |
| 422 | 1-161 |
| 423 | 1-420 |
| 424 | 1-432 |
| 425 | 1-276, 309-419 |
| 426 | 1-232 |
| 427 | 1-81 |
| 428 | 1-96 |
| 429 | 1-165 |
| 431 | 1-58, 186-237, 327-354 |
| 433 | 1-65 |
| 434 | 1-83 |
| 435 | 1-386 |
| 436 | 405-447 |
| 438 | 1-106 |
| 439 | 45-105, 168-255, 284-447 |
| 441 | 1-409 |
| 442 | 1-320 |
| 443 | 1-256 |
| 444 | 1-284 |
| 445 | 1-240 |
| 446 | 1-149 |
| 447 | 1-360 |
| 448 | 1-123 |
| 449 | 1-94 |
| 450 | 1-302 |
| 452 | 1-349 |
| 453 | 1-270 |
| 454 | 1-492 |
| 455 | 17-105 |
| 456 | 1-102 |
| 457 | 1-108 |
| 458 | 1-285 |
| 459 | 1-311 |
| 460 | 1-191 |
| 461 | 312-420 |
| 462 | 1-257 |
| 463 | 1-117 |
| 464 | 1-142 |
| 466 | 1-235 |
| 467 | 1-29 |
| 468 | 1-41 |
| 469 | 1-438 |
| 470 | 1-131 |
| 471 | 1-211 |
| 472 | 1-150 |
| 473 | 1-352 |
| 474 | 1-141 |
| 476 | 1-232 |
| 478 | 1-201 |
| 479 | 1-151 |
| 480 | 1-104 |
| 481 | 7-429 |

| | |
|---|---|
| 482 | 1-385 |
| 486 | 1-226 |
| 488 | 1-296 |
| 489 | 1-72, 323-377 |
| 491 | 1-348 |
| 492 | 33-126 |
| 493 | 1-300 |
| 494 | 1-295 |
| 495 | 1-244 |
| 496 | 1-215 |
| 497 | 1-255 |
| 499 | 1-174, 384-474 |
| 500 | 1-50, 102-241 |
| 501 | 153-430 |
| 502 | 91-132 |
| 503 | 1-64 |
| 504 | 21-63, 356-420 |
| 505 | 37-68, 187-234 |
| 506 | 1-315 |
| 507 | 101-208 |
| 510 | 1-402 |
| 511 | 1-343 |
| 512 | 1-140, 170-246, 276-420 |
| 513 | 1-324 |
| 514 | 1-303 |
| 515 | 13-340 |
| 516 | 1-263, 293-360 |
| 518 | 1-245 |
| 519 | 111-275 |
| 520 | 62-182 |
| 521 | 1-218 |
| 523 | 1-502 |
| 524 | 1-118 |
| 525 | 1-276 |
| 526 | 223-366 |
| 527 | 1-428 |
| 528 | 297-342 |
| 529 | 1-244 |
| 530 | 1-88, 375-434 |
| 531 | 1-406 |
| 533 | 1-149 |
| 534 | 1-145 |
| 535 | 1-116 |
| 536 | 1-207 |
| 537 | 1-394 |
| 538 | 1-415 |
| 539 | 1-160 |
| 540 | 1-327 |
| 541 | 1-38, 73-396 |
| 542 | 1-247 |
| 543 | 1-221 |
| 544 | 1-375 |
| 545 | 1-376 |

| | |
|---|---|
| 546 | 1-109 |
| 547 | 1-160, 223-306 |
| 548 | 1-148 |
| 551 | 1-231 |
| 552 | 1-229 |
| 553 | 1-232 |
| 554 | 1-141 |
| 555 | 1-376 |
| 556 | 1-279 |
| 557 | 1-340 |
| 558 | 1-51 |
| 559 | 1-354 |
| 562 | 1-188 |
| 563 | 1-229 |
| 564 | 184-352 |
| 566 | 308-341 |
| 567 | 1-218 |
| 568 | 1-79 |
| 569 | 1-142 |
| 570 | 1-207 |
| 571 | 1-373 |
| 572 | 1-195 |
| 573 | 1-352 |
| 574 | 1-121 |
| 575 | 1-222 |
| 576 | 151-288 |
| 577 | 1-264 |
| 578 | 1-205 |
| 580 | 1-171, 273-328 |
| 581 | 1-356 |
| 582 | 1-239 |
| 583 | 1-144 |
| 584 | 1-282 |
| 585 | 1-338 |
| 586 | 1-436 |
| 588 | 1-380 |
| 589 | 1-60 |
| 590 | 1-178 |
| 592 | 1-66 |
| 593 | 1-215 |
| 594 | 1-161 |
| 596 | 1-407 |
| 597 | 31-83 |
| 598 | 1-417 |
| 599 | 1-329 |
| 600 | 1-311 |
| 601 | 1-61, 99-214 |
| 602 | 1-154, 197-463 |
| 603 | 135-269 |
| 604 | 1-351 |
| 605 | 1-195 |
| 608 | 1-357 |
| 609 | 1-201 |

| | |
|---|---|
| 612 | 1-176 |
| 613 | 1-342 |
| 615 | 1-272 |
| 616 | 1-114 |
| 617 | 1-46 |
| 618 | 1-208 |
| 619 | 1-257 |
| 620 | 1-28 |
| 621 | 1-26 |
| 622 | 1-221 |
| 623 | 1-432 |
| 624 | 1-233 |
| 625 | 1-26 |
| 627 | 1-43 |
| 628 | 1-318 |
| 629 | 1-170 |
| 630 | 1-196 |
| 631 | 248-339 |
| 632 | 1-433 |
| 633 | 1-154 |
| 634 | 1-41 |
| 635 | 1-137 |
| 636 | 1-172 |
| 637 | 1-253 |
| 638 | 1-185 |
| 639 | 1-206 |
| 641 | 334-483 |
| 642 | 1-309 |
| 643 | 1-75, 162-213 |
| 644 | 107-211 |
| 645 | 1-98 |
| 646 | 1-347 |
| 647 | 1-49, 81-143 |
| 648 | 1-232 |
| 649 | 74-133 |
| 650 | 1-37 |
| 651 | 1-276 |
| 652 | 1-170 |
| 653 | 1-178 |
| 654 | 1-121 |
| 656 | 1-197 |
| 657 | 1-246 |
| 659 | 1-197 |
| 660 | 116-172 |
| 661 | 1-411 |
| 662 | 1-146 |
| 663 | 1-65 |
| 664 | 1-182 |
| 665 | 1-320 |
| 666 | 1-273 |
| 667 | 1-149 |
| 668 | 1-122 |
| 670 | 1-160 |

| | |
|---|---|
| 671 | 1-137 |
| 673 | 1-263 |
| 674 | 1-263 |
| 675 | 1-107 |
| 677 | 1-441 |
| 678 | 134-191 |
| 679 | 1-235 |
| 680 | 1-26 |
| 682 | 1-58, 269-328 |
| 683 | 1-447 |
| 684 | 1-217 |
| 685 | 1-132 |
| 686 | 1-60 |
| 688 | 1-107 |
| 689 | 132-221, 327-377 |
| 690 | 1-388 |
| 691 | 1-141, 171-408 |
| 692 | 1-322 |
| 693 | 1-153 |
| 695 | 1-455 |
| 698 | 1-58, 117-174 |
| 699 | 240-300 |
| 700 | 1-159 |
| 701 | 1-69 |
| 702 | 1-175 |
| 703 | 1-298 |
| 704 | 1-136 |
| 705 | 1-168 |
| 706 | 1-419 |
| 707 | 1-382 |
| 708 | 8-245, 296-384 |
| 709 | 1-149 |
| 710 | 1-167 |
| 711 | 1-35 |
| 712 | 1-80, 116-156, 206-241 |
| 713 | 33-376 |
| 714 | 1-304 |
| 715 | 1-242 |
| 717 | 1-145 |
| 718 | 1-350 |
| 720 | 1-257 |
| 721 | 1-360 |
| 722 | 1-191 |
| 724 | 1-139 |
| 726 | 1-207 |
| 727 | 99-164 |
| 728 | 1-321 |
| 730 | 156-372 |
| 731 | 1-109, 256-290 |
| 735 | 25-192 |
| 737 | 1-160 |
| 738 | 1-227 |
| 739 | 441-514 |

| | |
|---|---|
| 742 | 217-280 |
| 743 | 10-275 |
| 747 | 1-179 |
| 749 | 2-31, 139-168 |
| 750 | 349-410 |
| 752 | 1-119 |
| 753 | 1-121 |
| 754 | 1-28 |
| 760 | 25-175 |
| 761 | 1-212 |
| 763 | 8-75 |
| 766 | 1-59, 102-248, 295-320 |
| 769 | 53-85 |
| 771 | 1-370 |
| 774 | 1-347 |
| 776 | 1-200 |
| 778 | 39-342 |
| 779 | 4-28 |
| 780 | 1-49, 407-472 |
| 781 | 116-426 |
| 782 | 1-59 |
| 783 | 1-53, 219-453 |
| 784 | 29-53, 219-263, 426-494 |
| 785 | 99-347, 386-461 |
| 786 | 2-28 |
| 788 | 1-279 |
| 789 | 1-58 |
| 790 | 226-268 |
| 792 | 129-218 |
| 794 | 265-431 |
| 796 | 5-86 |
| 797 | 1-34 |
| 799 | 1-344 |
| 802 | 46-477 |
| 806 | 64-384 |
| 807 | 135-301 |
| 808 | 2-314 |
| 810 | 6-39 |
| 1600 | 1-25 |
| 1601 | 1-225 |
| 1602 | 23-139 |
| 1603 | 1-294 |
| 1606 | 15-44 |
| 1607 | 1-361 |
| 1611 | 85-228 |
| 1612 | 1-221 |
| 1613 | 138-281 |
| 1614 | 65-171 |
| 1615 | 2-142 |
| 1616 | 1-46 |
| 1617 | 1-95 |
| 1620 | 1-187 |
| 1621 | 1-136 |

| | |
|---|---|
| 1622 | 32-280, 311-400 |

Table IV

| SEQ ID NO | Positions of Preferred Fragments |
|---|---|
| 35 | 1-52 |
| 41 | 1-115 |
| 45 | 1-47 |
| 46 | 1-33 |
| 66 | 400-428 |
| 82 | 83-149 |
| 93 | 399-508 |
| 105 | 1-36 |
| 114 | 1-79 |
| 120 | 1-386 |
| 121 | 1-190 |
| 124 | 1-249 |
| 125 | 295-328 |
| 139 | 1-81, 125-268 |
| 159 | 1-139, 180-230 |
| 165 | 1-78 |
| 170 | 179-205, 248-280 |
| 194 | 1-150 |
| 213 | 1-158 |
| 247 | 1-104, 155-183, 280-359 |
| 269 | 31-143 |
| 350 | 139-386 |
| 368 | 228-446 |
| 385 | 1-72, 143-193 |
| 415 | 95-229 |
| 435 | 1-386 |
| 436 | 446-472 |
| 441 | 1-361 |
| 454 | 1-349 |
| 455 | 1-105 |
| 459 | 35-161, 200-311 |
| 460 | 1-26, 56-140 |
| 481 | 1-429 |
| 489 | 1-84 |
| 496 | 1-44, 84-215 |
| 501 | 153-430 |
| 502 | 1-91 |
| 504 | 1-63 |

| | |
|---|---|
| 505 | 1-68 |
| 514 | 1-303 |
| 515 | 237-351 |
| 519 | 1-145 |
| 526 | 231-366 |
| 530 | 1-88 |
| 535 | 1-55 |
| 570 | 76-207 |
| 576 | 168-218, 261-288 |
| 588 | 1-331 |
| 597 | 1-83 |
| 627 | 1-43 |
| 634 | 1-41 |
| 641 | 1-55, 334-483 |
| 672 | 1-34 |
| 687 | 1-129 |
| 708 | 1-245, 296-384 |
| 710 | 1-26, 104-167 |
| 722 | 1-191 |
| 730 | 1-465 |
| 731 | 1-43 |
| 735 | 1-91 |
| 737 | 1-160 |
| 738 | 1-186 |
| 739 | 1-48 |
| 742 | 1-62, 99-248 |
| 743 | 1-315, 412-459 |
| 744 | 1-31 |
| 747 | 1-63 |
| 749 | 1-32 |
| 750 | 1-38 |
| 752 | 1-139 |
| 753 | 1-193 |
| 754 | 1-28 |
| 759 | 1-38 |
| 760 | 1-115 |
| 763 | 1-62 |
| 765 | 1-126 |
| 769 | 1-85 |
| 770 | 1-40 |
| 771 | 1-148 |
| 774 | 1-134 |
| 775 | 265-531 |
| 776 | 71-203 |
| 777 | 333-469 |
| 778 | 144-468 |
| 779 | 1-28 |
| 780 | 1-49 |
| 781 | 1-102 |
| 782 | 1-59 |
| 783 | 1-53 |
| 784 | 1-220, 262-390 |
| 785 | 1-339, 408-461 |

| | |
|---|---|
| 786 | 1-28 |
| 789 | 1-58 |
| 791 | 1-126 |
| 792 | 1-31, 129-220 |
| 793 | 1-31 |
| 794 | 355-431 |
| 795 | 1-33 |
| 797 | 1-31 |
| 798 | 1-31 |
| 799 | 1-401 |
| 801 | 1-117 |
| 802 | 1-92 |
| 806 | 64-384 |
| 807 | 1-331 |
| 808 | 1-351 |
| 810 | 1-39 |
| 1600 | 1-25 |
| 1603 | 1-341 |
| 1606 | 1-31 |
| 1607 | 1-361 |
| 1608 | 164-305 |
| 1611 | 85-228 |
| 1612 | 1-221 |
| 1613 | 112-360 |
| 1614 | 1-171 |
| 1615 | 94-193 |
| 1617 | 1-155 |
| 1620 | 1-246 |

**III. Evaluation of Spatial and Temporal Expression of mRNAs Corresponding to the 5'ESTs, Consensus Contigated 5'ESTs, or EST-related nucleic acids**

**EXAMPLE 17**

Expression Patterns of mRNAs From Which the 5'ESTs were obtained

Each of the SEQ ID NOs. 24-811 and 1600-1622 was also categorized based on the tissue from which its corresponding mRNA was obtained, as follows.

Table V shows the spatial distribution of each nucleic acid sequence of the invention (SEQ ID NOs. 24-811 and 1600-1622) referred to by its sequence identification number in the first column. In the second column entitled tissue distribution, the spatial distribution is represented by the number of individual 5'ESTs used to assemble the consensus contigated 5'ESTs for a given tissue. Each type of tissue listed in Table V is encoded by a letter. The correspondence between the letter code and the tissue type is given in Table VI.

Table V

| SEQ ID NO | Tissue Distribution |
|---|---|
| 24 | AA:1 |
| 25 | S:1 |
| 26 | P:1 |
| 27 | W:1 |
| 28 | P:1 |
| 29 | S:1 |
| 30 | P:1 |
| 31 | P:1 |
| 32 | P:1 |
| 33 | P:1 |
| 34 | AB:1 |
| 35 | G:3; P:1; S:1; W:3; AA:4 |
| 36 | P:1 |
| 37 | S:1 |
| 38 | Q:1 |
| 39 | P:1 |
| 40 | AB:1 |
| 41 | B:1; C:3; F:1; G:1; H:4; S:2; T:8; W:1; Z:1; AA:3; AC:1; AD:3 |
| 42 | A:1 |
| 43 | N:2 |
| 44 | P:1 |
| 45 | C:2; K:1; O:1; S:5 |
| 46 | K:1; S:2; AA:1 |
| 47 | AA:1 |
| 48 | C:1; O:1; P:8 |
| 49 | P:1 |
| 50 | P:1 |
| 51 | P:1 |
| 52 | S:1 |
| 53 | AA:1 |
| 54 | T:1 |
| 55 | P:1 |
| 56 | P:1 |
| 57 | P:1 |
| 58 | P:1 |
| 59 | P:7; T:2; Z:1 |
| 60 | R:1 |
| 61 | C:1 |
| 62 | P:1 |
| 63 | F:1 |
| 64 | AA:1 |
| 65 | F:1 |

| | |
|---|---|
| 66 | P:4; T:2; Z:1 |
| 67 | S:1 |
| 68 | AA:1 |
| 69 | P:1 |
| 70 | P:1 |
| 71 | S:1 |
| 72 | W:1 |
| 73 | G:1 |
| 74 | P:1 |
| 75 | N:1 |
| 76 | P:1 |
| 77 | S:1 |
| 78 | U:1 |
| 79 | B:1 |
| 80 | P:1 |
| 81 | AC:1 |
| 82 | K:1; O:1 |
| 83 | G:1 |
| 84 | C:1; K:2; P:29; S:2; T:1; X:2; Y:1; AA:2 |
| 85 | K:1 |
| 86 | C:1 |
| 87 | F:1 |
| 88 | AB:1 |
| 89 | H:1 |
| 90 | M:1 |
| 91 | B:1 |
| 92 | K:1 |
| 93 | AC:2 |
| 94 | P:1 |
| 95 | M:1 |
| 96 | Z:2 |
| 97 | K:1; P:11; S:1; X:1; AA:1 |
| 98 | W:1 |
| 99 | X:1 |
| 100 | P:1 |
| 101 | AB:1 |
| 102 | F:1 |
| 103 | AA:1 |
| 104 | K:1 |
| 105 | B:4; C:6; E:2; H:3; O:2; Q:1; S:3; AC:2 |
| 106 | T:1 |
| 107 | O:1 |
| 108 | P:1 |
| 109 | G:1 |
| 110 | AA:1 |
| 111 | T:1 |
| 112 | P:1 |
| 113 | F:1 |

| | |
|---|---|
| 114 | B:3; C:4; K:5; S:4; Y:1 |
| 115 | U:1 |
| 116 | W:1 |
| 117 | T:1 |
| 118 | T:2 |
| 119 | T:1 |
| 120 | H:3 |
| 121 | AA:3 |
| 122 | K:1 |
| 123 | H:2 |
| 124 | AA:2 |
| 125 | B:1; G:1; J:3; T:13; Y:5; AA:5; AD:2 |
| 126 | H:1; P:1 |
| 127 | K:1 |
| 128 | F:1 |
| 129 | G:1 |
| 130 | P:1 |
| 131 | B:1 |
| 132 | AA:1 |
| 133 | W:1 |
| 134 | P:1 |
| 135 | K:1 |
| 136 | B:1; C:1 |
| 137 | B:1 |
| 138 | H:1 |
| 139 | AC:2 |
| 140 | T:1 |
| 141 | B:1 |
| 142 | H:1 |
| 143 | T:1 |
| 144 | H:1 |
| 145 | B:1 |
| 146 | R:1 |
| 147 | P:1 |
| 148 | C:1; H:2; O:1; S:2; T:1; AC:2 |
| 149 | H:1 |
| 150 | AA:1 |
| 151 | W:1 |
| 152 | S:1 |
| 153 | F:1 |
| 154 | M:1 |
| 155 | B:1 |
| 156 | R:1 |
| 157 | W:1 |
| 158 | T:1 |
| 159 | C:1; AA:1 |
| 160 | F:1 |
| 161 | H:1 |

| | |
|---|---|
| 162 | D:1 |
| 163 | AA:1 |
| 164 | AA:1 |
| 165 | W:3 |
| 166 | AA:1 |
| 167 | W:1 |
| 168 | F:1 |
| 169 | B:1 |
| 170 | G:2 |
| 171 | E:1 |
| 172 | B:1 |
| 173 | F:1 |
| 174 | B:1 |
| 175 | W:1 |
| 176 | K:1 |
| 177 | AA:1 |
| 178 | S:1 |
| 179 | K:1 |
| 180 | AA:1 |
| 181 | W:1 |
| 182 | K:1 |
| 183 | T:1 |
| 184 | P:1 |
| 185 | B:1 |
| 186 | W:1 |
| 187 | R:1 |
| 188 | T:1 |
| 189 | T:1 |
| 190 | W:1 |
| 191 | A:1 |
| 192 | F:1 |
| 193 | B:1 |
| 194 | G:3 |
| 195 | W:1 |
| 196 | O:1 |
| 197 | T:1 |
| 198 | O:1 |
| 199 | B:1 |
| 200 | AA:1 |
| 201 | G:1 |
| 202 | B:1 |
| 203 | G:1 |
| 204 | P:1 |
| 205 | AA:1 |
| 206 | Y:1 |
| 207 | Y:1 |
| 208 | AA:1 |
| 209 | G:1 |

| | |
|---|---|
| 210 | H:1 |
| 211 | C:1 |
| 212 | H:1 |
| 213 | W:2 |
| 214 | Y:1 |
| 215 | AB:1 |
| 216 | K:1 |
| 217 | M:1 |
| 218 | AD:1 |
| 219 | A:1 |
| 220 | AA:1 |
| 221 | G:1 |
| 222 | G:1 |
| 223 | G:1; H:2; S:2; X:1 |
| 224 | G:1 |
| 225 | G:1 |
| 226 | B:1 |
| 227 | P:1 |
| 228 | O:1 |
| 229 | G:1 |
| 230 | T:1 |
| 231 | T:1 |
| 232 | K:1 |
| 233 | S:1 |
| 234 | O:1 |
| 235 | F:1 |
| 236 | T:1 |
| 237 | B:1 |
| 238 | W:1 |
| 239 | G:1 |
| 240 | R:1 |
| 241 | A:1 |
| 242 | W:1 |
| 243 | P:1 |
| 244 | H:1 |
| 245 | D:1 |
| 246 | C:1 |
| 247 | B:2 |
| 248 | P:1 |
| 249 | F:1 |
| 250 | AB:1 |
| 251 | W:1 |
| 252 | H:1 |
| 253 | B:1 |
| 254 | S:1 |
| 255 | T:1 |
| 256 | W:1 |
| 257 | T:1 |

| | |
|---|---|
| 258 | AA:2 |
| 259 | P:1 |
| 260 | W:1 |
| 261 | H:1 |
| 262 | K:1 |
| 263 | K:1 |
| 264 | C:1; E:1; F:1; I:4; L:1; N:22; O:1; P:1; S:1; T:9; AA:1 |
| 265 | A:1 |
| 266 | T:1 |
| 267 | K:1 |
| 268 | H:1 |
| 269 | T:2 |
| 270 | T:1 |
| 271 | T:1 |
| 272 | B:1 |
| 273 | Y:1 |
| 274 | T:1 |
| 275 | G:1 |
| 276 | AA:1 |
| 277 | T:1 |
| 278 | AB:1 |
| 279 | T:1 |
| 280 | W:1 |
| 281 | F:1 |
| 282 | K:1 |
| 283 | H:1 |
| 284 | O:1 |
| 285 | W:1 |
| 286 | B:21; C:7; H:5; K:5; O:8; S:16; W:1; Y:3; Z:4; AA:2; AC:1 |
| 287 | K:2; P:12; W:1; AC:2 |
| 288 | S:1 |
| 289 | K:2; P:8; W:1; AC:2 |
| 290 | S:1 |
| 291 | H:1 |
| 292 | B:11; C:2; E:1; H:7; K:1; N:3; S:1; T:8; W:1; AA:28; AC:1 |
| 293 | B:6; C:3; G:1; H:6; K:4; N:4; O:3; Q:2; S:5; T:1; U:1; V:2; Y:3; AA:1 |
| 294 | B:1 |
| 295 | H:1 |
| 296 | AA:1 |
| 297 | T:1 |
| 298 | T:1 |
| 299 | T:1 |
| 300 | H:1; S:1 |
| 301 | H:1 |
| 302 | W:1 |
| 303 | W:1 |
| 304 | H:1 |
| 305 | G:1 |

| | |
|---|---|
| 306 | K:1 |
| 307 | H:1 |
| 308 | A:1 |
| 309 | H:1 |
| 310 | H:1 |
| 311 | Y:1 |
| 312 | G:1 |
| 313 | H:1 |
| 314 | K:1 |
| 315 | Y:1 |
| 316 | P:1 |
| 317 | H:1 |
| 318 | AA:1 |
| 319 | H:1 |
| 320 | O:1 |
| 321 | Y:1 |
| 322 | B:1 |
| 323 | P:1 |
| 324 | P:1 |
| 325 | K:1 |
| 326 | H:1 |
| 327 | H:1 |
| 328 | Q:1 |
| 329 | S:1 |
| 330 | B:1 |
| 331 | T:1 |
| 332 | T:1 |
| 333 | B:1 |
| 334 | T:1 |
| 335 | W:1 |
| 336 | P:1 |
| 337 | A:1 |
| 338 | AA:1 |
| 339 | AA:1 |
| 340 | G:1 |
| 341 | C:1 |
| 342 | K:1 |
| 343 | S:1 |
| 344 | G:1 |
| 345 | B:1 |
| 346 | Y:1 |
| 347 | G:1 |
| 348 | F:1 |
| 349 | AA:5 |
| 350 | B:15; C:1; G:1; H:1; O:1; Q:2; S:1; X:1; Y:1 |
| 351 | F:1 |
| 352 | R:1 |
| 353 | O:1 |

| | |
|---|---|
| 354 | H:1 |
| 355 | W:1 |
| 356 | F:1 |
| 357 | T:1 |
| 358 | S:1 |
| 359 | X:1 |
| 360 | T:1 |
| 361 | K:1 |
| 362 | K:1 |
| 363 | G:1 |
| 364 | K:1 |
| 365 | G:1 |
| 366 | AA:1 |
| 367 | F:1 |
| 368 | C:2; H:2; X:1 |
| 369 | E:1 |
| 370 | T:1 |
| 371 | H:1 |
| 372 | G:1 |
| 373 | AA:1 |
| 374 | G:1 |
| 375 | F:1 |
| 376 | F:1 |
| 377 | R:1 |
| 378 | AA:1 |
| 379 | AA:1 |
| 380 | C:1 |
| 381 | H:1 |
| 382 | T:1 |
| 383 | W:1 |
| 384 | S:1 |
| 385 | AA:2 |
| 386 | D:1 |
| 387 | O:1 |
| 388 | W:1 |
| 389 | F:1 |
| 390 | W:1 |
| 391 | K:1 |
| 392 | W:1 |
| 393 | K:1 |
| 394 | T:1 |
| 395 | H:1 |
| 396 | T:1 |
| 397 | T:1 |
| 398 | G:1 |
| 399 | C:1 |
| 400 | K:1 |
| 401 | B:1 |

| | |
|---|---|
| 402 | H:1 |
| 403 | B:1 |
| 404 | B:1 |
| 405 | H:1 |
| 406 | AB:1 |
| 407 | O:1 |
| 408 | P:1 |
| 409 | X:1 |
| 410 | H:1 |
| 411 | B:9; C:3; K:3; L:2; O:1; S:2; X:1; AA:1 |
| 412 | G:1; S:2; V:2; W:1; Y:1; Z:1 |
| 413 | W:1 |
| 414 | G:1 |
| 415 | B:3; C:3; F:1; G:2; H:4; J:1; K:1; O:1; P:3; S:1; V:1 |
| 416 | I:1 |
| 417 | F:1 |
| 418 | F:1 |
| 419 | F:1 |
| 420 | AA:1 |
| 421 | F:1 |
| 422 | T:1 |
| 423 | P:1 |
| 424 | B:1 |
| 425 | Y:1 |
| 426 | W:1 |
| 427 | AA:1 |
| 428 | W:1 |
| 429 | H:1 |
| 430 | Y:1 |
| 431 | J:1 |
| 432 | AA:1 |
| 433 | G:1 |
| 434 | AA:1 |
| 435 | B:3; H:1 |
| 436 | B:9; G:4; H:8; K:2; O:2; W:1; Z:2; AA:2; AD:3 |
| 437 | H:1; T:1 |
| 438 | T:1 |
| 439 | R:1 |
| 440 | M:1 |
| 441 | H:2 |
| 442 | W:1 |
| 443 | B:1 |
| 444 | W:1 |
| 445 | AB:1 |
| 446 | F:1 |
| 447 | AD:1 |
| 448 | AB:1 |
| 449 | N:1 |

| | |
|---|---|
| 450 | T:1 |
| 451 | W:1 |
| 452 | O:1 |
| 453 | AA:1 |
| 454 | D:28 |
| 455 | W:1 |
| 456 | T:1 |
| 457 | G:1 |
| 458 | W:1 |
| 459 | Y:4 |
| 460 | B:3 |
| 461 | P:2 |
| 462 | K:1 |
| 463 | T:1 |
| 464 | H:1 |
| 465 | G:1 |
| 466 | AC:1 |
| 467 | R:1 |
| 468 | S:1 |
| 469 | B:1 |
| 470 | S:1 |
| 471 | T:1 |
| 472 | AA:1 |
| 473 | W:1 |
| 474 | T:1 |
| 475 | S:1 |
| 476 | T:1 |
| 477 | AA:1 |
| 478 | G:1 |
| 479 | W:1 |
| 480 | B:1 |
| 481 | O:2 |
| 482 | K:1 |
| 483 | P:1 |
| 484 | W:1 |
| 485 | P:1 |
| 486 | B:1 |
| 487 | Y:1 |
| 488 | H:1 |
| 489 | P:1; Q:1; S:3 |
| 490 | C:1 |
| 491 | S:1 |
| 492 | H:1 |
| 493 | B:1 |
| 494 | H:1 |
| 495 | G:1 |
| 496 | N:2 |
| 497 | B:1 |

| | |
|---|---|
| 498 | G:1 |
| 499 | P:1 |
| 500 | G:1 |
| 501 | C:1; K:1; Q:1 |
| 502 | B:4 |
| 503 | R:1 |
| 504 | B:5; H:2; W:2 |
| 505 | G:2; H:1 |
| 506 | W:1 |
| 507 | B:1 |
| 508 | W:1 |
| 509 | AB:1 |
| 510 | H:1 |
| 511 | N:1 |
| 512 | J:1 |
| 513 | AA:1 |
| 514 | T:2 |
| 515 | AA:5 |
| 516 | F:1 |
| 517 | C:1; O:1 |
| 518 | W:1 |
| 519 | T:4 |
| 520 | B:1 |
| 521 | H:1 |
| 522 | H:2; T:3 |
| 523 | H:1 |
| 524 | AA:1 |
| 525 | W:1 |
| 526 | C:2; E:1; J:1; R:3; S:4; AA:1 |
| 527 | H:1 |
| 528 | S:1 |
| 529 | P:1 |
| 530 | B:1; H:1 |
| 531 | O:1 |
| 532 | Y:1 |
| 533 | H:1 |
| 534 | T:1 |
| 535 | T:2 |
| 536 | B:1 |
| 537 | AD:1 |
| 538 | AA:1 |
| 539 | T:1 |
| 540 | F:1 |
| 541 | AD:1 |
| 542 | W:1 |
| 543 | W:1 |
| 544 | F:1 |
| 545 | T:1 |

| | |
|---|---|
| 546 | F:1 |
| 547 | K:1 |
| 548 | Y:1 |
| 549 | S:1 |
| 550 | B:1 |
| 551 | B:1 |
| 552 | B:1 |
| 553 | H:1 |
| 554 | P:1 |
| 555 | G:1 |
| 556 | H:1 |
| 557 | K:1 |
| 558 | B:1 |
| 559 | R:1 |
| 560 | AB:1 |
| 561 | C:1; S:1; V:1 |
| 562 | AA:1 |
| 563 | K:1 |
| 564 | P:1 |
| 565 | K:1 |
| 566 | G:1 |
| 567 | W:1 |
| 568 | E:1; W:2 |
| 569 | W:1 |
| 570 | B:2 |
| 571 | O:1 |
| 572 | T:1 |
| 573 | B:1 |
| 574 | T:1 |
| 575 | B:1 |
| 576 | B:3 |
| 577 | B:1 |
| 578 | X:1 |
| 579 | H:1 |
| 580 | AA:1 |
| 581 | AA:1 |
| 582 | AA:1 |
| 583 | AA:1 |
| 584 | AA:1 |
| 585 | D:1 |
| 586 | H:1 |
| 587 | H:1 |
| 588 | AA:3 |
| 589 | K:1 |
| 590 | W:1 |
| 591 | K:1 |
| 592 | W:1 |
| 593 | B:1 |

| | |
|---|---|
| 594 | V:1 |
| 595 | R:1 |
| 596 | P:1 |
| 597 | G:1; X:2; Z:1 |
| 598 | X:1 |
| 599 | F:1 |
| 600 | F:1 |
| 601 | Y:1 |
| 602 | F:1 |
| 603 | W:1 |
| 604 | H:1 |
| 605 | G:1 |
| 606 | C:2; H:1; S:3; W:2; AD:3 |
| 607 | W:1 |
| 608 | C:1 |
| 609 | F:1 |
| 610 | K:1 |
| 611 | M:1 |
| 612 | AD:1 |
| 613 | H:1 |
| 614 | T:1 |
| 615 | H:1 |
| 616 | F:1 |
| 617 | T:1 |
| 618 | G:1 |
| 619 | G:1 |
| 620 | B:1 |
| 621 | W:1 |
| 622 | W:1 |
| 623 | T:1 |
| 624 | AA:1 |
| 625 | G:1 |
| 626 | M:1 |
| 627 | C:2; T:2; W:1; Y:1 |
| 628 | T:1 |
| 629 | J:1 |
| 630 | T:1 |
| 631 | P:1 |
| 632 | H:1 |
| 633 | H:1 |
| 634 | C:1; S:1; T:1; AD:1 |
| 635 | J:1 |
| 636 | G:1 |
| 637 | W:1 |
| 638 | AA:1 |
| 639 | W:1 |
| 640 | B:6; C:3; G:1; H:2; K:6; O:4; Q:1; R:2; S:1; T:3; Y:3; Z:2; AA:2; AC:2; AD:3 |

| | |
|---|---|
| 641 | B:21; C:2; G:5; W:4; Y:1 |
| 642 | AA:1 |
| 643 | P:1 |
| 644 | AA:1 |
| 645 | T:1 |
| 646 | K:1 |
| 647 | F:1 |
| 648 | F:1 |
| 649 | F:1 |
| 650 | T:1 |
| 651 | W:1 |
| 652 | T:1 |
| 653 | T:1 |
| 654 | P:1 |
| 655 | B:1; H:2; N:1; T:3; Y:1 |
| 656 | B:1 |
| 657 | T:1 |
| 658 | R:1 |
| 659 | K:1 |
| 660 | W:1 |
| 661 | AA:1 |
| 662 | Y:1 |
| 663 | W:1 |
| 664 | G:1 |
| 665 | S:1 |
| 666 | Y:1 |
| 667 | F:1 |
| 668 | T:1 |
| 669 | B:1 |
| 670 | F:1 |
| 671 | T:1 |
| 672 | A:2; B:6; C:1; G:1; H:3; J:1; L:1; P:2; Q:1; S:4; T:1; V:3; W:2; Y:1; AA:3; AD:2 |
| 673 | T:1 |
| 674 | G:1 |
| 675 | F:1 |
| 676 | M:1 |
| 677 | G:1 |
| 678 | Y:1 |
| 679 | D:1 |
| 680 | P:1 |
| 681 | D:1 |
| 682 | AA:1 |
| 683 | G:1 |
| 684 | K:1 |
| 685 | G:1 |
| 686 | P:1 |
| 687 | B:3; C:2; D:2; E:2; J:4; V:2; AC:6 |

| | |
|---|---|
| 688 | AA:1 |
| 689 | S:1 |
| 690 | AA:1 |
| 691 | H:1 |
| 692 | AA:1 |
| 693 | S:1 |
| 694 | AB:1 |
| 695 | T:1 |
| 696 | H:1 |
| 697 | B:4; E:1; F:1; P:1; T:2; Z:2 |
| 698 | O:1 |
| 699 | W:1 |
| 700 | S:1 |
| 701 | O:1 |
| 702 | B:1 |
| 703 | AB:1 |
| 704 | H:1 |
| 705 | B:1 |
| 706 | H:1 |
| 707 | G:1 |
| 708 | F:1; H:1; K:1; W:2; AA:1 |
| 709 | H:1 |
| 710 | T:2 |
| 711 | C:1 |
| 712 | G:1 |
| 713 | Y:1 |
| 714 | C:1 |
| 715 | Y:1 |
| 716 | Z:1 |
| 717 | P:1 |
| 718 | G:1 |
| 719 | S:1 |
| 720 | K:1 |
| 721 | M:1 |
| 722 | T:2 |
| 723 | O:1; P:2; S:2 |
| 724 | T:1 |
| 725 | T:1 |
| 726 | N:1 |
| 727 | T:1 |
| 728 | T:1 |
| 729 | C:2; H:2; K:2; V:1; AC:1 |
| 730 | B:7; H:2; Y:1 |
| 731 | B:5; W:3 |
| 732 | B:1; C:2; G:2; S:2; AA:9 |
| 733 | B:6; C:2; G:1; H:10; O:2; P:6; Q:1; S:2; W:4; AC:2 |
| 734 | B:6; O:1; V:1 |
| 735 | C:1; O:2 |

| | |
|---|---|
| 736 | B:1; H:2; N:1; T:3; Y:1 |
| 737 | T:2 |
| 738 | T:2 |
| 739 | B:3; C:8; D:1; E:6; G:3; H:11; I:1; J:1; N:1; O:3; P:12; Q:3; S:2; T:2; W:1; AC:1; AD:8 |
| 740 | H:2; Y:1 |
| 741 | C:2; H:1 |
| 742 | B:12; C:1; G:1; H:4; K:2; O:2; S:4; T:2; Y:2 |
| 743 | AA:4 |
| 744 | B:1; G:1; H:6; T:1; W:1 |
| 745 | C:7; E:1; G:3; H:2; P:2; S:2; T:1; W:1; AD:2 |
| 746 | G:2; S:1 |
| 747 | T:2 |
| 748 | S:3 |
| 749 | H:1; O:2; S:2 |
| 750 | Y:1; AD:1 |
| 751 | B:8; G:2; H:2; I:1; Q:2; S:2; T:1; W:2 |
| 752 | T:3 |
| 753 | P:4 |
| 754 | B:1; H:2 |
| 755 | B:7; C:1; G:6; H:2; K:1; U:2; V:1; Z:1 |
| 756 | C:1; H:1; J:2; O:2; S:1; T:2; W:1; AA:1 |
| 757 | B:1; C:1; K:3; S:1; V:1; Y:1 |
| 758 | E:1; H:2; K:1; P:1; Q:1; AD:5 |
| 759 | B:6; C:1; Y:1 |
| 760 | B:4 |
| 761 | W:2 |
| 762 | B:3; C:7; H:9; N:1; S:1; T:1; Y:1; AA:1 |
| 763 | N:1; S:1; AA:5 |
| 764 | H:3 |
| 765 | B:3; G:1; W:1 |
| 766 | H:2 |
| 767 | C:1; AA:3 |
| 768 | B:2; C:6; H:9; N:1; S:1; T:1; Y:1; AA:1 |
| 769 | A:1; B:4; C:4; F:4; G:6; H:10; K:2; O:8; P:2; R:1; S:8; T:2; W:3; AA:2; AC:1 |
| 770 | A:2; P:16; X:1 |
| 771 | AA:3 |
| 772 | O:4 |
| 773 | B:1; C:1; W:1 |
| 774 | P:2; X:4 |
| 775 | B:18; C:6; H:5; K:3; O:7; S:10; W:1; Y:3; Z:2; AA:2; AC:1 |
| 776 | H:7 |
| 777 | B:26; C:8; H:5; K:4; O:10; S:17; W:1; Y:4; Z:4; AA:4; AC:2 |
| 778 | B:6 |
| 779 | B:3; C:1; G:1; H:2; K:1; Q:1; S:8; W:2; Y:9; AA:4 |
| 780 | B:3; C:1; F:1; P:1; W:1; AC:1 |
| 781 | I:2; N:1; P:1; R:3; AA:1 |
| 782 | B:2 |

| | |
|---|---|
| 783 | H:1; P:2; S:3; AD:1 |
| 784 | H:1; P:1; S:4; AD:1 |
| 785 | T:2 |
| 786 | D:1; AC:9 |
| 787 | H:1; L:1; S:1 |
| 788 | B:6; S:4 |
| 789 | S:1; T:1 |
| 790 | B:1; C:2; H:5; W:1; AD:1 |
| 791 | B:3; C:2; D:3; E:2; J:4; V:3; AC:5 |
| 792 | B:3; D:1; K:2; S:2; Y:1 |
| 793 | B:2; G:2; AA:1 |
| 794 | B:25; C:4; D:1; E:1; F:3; G:6; J:1; K:6; N:1; O:1; P:2; R:1; S:3; T:2; W:2; X:1; Y:1; Z:1; AA:1; AC:2; AD:1 |
| 795 | B:4; C:1; E:2; H:4; J:1; L:1; O:4; S:1; V:1; Y:3; Z:1 |
| 796 | H:5 |
| 797 | B:2; E:1; N:2 |
| 798 | B:1; G:1; H:6; T:1; W:1 |
| 799 | H:2 |
| 800 | H:2; I:2; AA:1 |
| 801 | A:2; B:4; C:14; D:1; H:2; K:1; N:2; S:4; T:1; W:2; AA:20 |
| 802 | AA:17 |
| 803 | B:2; G:3; H:3; S:1; U:1; AC:1; AD:2 |
| 804 | C:1; S:2; T:2; X:2; AA:1; AC:1 |
| 805 | B:5; C:6; D:5; H:17; J:2; K:4; N:1; O:6; P:2; S:5; T:5; W:1; X:1; Z:2; AA:13; AC:3 |
| 806 | B:2; C:3; D:3; H:6; J:2; K:1; N:1; O:3; P:1; S:2; T:4; W:1; X:1; Z:1; AA:5; AC:1 |
| 807 | H:1; AC:4 |
| 808 | R:13 |
| 809 | B:3; W:4 |
| 810 | B:16; S:1; Y:14 |
| 811 | B:8; C:5; G:1; H:1; K:5; O:2; Q:2; R:2; S:2; T:3; Y:4; Z:2; AA:1; AC:1; AD:2 |
| 1600 | T:4 |
| 1601 | AA:3 |
| 1602 | C:3; H:1 |
| 1603 | H:2; AC:2 |
| 1604 | B:7; C:1; E:1; H:1; P:2; R:3; S:2; T:2; Z:3; AA:2 |
| 1605 | C:4; H:3; O:1 |
| 1606 | A:3; B:13; C:14; D:2; E:10; F:3; G:19; H:32; K:11; O:5; P:2; R:3; S:16; T:4; W:2; Y:10; Z:8; AA:1; AC:3 |
| 1607 | T:3 |
| 1608 | B:3; P:2 |
| 1609 | R:4 |
| 1610 | B:4 |
| 1611 | B:3; T:1 |
| 1612 | T:2 |
| 1613 | V:5 |
| 1614 | D:3 |

| | |
|---|---|
| 1615 | AA:10 |
| 1616 | B:4 |
| 1617 | T:2 |
| 1618 | K:2; S:8; AA:1 |
| 1619 | B:2 |
| 1620 | W:2 |
| 1621 | H:1; AB:1 |
| 1622 | H:2 |

**Table VI**

| Tissue code | Tissue type |
|---|---|
| A | Bone Marrow |
| B | Brain |
| c | Cancerous prostate |
| D | Cerebellum |
| E | Colon |
| F | Dystrophic muscle |
| G | Fetal brain |
| H | Fetal kidney |
| I | Fetal liver |
| J | Heart |
| K | Hypertrophic prostate |
| L | Kidney |
| M | Large intestine |
| N | Liver |
| O | Lung |
| P | Lymph ganglia |
| Q | Lymphocytes |
| R | Muscle |
| S | Prostate |
| T | Ovary |
| U | Pancreas |
| V | Placenta |
| W | Spinal cord |
| X | Spleen |
| Y | Substantia nigra |
| Z | Surrenals |
| AA | Testis |
| AB | Thyroid |
| AC | Umbilical cord |
| AD | Uterus |

In addition to categorizing the 5' ESTs and consensus contigated 5' ESTs with respect to their tissue of origin, the spatial and temporal expression patterns of the mRNAs corresponding to the 5' ESTs and consensus contigated 5' ESTs, as well as their expression levels, may be determined as described in Example 18 below.

Characterization of the spatial and temporal expression patterns and expression levels of these mRNAs is useful for constructing expression vectors capable of producing a desired level of gene product in a desired spatial or temporal manner, as will be discussed in more detail below.

Furthermore, 5' ESTs and consensus contigated 5' ESTs whose corresponding mRNAs are associated with disease states may also be identified. For example, a particular disease may result from the lack of expression, over expression, or under expression of a mRNA corresponding to a 5' EST or consensus contigated 5' EST. By comparing mRNA expression patterns and quantities in samples taken from healthy individuals with those from individuals suffering from a particular disease, 5' ESTs or consensus contigated 5' ESTs responsible for the disease may be identified.

It will be appreciated that the results of the above characterization procedures for 5' ESTs and consensus contigated 5' ESTs also apply to extended cDNAs (obtainable as described below) which contain sequences adjacent to the 5' ESTs and consensus contigated 5' ESTs. It will also be appreciated that if desired, characterization may be delayed until extended cDNAs have been obtained rather than characterizing the 5' ESTs or consensus contigated 5' ESTs themselves.

## EXAMPLE 18

### Evaluation of Expression Levels and Patterns of mRNAs Corresponding to EST-Related Nucleic Acids

Expression levels and patterns of mRNAs corresponding to EST-related nucleic acids may be analyzed by solution hybridization with long probes as described in International Patent Application No. WO 97/05277. Briefly, an EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid corresponding to the gene encoding the mRNA to be characterized is inserted at a cloning site immediately downstream of a bacteriophage (T3, T7 or SP6) RNA polymerase promoter to produce antisense RNA. Preferably, the EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid is 100 or more nucleotides in length. The plasmid is linearized and transcribed in the presence of ribonucleotides comprising modified ribonucleotides (*i.e.* biotin-UTP and DIG-UTP). An excess of this doubly labeled RNA is hybridized in solution with mRNA isolated from cells or tissues of interest. The hybridizations are performed under standard stringent conditions (40-50°C for 16 hours in an 80% formamide, 0.4 M NaCl buffer, pH 7-8). The unhybridized probe is removed by digestion with ribonucleases specific for single-stranded RNA (*i.e.* RNases CL3, T1, Phy M, U2 or A). The presence of the biotin-UTP modification enables capture of the hybrid on a microtitration plate coated with streptavidin. The presence of the DIG modification enables the hybrid to be detected and quantified by ELISA using an anti-DIG antibody coupled to alkaline phosphatase.

The EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid may also be

tagged with nucleotide sequences for the serial analysis of gene expression (SAGE) as disclosed in UK Patent Application No. 2 305 241 A. In this method, cDNAs are prepared from a cell, tissue, organism or other source of nucleic acid for which gene expression patterns must be determined. The resulting cDNAs are separated into two pools. The cDNAs in each pool are cleaved with a first restriction endonuclease, called an anchoring enzyme, having a recognition site which is likely to be present at least once in most cDNAs. The fragments which contain the 5' or 3' most region of the cleaved cDNA are isolated by binding to a capture medium such as streptavidin coated beads. A first oligonucleotide linker having a first sequence for hybridization of an amplification primer and an internal restriction site for a so called tagging endonuclease is ligated to the digested cDNAs in the first pool. Digestion with the second endonuclease produces short tag fragments from the cDNAs.

A second oligonucleotide having a second sequence for hybridization of an amplification primer and an internal restriction site is ligated to the digested cDNAs in the second pool. The cDNA fragments in the second pool are also digested with the tagging endonuclease to generate short tag fragments derived from the cDNAs in the second pool. The tags resulting from digestion of the first and second pools with the anchoring enzyme and the tagging endonuclease are ligated to one another to produce so called ditags. In some embodiments, the ditags are concatamerized to produce ligation products containing from 2 to 200 ditags. The tag sequences are then determined and compared to the sequences of the EST-related nucleic acid, fragment of an EST-related nucleic acid, positional segment of an EST-related nucleic acid, or fragment of a positional segment of an EST-related nucleic acid to determine which 5' ESTs, consensus contigated 5' ESTs, or extended cDNAs are expressed in the cell, tissue, organism, or other source of nucleic acids from which the tags were derived. In this way, the expression pattern of the 5' ESTs, consensus contigated 5' ESTs, or extended cDNAs in the cell, tissue, organism, or other source of nucleic acids is obtained.

Quantitative analysis of gene expression may also be performed using arrays. As used herein, the term array means a one dimensional, two dimensional, or multidimensional arrangement of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids. Preferably, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are at least 10, 12, 15, 18, 20, 23, 25, 28, 30, 35, 40, or 50 nucleotides in length. More preferably, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are at least 100 nucleotide long. More preferably, the fragments are more than 100 nucleotides in length. In some embodiments, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids may be more than 500 nucleotides long.

For example, quantitative analysis of gene expression may be performed with EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or

fragments of positional segments of EST-related nucleic acids in a complementary DNA microarray as described by Schena *et al.* (*Science* 270:467-470, 1995; *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619, 1996). EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are amplified by PCR and arrayed from 96-well microtiter plates onto silylated microscope slides using high-speed robotics. Printed arrays are incubated in a humid chamber to allow rehydration of the array elements and rinsed, once in 0.2% SDS for 1 min, twice in water for 1 min and once for 5 min in sodium borohydride solution. The arrays are submerged in water for 2 min at 95°C, transferred into 0.2% SDS for 1 min, rinsed twice with water, air dried and stored in the dark at 25°C.

Cell or tissue mRNA is isolated or commercially obtained and probes are prepared by a single round of reverse transcription. Probes are hybridized to 1 $cm^2$ microarrays under a 14 x 14 mm glass coverslip for 6-12 hours at 60°C. Arrays are washed for 5 min at 25°C in low stringency wash buffer (1 x SSC/0.2% SDS), then for 10 min at room temperature in high stringency wash buffer (0.1 x SSC/0.2% SDS). Arrays are scanned in 0.1 x SSC using a fluorescence laser scanning device fitted with a custom filter set. Accurate differential expression measurements are obtained by taking the average of the ratios of two independent hybridizations.

Quantitative analysis of the expression of genes may also be performed with EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids in complementary DNA arrays as described by Pietu *et al.* (*Genome Research* 6:492-503, 1996). The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids thereof are PCR amplified and spotted on membranes. Then, mRNAs originating from various tissues or cells are labeled with radioactive nucleotides. After hybridization and washing in controlled conditions, the hybridized mRNAs are detected by phospho-imaging or autoradiography. Duplicate experiments are performed and a quantitative analysis of differentially expressed mRNAs is then performed.

Alternatively, expression analysis of the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids can be done through high density nucleotide arrays as described by Lockhart *et al.* (*Nature Biotechnology* 14: 1675-1680, 1996) and Sosnowsky *et al.* (*Proc. Natl. Acad. Sci.* 94:1119-1123, 1997). Oligonucleotides of 15-50 nucleotides corresponding to sequences of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are synthesized directly on the chip (Lockhart *et al.*, *supra*) or synthesized and then addressed to the chip (Sosnowsky *et al.*, *supra*). Preferably, the oligonucleotides are about 20 to 25 nucleotides in length.

cDNA probes labeled with an appropriate compound, such as biotin, digoxigenin or fluorescent dye, are synthesized from the appropriate mRNA population and then randomly fragmented to an

average size of 50 to 100 nucleotides. The said probes are then hybridized to the chip. After washing as described in Lockhart *et al, supra* and application of different electric fields (Sonowsky et *al, supra*.), the dyes or labeling compounds are detected and quantified. Duplicate hybridizations are performed. Comparative analysis of the intensity of the signal originating from cDNA probes on the same target oligonucleotide in different cDNA samples indicates a differential expression of the mRNA corresponding to the 5' EST, consensus contigated 5' EST or extended cDNA from which the oligonucleotide sequence has been designed.

**IV. Use of 5' ESTs to Clone Extended cDNAs and to Clone the Corresponding Genomic DNAs**

Once 5' ESTs or consensus contigated 5' ESTs which include the 5' end of the corresponding mRNAs have been selected using the procedures described above, they can be utilized to isolate extended cDNAs which contain sequences adjacent to the 5' ESTs or consensus contigated 5' ESTs. The extended cDNAs may include the entire coding sequence of the protein encoded by the corresponding mRNA, including the authentic translation start site. If the extended cDNA encodes a secreted protein, it may contain the signal sequence, and the sequence encoding the mature protein remaining after cleavage of the signal peptide.

Extended cDNAs which include the entire coding sequence of the protein encoded by the corresponding mRNA are referred to herein as "full-length cDNAs." Alternatively, the extended cDNAs may not include the entire coding sequence of the protein encoded by the corresponding mRNA, although they do include sequences adjacent to the 5'ESTs or consensus contigated 5' ESTs. In some embodiments in which the extended cDNAs are derived from an mRNA encoding a secreted protein, the extended cDNAs may include only the sequence encoding the mature protein remaining after cleavage of the signal peptide, or only the sequence encoding the signal peptide.

Examples 19 and 20 below describe a general method for obtaining extended cDNAs using 5' ESTs or consensus contigated 5' ESTs and nucleic acid homologous thereto. Example 21 below describes the cloning and sequencing of several extended cDNAs, including full-length cDNAs which include the authentic 5' end of the corresponding mRNA for several secreted proteins.

The methods of Examples 19 and 20 can also be used to obtain extended cDNAs which encode less than the entire coding sequence of proteins encoded by the genes corresponding to the 5' ESTs or consensus contigated 5'ESTs. In some embodiments, the extended cDNAs isolated using these methods encode at least 5,10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the proteins encoded by the sequences of SEQ ID NOs. 24-811 and 1600-1622. In some embodiments, the extended cDNAs isolated using these methods encode at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of one of the proteins encoded by the sequences of SEQ ID NOs. 24-811.

**EXAMPLE 19**

General Method for Using 5' ESTs or Consensus Contigated 5'ESTs to Clone and Sequence Extended cDNAs which Include the Entire Coding Region and the Authentic 5'End of the Corresponding mRNA

The following general method may be used to quickly and efficiently isolate extended cDNAs including sequence adjacent to the sequences of the 5' ESTs or Consensus Contigated 5'ESTs used to obtain them. This method may be applied to obtain extended cDNAs for any 5' EST or consensus contigated 5' EST of the invention, including those 5' ESTs and consensus contigated 5' ESTs encoding secreted proteins. This method is illustrated in Figure 3.

1. Obtaining Extended cDNAs

The method takes advantage of the known 5' sequence of the mRNA. A reverse transcription reaction is conducted on purified mRNA with a poly dT primer containing a nucleotide sequence at its 5' end allowing the addition of a known sequence at the end of the cDNA which corresponds to the 3' end of the mRNA. Such a primer and a commercially-available reverse transcriptase enzyme are added to a buffered mRNA sample yielding a reverse transcript anchored at the 3' polyA site of the RNAs. Nucleotide monomers are then added to complete the first strand synthesis.

After removal of the mRNA hybridized to the first cDNA strand by alkaline hydrolysis, the products of the alkaline hydrolysis and the residual poly dT primer can be eliminated with an exclusion column.

Subsequently, a pair of nested primers on each end is designed based on the known 5' sequence from the 5' EST or consensus contigated 5' EST and the known 3' end added by the poly dT primer used in the first strand synthesis. Software used to design primers are either based on GC content and melting temperatures of oligonucleotides, such as OSP (Illier and Green, *PCR Meth. Appl.* 1:124-128, 1991), or based on the octamer frequency disparity method (Griffais *et al.*, *Nucleic Acids Res.* 19: 3887-3891, 1991 ) such as PC-Rare (http:// bioinformatics.weizmann.ac.il/software/PC-Rare/doc/manuel.html). Preferably, the nested primers at the 5' end and the nested primers at the 3' end are separated from one another by four to nine bases. These primer sequences may be selected to have melting temperatures and specificities suitable for use in PCR.

A first PCR run is performed using the outer primer from each of the nested pairs. A second PCR run using the inner primer from each of the nested pairs is then performed on a small sample of the first PCR product. Thereafter, the primers and remaining nucleotide monomers are removed.

2. Sequencing Extended cDNAs or Fragments Thereof

Due to the lack of position constraints on.the design of 5' nested primers compatible for PCR use using the OSP software, amplicons of two types are obtained. Preferably, the second 5' primer is located upstream of the translation initiation codon thus yielding a nested PCR product containing the entire coding sequence. Such an extended cDNA may be used in a direct cloning procedure as described in section a below. However, in some cases, the second 5' primer is located downstream of the translation initiation codon, thereby yielding a PCR product containing only part of the ORF. Such incomplete PCR products are submitted to a modified procedure described in section b below.

*a) Nested PCR products containing complete ORFs*

When the resulting nested PCR product contains the complete coding sequence, as predicted from the 5'EST or consensus contigated 5' EST sequence, it is directly cloned in an appropriate vector as described in section 3.

*b) Nested PCR products containing incomplete ORFs*

When the amplicon does not contain the complete coding sequence, intermediate steps are necessary to obtain both the complete coding sequence and a PCR product containing the full coding sequence. The complete coding sequence can be assembled from several partial sequences determined directly from different PCR products.

Once the full coding sequence has been completely determined, new primers compatible for PCR use are then designed to obtain amplicons containing the whole coding region. However, in such cases, 3' primers compatible for PCR use are located inside the 3' UTR of the corresponding mRNA, thus yielding amplicons which lack part of this region, *i.e.* the polyA tract and sometimes the polyadenylation signal, as illustrated in Figure 3. Such extended cDNAs are then cloned into an appropriate vector as described in section 3.

*c) Sequencing extended cDNAs*

Sequencing of extended cDNAs can be performed using a Die Terminator approach with the AmpliTaq DNA polymerase FS kit available from Perkin Elmer.

In order to sequence long PCR fragments, primer walking is performed using software such as OSP to choose primers and automated computer software such as ASMG (Sutton *et al., Genome Science Technol.* 1: 9-19, 1995) to construct contigs of walking sequences including the initial 5' tag. Preferably, primer walking is performed until the sequences of full length cDNAs are obtained.

Completion of the sequencing of a given extended cDNA fragment may be assessed by comparing the sequence length to the size of the corresponding nested PCR product. When Northern blot data are available, the size of the mRNA detected for a given PCR product may also be used to finally assess that the sequence is complete. Sequences which do not fulfill these criteria are discarded and will undergo a new isolation procedure.

3. Cloning Extended cDNAs

The PCR product containing the full coding sequence is then cloned in an appropriate vector. For example, the extended cDNAs can be cloned into any expression vector known in the art, such as pED6dpc2 (DiscoverEase, Genetics Institute, Cambridge, MA).

Cloned PCR products are then entirely sequenced in order to obtain at least two sequences per clone. Preferably, the sequences are obtained from both sense and antisense strands according to the aforementioned procedure with the following modifications. First, both 5' and 3' ends of cloned PCR products are sequenced in order to confirm the identity of the clone. Second, primer walking is performed if the full coding coding region has not been obtained yet. Contigation is then performed using primer walking sequences for cloned products as well as walking sequences that have already

contigated for uncloned PCR products. The sequence is considered complete when the resulting contigs include the whole coding region as well as overlapping sequences with vector DNA on both ends. All the contigated sequences for each cloned amplicon are then used to obtain a consensus sequence.

4. Selection of Cloned Full length Sequences

*a) Computer analysis of extended cDNAs*

Following identification of contaminants and masking of repeats, structural features, e.g. polyA tail and polyadenylation signal, of the sequences of extended cDNAs are subsequently determined using methods known to those skilled in the art. For example, algorithm, parameters and criteria defined in Figure 10 may be used. Briefly, a polyA tail is defined as a homopolymeric stretch of at least 11 A with at most one alternative base within it. The polyA tail search is restricted to the last 20 nucleotides of the sequence and limited to stretches of 11 consecutive A's because sequencing reactions are often not readable after such a polyA stretch. To search for a polyadenylation signal, the polyA tail is clipped from the full-length sequence. The 50 nucleotides preceding the polyA tail are searched for the canonic polyadenylation AAUAAA signal allowing one mismatch to account for possible sequencing errors as well as known variation in the canonical sequence of the polyadenylation signal.

Functional features, e.g. ORFs and signal sequences, of the sequences of extended cDNAs are subsequently determined as follows. The 3 upper strand frames of extended cDNAs are searched for ORFs defined as the maximum length fragments beginning with a translation initiation codon and ending with a stop codon. ORFs encoding at least 80 amino acids are preferred. If extended cDNAs encoding secreted proteins are desired, each found ORF is then scanned for the presence of a signal peptide using the matrix method described in Example 13.

Sequences of extended cDNAs are then compared, on a nucleotidic or proteic basis, to public sequences available at the time of filing.

*b) Selection of full-length cDNAs of interest*

A negative selection may then be performed in order to eliminate unwanted cloned sequences resulting from either contaminants or PCR artifacts as follows. Sequences matching contaminant sequences such as vector DNA, tRNA, mtRNA, rRNA sequences are discarded as well as those encoding ORF sequences exhibiting extensive homology to repeats. Sequences obtained by direct cloning (section 1a) but lacking polyA tail may be discarded. Only ORFs ending either before the polyA tail (section 1a) or before the end of the cloned 3'UTR (section 1b) may be selected. If extended cDNAs encoding secreted proteins are desired, ORFs containing a signal peptide are considered. In addition, ORFs containing unlikely mature proteins such as mature proteins which size is less than 20 amino acids or less than 25% of the immature protein size may be eliminated.

Then, for each remaining full length cDNA containing several ORFs, a preselection of ORFs may be performed using the following criteria. The longest ORF is preferred. If extended cDNAs

encoding secreted proteins are desired and if the ORF sizes are similar, the chosen ORF is the one which signal peptide has the highest score according to Von Heijne method.

Sequences of full length cDNA clones may then be compared pairwise after masking of the repeat sequences. Full-length cDNA sequences exhibiting extensive homology may be clustered in the same class. Each cluster may then be subjected to a cluster analysis that detects sequences resulting from internal priming or from alternative splicing, identical sequences or sequences with several frameshifts. A selection may be operated between clones belonging to the same class in order to detect clones encoding homologous but distinct ORFs which may be both selected if they both contain sequences of interest.

Selection of full-length cDNA clones encoding sequences of interest may subsequently be performed using the following criteria. Structural parameters (initial tag, polyadenylation site and signal) are first checked. Then, homologies with known nucleic acids and proteins are examined in order to determine whether the clone sequence match a known nucleotide/protein sequence and, in the latter case, its covering rate and the date at which the sequence became public. If there is no extensive match with sequences other than ESTs or genomic DNA, or if the clone sequence brings substantial new information, such as encoding a protein resulting from alternative splicing of an mRNA coding for an already known protein, the sequence is kept. Examples of such cloned full-length cDNAs containing sequences of interest are described in Example 21. Sequences resulting from chimera or double inserts or located on chromosome breaking points as assessed by homology to other sequences may be discarded during this procedure.

Extended cDNAs prepared as described above may be subsequently engineered to obtain nucleic acids which include desired portions of the extended cDNA using conventional techniques such as subcloning, PCR, or *in vitro* oligonucleotide synthesis. For example, nucleic acids which include only the full coding sequences may be obtained using techniques known to those skilled in the art. Alternatively, conventional techniques may be applied to obtain nucleic acids which contain only part of the coding sequences. In the case of nucleic acids encoding secreted proteins, nucleic acids containing only the coding sequence for the mature protein remaining after the signal peptide is cleaved off or nucleic acids which contain only the coding sequences for the signal peptides may be obtained.

Similarly, nucleic acids containing any other desired portion of the coding sequences for the encoded protein may be obtained. For example, the nucleic acid may contain at least 10, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 consecutive bases of an extended cDNA.

Once an extended cDNA has been obtained, it can be sequenced to determine the amino acid sequence it encodes. Once the encoded amino acid sequence has been determined, one can create and identify any of the many conceivable cDNAs that will encode that protein by simply using the degeneracy of the genetic code. For example, allelic variants or other homologous nucleic acids can be identified as described below. Alternatively, nucleic acids encoding the desired amino acid sequence can be synthesized *in vitro*.

In a preferred embodiment, the coding sequence may be selected using the known codon or codon pair preferences for the host organism in which the cDNA is to be expressed.

In addition to PCR based methods for obtaining cDNAs which include the authentic 5'end of the corresponding mRNA as well as the complete protein coding sequence of the corresponding mRNA, traditional hybridization based methods may also be employed. These methods may also be used to obtain the genomic DNAs which encode the mRNAs from which the 5' ESTs or consensus contigated 5' ESTS were derived, mRNAs corresponding to the extended cDNAs, or nucleic acids which are homologous to extended cDNAs, 5' ESTs, or consensus contigated 5' ESTs. Example 19 below provides examples of such methods.

## EXAMPLE 20

Methods for Obtaining Extended cDNAs which Include the Entire Coding Region and the Authentic 5'End of the Corresponding mRNA or Nucleic Acids Homologous to Extended cDNAs, 5' ESTs or Consensus Contigated 5' ESTs

A full-length cDNA library can be made using the strategies described in Example 7. Alternatively, a cDNA library or genomic DNA library may be obtained from a commercial source or made using techniques familiar to those skilled in the art.

Such cDNA or genomic DNA libraries may be used to isolate extended cDNAs obtained from 5' ESTs or consensus contigated 5' ESTs or nucleic acids homologous to extended cDNAs, 5' ESTs, or consensus contigated 5' ESTs as follows. The cDNA library or genomic DNA library is hybridized to a detectable probe. The detectable probe may comprise at least 10, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 consecutive nucleotides of the 5' EST, consensus contigated 5' EST, or extended cDNA.

Techniques for identifying cDNA clones in a cDNA library which hybridize to a given probe sequence are disclosed in Sambrook *et al., Molecular Cloning: A Laboratory Manual 2d Ed.*, Cold Spring Harbor Laboratory Press, 1989. The same techniques may be used to isolate genomic DNAs. Briefly, cDNA or genomic DNA clones which hybridize to the detectable probe are identified and isolated for further manipulation as follows. The detectable probe described in the preceding paragraph is labeled with a detectable label such as a radioisotope or a fluorescent molecule. Techniques for labeling the probe are well known and include phosphorylation with polynucleotide kinase, nick translation, *in vitro* transcription, and non radioactive techniques. The cDNAs or genomic DNAs in the library are transferred to a nitrocellulose or nylon filter and denatured. After blocking of non specific sites, the filter is incubated with the labeled probe for an amount of time sufficient to allow binding of the probe to cDNAs or genomic DNAs containing a sequence capable of hybridizing thereto.

By varying the stringency of the hybridization conditions used to identify cDNAs or genomic DNAs which hybridize to the detectable probe, cDNAs or genomic DNAs having different levels of homology to the probe can be identified and isolated as described below.

1. Identification of cDNA or Genomic DNA Sequences Having a High Degree of Homology to the Labeled Probe

To identify cDNAs or genomic DNAs having a high degree of homology to the probe sequence, the melting temperature of the probe may be calculated using the following formulas:

For probes between 14 and 70 nucleotides in length the melting temperature (Tm) is calculated using the formula: Tm=81.5+16.6(log (Na+))+0.41(fraction G+C)-(600/N) where N is the length of the probe.

If the hybridization is carried out in a solution containing formamide, the melting temperature may be calculated using the equation Tm=81.5+16.6(log (Na+))+0.41(fraction G+C)-(0.63% formamide)-(600/N) where N is the length of the probe.

Prehybridization may be carried out in 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 µg denatured fragmented salmon sperm DNA or 6X SSC, 5X Denhardt's reagent, 0.5% SDS, 100 µg denatured fragmented salmon sperm DNA, 50% formamide. The formulas for SSC and Denhardt's solutions are listed in Sambrook *et al.*, *supra*.

Hybridization is conducted by adding the detectable probe to the prehybridization solutions listed above. Where the probe comprises double stranded DNA, it is denatured before addition to the hybridization solution. The filter is contacted with the hybridization solution for a sufficient period of time to allow the probe to hybridize to extended cDNAs or genomic DNAs containing sequences complementary thereto or homologous thereto. For probes over 200 nucleotides in length, the hybridization may be carried out at 15-25°C below the Tm. For shorter probes, such as oligonucleotide probes, the hybridization may be conducted at 15-25°C below the Tm. Preferably, for hybridizations in 6X SSC, the hybridization is conducted at approximately 68°C. Preferably, for hybridizations in 50% formamide containing solutions, the hybridization is conducted at approximately 42°C.

All of the foregoing hybridizations would be considered to be under "stringent" conditions.

Following hybridization, the filter is washed in 2X SSC, 0.1% SDS at room temperature for 15 minutes. The filter is then washed with 0.1X SSC, 0.5% SDS at room temperature for 30 minutes to 1 hour. Thereafter, the solution is washed at the hybridization temperature in 0.1X SSC, 0.5% SDS. A final wash is conducted in 0.1X SSC at room temperature.

cDNAs or genomic DNAs which have hybridized to the probe are identified by autoradiography or other conventional techniques.

2. Obtaining cDNA or Genomic DNA Sequences Having Lower Degrees of Homology to the Labeled Probe

The above procedure may be modified to identify cDNAs or genomic DNAs having decreasing levels of homology to the probe sequence. For example, to obtain cDNAs or genomic DNAs of decreasing homology to the detectable probe, less stringent conditions may be used. For example, the hybridization temperature may be decreased in increments of 5°C from 68°C to 42°C in a hybridization buffer having a sodium concentration of approximately 1M. Following hybridization, the filter may be

washed with 2X SSC, 0.5% SDS at the temperature of hybridization. These conditions are considered to be "moderate" conditions above 50°C and "low" conditions below 50°C.

Alternatively, the hybridization may be carried out in buffers, such as 6X SSC, containing formamide at a temperature of 42°C. In this case, the concentration of formamide in the hybridization buffer may be reduced in 5% increments from 50% to 0% to identify clones having decreasing levels of homology to the probe. Following hybridization, the filter may be washed with 6X SSC, 0.5% SDS at 50°C. These conditions are considered to be "moderate" conditions above 25% formamide and "low" conditions below 25% formamide. cDNAs or genomic DNAs which have hybridized to the probe are identified by autoradiography.

3. Determination of the Degree of Homology between the Obtained cDNAs or Genomic DNAs and 5'ESTs, Consensus Contigated 5'ESTs, or Extended cDNAs or Between the Polypeptides Encoded by the Obtained cDNAs or Genomic DNAs and the Polypeptides Encoded by the 5'ESTs, Consensus Contigated 5'ESTs, or Extended cDNAs

To determine the level of homology between the hybridized cDNA or genomic DNA and the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived, the nucleotide sequences of the hybridized nucleic acid and the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived are compared. The sequences of the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived and the sequences of the cDNA or genomic DNA which hybridized to the detectable probe may be stored on a computer readable medium as described below and compared to one another using any of a variety of algorithms familiar to those skilled in the art, those described below.

To determine the level of homology between the polypeptide encoded by the hybridizing cDNA or genomic DNA and the polypeptide encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived, the polypeptide sequence encoded by the hybridized nucleic acid and the polypeptide sequence encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived are compared. The sequences of the polypeptide encoded by the 5'EST, consensus contigated 5'EST or extended cDNA from which the probe was derived and the polypeptide sequence encoded by the cDNA or genomic DNA which hybridized to the detectable probe may be stored on a computer readable medium as described below and compared to one another using any of a variety of algorithms familiar to those skilled in the art, those described below.

Protein and/or nucleic acid sequence homologies may be evaluated using any of the variety of sequence comparison algorithms and programs known in the art. Such algorithms and programs include, but are by no means limited to, TBLASTN, BLASTP, FASTA, TFASTA, and CLUSTALW (Pearson and Lipman, 1988, *Proc. Natl. Acad. Sci. USA 85(8)*:2444-2448; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Thompson *et al.*, 1994, *Nucleic Acids Res. 22(2)*:4673-4680; Higgins *et al.*, 1996, *Methods Enzymol. 266*:383-402; Altschul *et al.*, 1990, *J. Mol. Biol. 215(3)*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272).

In a particularly preferred embodiment, protein and nucleic acid sequence homologies are evaluated using the Basic Local Alignment Search Tool ("BLAST") which is well known in the art (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad. Sci. USA 87*:2267-2268; Altschul *et al.*, 1990, *J. Mol. Biol. 215*:403-410; Altschul *et al.*, 1993, *Nature Genetics 3*:266-272; Altschul *et al.*, 1997, *Nuc. Acids Res. 25*:3389-3402). In particular, five specific BLAST programs are used to perform the following task:

(1) BLASTP and BLAST3 compare an amino acid query sequence against a protein sequence database;

(2) BLASTN compares a nucleotide query sequence against a nucleotide sequence database;

(3) BLASTX compares the six-frame conceptual translation products of a query nucleotide sequence (both strands) against a protein sequence database;

(4) TBLASTN compares a query protein sequence against a nucleotide sequence database translated in all six reading frames (both strands); and

(5) TBLASTX compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

The BLAST programs identify homologous sequences by identifying similar segments, which are referred to herein as "high-scoring segment pairs," between a query amino or nucleic acid sequence and a test sequence which is preferably obtained from a protein or nucleic acid sequence database. High-scoring segment pairs are preferably identified (*i.e.*, aligned) by means of a scoring matrix, many of which are known in the art. Preferably, the scoring matrix used is the BLOSUM62 matrix (Gonnet *et al.*, 1992, *Science 256*:1443-1445; Henikoff and Henikoff, 1993, *Proteins 17*:49-61). Less preferably, the PAM or PAM250 matrices may also be used (see, *e.g.*, Schwartz and Dayhoff, eds., 1978, *Matrices for Detecting Distance Relationships: Atlas of Protein Sequence and Structure*, Washington: National Biomedical Research Foundation)

The BLAST programs evaluate the statistical significance of all high-scoring segment pairs identified, and preferably selects those segments which satisfy a user-specified threshold of significance, such as a user-specified percent homology. Preferably, the statistical significance of a high-scoring segment pair is evaluated using the statistical significance formula of Karlin (see, *e.g.*, Karlin and Altschul, 1990, *Proc. Natl. Acad: Sci. USA 87*:2267-2268).

The parameters used with the above algorithms may be adapted depending on the sequence length and degree of homology studied. In some embodiments, the parameters may be the default parameters used by the algorithms in the absence of instructions from the user.

In some embodiments, the level of homology between the hybridized nucleic acid and the extended cDNA, 5'EST, or 5' consensus contigated 5'EST from which the probe was derived may be determined using the FASTDB algorithm described in Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990. In such analyses the parameters may be selected as follows: Matrix=Unitary, k-tuple=4,

Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the sequence which hybridizes to the probe, whichever is shorter. Because the FASTDB program does not consider 5' or 3' truncations when calculating homology levels, if the sequence which hybridizes to the probe is truncated relative to the sequence of the extended cDNA, 5'EST, or consensus contigated 5'EST from which the probe was derived the homology level is manually adjusted by calculating the number of nucleotides of the extended cDNA, 5'EST, or consensus contigated 5' EST which are not matched or aligned with the hybridizing sequence, determining the percentage of total nucleotides of the hybridizing sequence which the non-matched or non-aligned nucleotides represent, and subtracting this percentage from the homology level. For example, if the hybridizing sequence is 700 nucleotides in length and the extended cDNA, 5'EST, or consensus contigated 5' EST sequence is 1000 nucleotides in length wherein the first 300 bases at the 5'□end of the extended cDNA, 5'EST, or consensus contigated 5' EST are absent from the hybridizing sequence, and wherein the overlapping 700 nucleotides are identical, the homology level would be adjusted as follows. The non-matched, non-aligned 300 bases represent 30% of the length of the extended cDNA, 5'EST, or consensus contigated 5' EST. If the overlapping 700 nucleotides are 100% identical, th adjusted homology level would be 100-30=70% homology. It should be noted that the preceding adjustments are only made when the non-matched or non-aligned nucleotides are at the 5'or 3'ends. No adjustments are made if the non-matched or non-aligned sequences are internal or under any other conditions.

For example, using the above methods, nucleic acids having at least 95% nucleic acid homology, at least 96% nucleic acid homology, at least 97% nucleic acid homology, at least 98% nucleic acid homology, at least 99% nucleic acid homology, or more than 99% nucleic acid homology to the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived may be obtained and identified. Such nucleic acids may be allelic variants or related nucleic acids from other species. Similarly, by using progressively less stringent hybridization conditions one can obtain and identify nucleic acids having at least 90%, at least 85%, at least 80% or at least 75% homology to the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived.

Using the above methods and algorithms such as FASTA with parameters depending on the sequence length and degree of homology studied, for example the default parameters used by the algorithms in the absence of instructions from the user, one can obtain nucleic acids encoding proteins having at least 99%, at least 98%, at least 97%, at least 96%, at least 95%, at least 90%, at least 85%, at least 80% or at least 75% homology to the protein encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST from which the probe was derived. In some embodiments, the homology levels can be determined using the "default" opening penalty and the "default" gap penalty, and a scoring matrix such as PAM 250 (a standard scoring matrix; see Dayhoff *et al.*, in: Atlas of Protein Sequence and Structure, Vol. 5, Supp. 3 (1978)).

Alternatively, the level of polypeptide homology may be determined using the FASTDB algorithm described by Brutlag *et al.* Comp. App. Biosci. 6:237-245, 1990. In such analyses the parameters may be selected as follows: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=Sequence Length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the homologous sequence, whichever is shorter. If the homologous amino acid sequence is shorter than the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST as a result of an N terminal and/or C terminal deletion the results may be manually corrected as follows. First, the number of amino acid residues of the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST which are not matched or aligned with the homologous sequence is determined. Then, the percentage of the length of the sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST which the non-matched or non-aligned amino acids represent is calculated. This percentage is subtracted from the homology level. For example wherein the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST is 100 amino acids in length and the length of the homologous sequence is 80 amino acids and wherein the amino acid sequence encoded by the extended cDNA or 5'EST is truncated at the N terminal end with respect to the homologous sequence, the homology level is calculated as follows. In the preceding scenario there are 20 non-matched, non-aligned amino acids in the sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST. This represents 20% of the length of the amino acid sequence encoded by the extended cDNA, 5'EST, or consensus contigated 5' EST. If the remaining amino acids are 1005 identical between the two sequences, the homology level would be 100%-20%=80% homology. No adjustments are made if the non-matched or non-aligned sequences are internal or under any other conditions.

In addition to the above described methods, other protocols are available to obtain extended cDNAs using 5' ESTs or consensus contigated 5'ESTs as outlined in the following paragraphs.

Extended cDNAs may be prepared by obtaining mRNA from the tissue, cell, or organism of interest using mRNA preparation procedures utilizing polyA selection procedures or other techniques known to those skilled in the art. A first primer capable of hybridizing to the polyA tail of the mRNA is hybridized to the mRNA and a reverse transcription reaction is performed to generate a first cDNA strand.

The first cDNA strand is hybridized to a second primer containing at least 10 consecutive nucleotides of the sequences of SEQ ID NOs 24-811 and 1600-1622. Preferably, the primer comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides from the sequences of SEQ ID NOs 24-811 and 1600-1622. In some embodiments, the primer comprises more than 30 nucleotides from the sequences of SEQ ID NOs 24-811 and 1600-1622. If it is desired to obtain extended cDNAs containing the full protein coding sequence, including the authentic translation initiation site, the second primer used contains sequences located upstream of the translation initiation site. The second primer is

extended to generate a second cDNA strand complementary to the first cDNA strand. Alternatively, RT-PCR may be performed as described above using primers from both ends of the cDNA to be obtained.

Extended cDNAs containing 5' fragments of the mRNA may be prepared by hybridizing an mRNA comprising the sequences of SEQ ID NOs. 24-811 and 1600-1622 with a primer comprising a complementary to a fragment of an EST-related nucleic acid hybridizing the primer to the mRNAs, and reverse transcribing the hybridized primer to make a first cDNA strand from the mRNAs. Preferably, the primer comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides of the sequences complementary to SEQ ID NOs. 24-811 and 1600-1622.

Thereafter, a second cDNA strand complementary to the first cDNA strand is synthesized. The second cDNA strand may be made by hybridizing a primer complementary to sequences in the first cDNA strand to the first cDNA strand and extending the primer to generate the second cDNA strand.

The double stranded extended cDNAs made using the methods described above are isolated and cloned. The extended cDNAs may be cloned into vectors such as plasmids or viral vectors capable of replicating in an appropriate host cell. For example, the host cell may be a bacterial, mammalian, avian, or insect cell.

Techniques for isolating mRNA, reverse transcribing a primer hybridized to mRNA to generate a first cDNA strand, extending a primer to make a second cDNA strand complementary to the first cDNA strand, isolating the double stranded cDNA and cloning the double stranded cDNA are well known to those skilled in the art and are described *in Current Protocols in Molecular Biology*, John Wiley & Sons, Inc. 1997 and Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989.

Alternatively, other procedures may be used for obtaining full-length cDNAs or extended cDNAs. In one approach, full-length or extended cDNAs are prepared from mRNA and cloned into double stranded phagemids as follows. The cDNA library in the double stranded phagemids is then rendered single stranded by treatment with an endonuclease, such as the Gene II product of the phage F1 and an exonuclease (Chang *et al.*, **Gene 127**:95-8, 1993). A biotinylated oligonucleotide comprising the sequence of a fragment of an EST-related nucleic acid is hybridized to the single stranded phagemids. Preferably, the fragment comprises at least 10, 12, 15, 17, 18, 20, 23, 25, or 28 consecutive nucleotides of the sequences of SEQ ID NOs. 24-811 and 1600-1622.

Hybrids between the biotinylated oligonucleotide and phagemids are isolated by incubating the hybrids with streptavidin coated paramagnetic beads and retrieving the beads with a magnet (Fry *et al.*, *Biotechniques*, 13: 124-131, 1992). Thereafter, the resulting phagemids are released from the beads and converted into double stranded DNA using a primer specific for the 5' EST or consensus contigated 5'EST sequence used to design the biotinylated oligonucleotide. Alternatively, protocols such as the Gene Trapper kit (Gibco BRL) may be used. The resulting double stranded DNA is transformed into bacteria. Extended cDNAs or full length cDNAs containing the 5' EST or consensus contigated 5'EST sequence are identified by colony PCR or colony hybridization.

Using any of the above described methods in section III, a plurality of extended cDNAs containing full-length protein coding sequences or portions of the protein coding sequences may be provided as cDNA libraries for subsequent evaluation of the encoded proteins or use in diagnostic assays as described below.

## EXAMPLE 21

### Full Length cDNAs

The procedures described in Example 19 and 20 were used to obtain extended cDNAs or full length cDNAs derived from 5' ESTs in a variety of tissues. The following list provides a few examples of cDNAs obtained by these means.

Using this procedure, the full length cDNA of SEQ ID NO:1 (internal identification number 58-34-2-E7-FL2) was obtained. This cDNA encodes the signal peptide MWWFQQGLSFLPSALVIWTSA (SEQ ID NO:2) having a von Heijne score of 5.5.

Using this approach, the full length cDNA of SEQ ID NO:3 (internal identification number 48-19-3-G1-FL1) was obtained. This cDNA encodes the signal peptide MKKVLLLITAILAVAVG (SEQ ID NO: 4) having a von Heijne score of 8.2.

The full length cDNA of SEQ ID NO:5 (internal identification number 58-35-2-F10-FL2) was also obtained using this procedure. This cDNA encodes a signal peptide LWLLFFLVTAIHA (SEQ ID NO:6) having a von Heijne score of 10.7.

Furthermore, the polypeptides encoded by the extended or full-length cDNAs may be screened for the presence of known structural or functional motifs or for the presence of signatures, small amino acid sequences which are well conserved amongst the members of a protein family. The results obtained for the polypeptides encoded by a few full-length cDNAs derived from 5'ESTs that were screened for the presence of known protein signatures and motifs using the Proscan software from the GCG package and the Prosite 15.0 database are provided below.

The protein of SEQ ID NO: 8 encoded by the full-length cDNA SEQ ID NO: 7 (internal designation 78-8-3-E6-CL0_1C) and expressed in adult prostate belong to the phosphatidylethanolamine-binding protein from which it exhibits the characteristic PROSITE signature from positions 90 to 112. Proteins from this widespread family, from nematodes to fly, yeast, rodent and primate species, bind hydrophobic ligands such as phospholipids and nucleotides. They are mostly expressed in brain and in testis and are thought to play a role in cell growth and/or maturation, in regulation of the sperm maturation, motility and in membrane remodeling. They may act either through signal transduction or through oxidoreduction reactions (for a review see Schoentgen and Jollès, *FEBS Letters*, 369 :22-26 (1995)). Taken together, these data suggest that the protein of SEQ ID NO: 8 may play a role in cell growth, maturation and in membrane remodeling and/or may be related to male fertility. Thus, these protein may be useful in diagnosing and/or treating cancer, neurodegenerative diseases, and/or disorders related to male fertility and sterility.

The protein of SEQ ID No. 10 encoded by the full-length cDNA SEQ ID N0. 9 (internal designation 108-013-5-O-H9-FLC) shows homologies with a family of lysophospholipases conserved among eukaryotes (yeast, rabbit, rodents and human). In addition, some members of this family exhibit a calcium-independent phospholipase A2 activity (Portilla *et al, J. Am. Soc. Nephro.*, 9 :1178-1186 (1998)). All members of this family exhibit the active site consensus GXSXG motif of carboxylesterases that is also found in the protein of SEQ ID N0. 10 (position 54 to 58). In addition, this protein may be a membrane protein with one transmembrane domain as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, **10** :685-686 (1994)). Taken together, these data suggest that the protein of SEQ ID NO:10 may play a role in fatty acid metabolism, probably as a phospholipase. Thus, this protein or part therein, may be useful in diagnosing and/or treating several disorders including, but not limited to, cancer, diabetes, and neurodegenerative disorders such as Parkinson's and Alzheimer's diseases. It may also be useful in modulating inflammatory responses to infectious agents and/or to suppress graft rejection.

The protein of SEQ ID NO: 12 encoded by the full-length cDNA SEQ ID NO: 11 (internal designation 108-004-5-0-D10-FLC) shows remote homology to a subfamily of beta4-galactosyltransferases widely conserved in animals (human, rodents, cow and chicken). Such enzymes, usually type II membrane proteins located in the endoplasmic reticulum or in the Golgi apparatus, catalyzes the biosynthesis of glycoproteins, glycolipid glycans and lactose. Their characteristic features defined as those of subfamily A in Breton *et al, J. Biochem.*, **123**:1000-1009 (1998) are pretty well conserved in the protein of SEQ ID NO: 12, especially the region I containing the DVD motif (positions 163-165) thought to be involved either in UDP binding or in the catalytic process itself. In addition, the protein of SEQ ID NO: 12 has the typical structure of a type II protein. Indeed, it contains a short 28-amino-acid-long N-terminal tail, a transmembrane segment from positions 29 to 49 and a large 278-amino-acid-long C-terminal tail as predicted by the software TopPred II (Claros and von Heijne, *CABIOS applic. Notes*, **10** :685-686 (1994)). Taken together, these data suggest that the protein of SEQ ID NO: 12 may play a role in the biosynthesis of polysaccharides, and of the carbohydrate moieties of glycoproteins and glycolipids and/or in cell-cell recognition. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer, atherosclerosis, cardiovascular disorders, autoimmune disorders and rheumatic diseases including rheumatoid arthritis.

The protein of SEQ ID NO: 14 encoded by the full-length cDNA SEQ ID NO: 13 (internal designation 108-009-5-0-A2-FLC) shows extensive homology to the bZIP family of transcription factors, and especially to the human luman protein (Lu *et al., Mol. Cell. Biol.*, 17 :5117-5126 (1997))). The match include the whole bZIP domain composed of a basic DNA-binding domain and of a leucine zipper allowing protein dimerization. The basic domain is conserved in the protein of SEQ ID NO: 14 as shown by the characteristic PROSITE signature (positions 224-237) except for a conservative substitution of a glutamic acid with an aspartic acid in position 233. The typical

PROSITE signature for leucine zipper is also present (positions 259 to 280). Taken together, these data suggest that the protein of SEQ ID NO: 14 may bind to DNA, hence regulating gene expression as a transcription factor. Thus, this protein may be useful in diagnosing and/or treating several types of disorders including, but not limited to, cancer.

Bacterial clones containing plasmids containing the full length cDNAs described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the insertion. The PCR product which corresponds to the cDNA insert can then be manipulated using standard cloning techniques familiar to those skilled in the art.

## V. Expression of Proteins or Polypeptides Encoded by EST-related nucleic acids or Fragments thereof

EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, and fragments of positional segments of EST-related nucleic acids may be used to express the polypeptides which they encode. In particular, they may be used to express EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In some embodiments, the EST-related nucleic acids, positional segments of EST-related nucleic acids, and fragments of positional segments of EST-related nucleic acids may be used to express the full polypeptide (*i.e.* the signal peptide and the mature polypeptide) of a secreted protein, the mature protein (*i.e.* the polypeptide generated after cleavage of the signal peptide), or the signal peptide of a secreted protein. If desired, nucleic acids encoding the signal peptide may be used to facilitate secretion of the expressed protein. It will be appreciated that a plurality of EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids may be simultaneously cloned into expression vectors to create an expression library for analysis of the encoded proteins as described below.

### EXAMPLE 22

### Expression of the Proteins Encoded by the Genes Corresponding to the 5'ESTs or Consensus Contigated 5' ESTs

To express their encoded proteins, the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, or fragments of positional segments of EST-related nucleic acids are cloned into a suitable expression vector. In some instances, nucleic acids encoding EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides may be cloned into a suitable expression vector.

In some embodiments, the nucleic acids inserted into the expression vector may comprise the coding sequence of a sequence selected from the group consisting of SEQ ID NOs. 24-811. In other embodiments, the nucleic acids inserted into the expression vector may comprise may comprise the full coding sequence (*i.e.* the nucleotides encoding the signal peptide and the mature polypeptide) of one of SEQ ID Nos. 766-792. In some embodiments, the nucleic acid inserted into the expression vector may comprise the nucleotides of one of the sequences of SEQ ID Nos. 766-792 which encode the mature polypeptide (*i.e.* the nucleotides encoding the polypeptide generated after cleavage of the signal peptide). In further embodiments, the nucleic acids inserted into the expression vector may comprise the nucleotides of 24-728 and 766-792 which encode the signal peptide to facilitate secretion of the expressed protein. The nucleic acids inserted into the expression vectors may also contain sequences upstream of the sequences encoding the signal peptide, such as sequences which regulate expression levels or sequences which confer tissue specific expression.

The nucleic acid inserted into the expression vector may encode a polypeptide comprising the one of the sequences of SEQ ID Nos. 812-1599. In some embodiments, the nucleic acid inserted into the expression vector may encode the full polypeptide sequence (*i.e.* the signal peptide and the mature polypeptide) included in one of SEQ ID Nos. 1554-1580. In other embodiments, the nucleic acid inserted into the expression vector may encode the mature polypeptide (*i.e.* the polypeptide generated after cleavage of the signal peptide) included in one of the sequences of SEQ ID Nos. 1554-1580. In further embodiments, the nucleic acids inserted into the expression vector may encode the signal peptide included in one of the sequences of 812-1516 and 1554-1580.

The nucleic acid encoding the protein or polypeptide to be expressed is operably linked to a promoter in an expression vector using conventional cloning technology. The expression vector may be any of the mammalian, yeast, insect or bacterial expression systems known in the art. Commercially available vectors and expression systems are available from a variety of suppliers including Genetics Institute (Cambridge, MA), Stratagene (La Jolla, California), Promega (Madison, Wisconsin), and Invitrogen (San Diego, California). If desired, to enhance expression and facilitate proper protein folding, the codon context and codon pairing of the sequence may be optimized for the particular expression organism in which the expression vector is introduced, as explained by Hatfield, *et al.*, U.S. Patent No. 5,082,767.

The following is provided as one exemplary method to express the proteins encoded by the nucleic acids described above. In some instances the nucleic acid encoding the protein or polypeptide to

be expressed includes a methionine initiation codon and a polyA signal. If the nucleic acid encoding the polypeptide to be expressed lacks a methionine to serve as the initiation site, an initiating methionine can be introduced next to the first codon of the nucleic acid using conventional techniques. Similarly, if the nucleic acid encoding the protein or polypeptide to be expressed lacks a polyA signal, this sequence can be added to the construct by, for example, splicing out the polyA signal from pSG5 (Stratagene) using BglI and SalI restriction endonuclease enzymes and incorporating it into the mammalian expression vector pXT1 (Stratagene). pXT1 contains the LTRs and a portion of the *gag* gene from Moloney Murine Leukemia Virus. The position of the LTRs in the construct allow efficient stable transfection. The vector includes the Herpes Simplex thymidine kinase promoter and the selectable neomycin gene. The nucleic acid encoding the polypeptide to be expressed is obtained by PCR from the bacterial vector using oligonucleotide primers complementary to the nucleic acid encoding the protein or polypeptide to be expressed and containing restriction endonuclease sequences for Pst I incorporated into the 5'primer and BglII at the 5' end of 3' primer, taking care to ensure that the nucleic acid encoding the protein or polypeptide to be expressed is correctly positioned with respect to the poly A signal. The purified fragment obtained from the resulting PCR reaction is digested with PstI, blunt ended with an exonuclease, digested with Bgl II, purified and ligated to pXT1, now containing a poly A signal and digested with BglII.

The ligated product is transfected into mouse NIH 3T3 cells using Lipofectin (Life Technologies, Inc., Grand Island, New York) under conditions outlined in the product specification. Positive transfectants are selected after growing the transfected cells in 600 µg/ml G418 (Sigma, St. Louis, Missouri).

Alternatively, the nucleic acid encoding the protein or polypeptide to be expressed may be cloned into pED6dpc2. The resulting pED6dpc2 constructs may be transfected into a suitable host cell, such as COS 1 cells. Methotrexate resistant cells are selected and expanded. The expressed protein or polypeptide may be isolated, purified, or enriched as described above.

To confirm expression of the desired protein or polypeptide, the proteins or polypeptides produced by cells containing a vector with a nucleic acid insert encoding the protein or polypeptide are compared to those lacking such an insert. The expressed proteins are detected using techniques familiar to those skilled in the art such as Coomassie blue or silver staining or using antibodies against the protein or polypeptide encoded by the nucleic acid insert. Antibodies capable of specifically recognizing the protein of interest may be generated using synthetic 15-mer peptides having a sequence encoded by the appropriate nucleic acid. The synthetic peptides are injected into mice to generate antibody to the polypeptide encoded by the nucleic acid.

If the proteins or polypeptides encoded by the nucleic acid inserts are secreted, medium prepared from the host cells or organisms containing an expression vector which contains a nucleic acid insert encoding the desired protein or polypeptide is compared to medium prepared from the control cells or organism. The presence of a band in medium from the cells containing the nucleic acid insert which

is absent from preparations from the control cells indicates that the protein or polypeptide encoded by the nucleic acid insert is being expressed and secreted. Generally, the band corresponding to the protein encoded by the nucleic acid insert will have a mobility near that expected based on the number of amino acids in the open reading frame of the nucleic acid insert. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

Alternatively, if the protein expressed from the above expression vectors does not contain sequences directing its secretion, the proteins expressed from host cells containing an expression vector with an insert encoding a secreted protein or portion thereof can be compared to the proteins expressed in control host cells containing the expression vector without an insert. The presence of a band in samples from cells containing the expression vector with an insert which is absent in samples from cells containing the expression vector without an insert indicates that the desired protein or portion thereof is being expressed. Generally, the band will have the mobility expected for the secreted protein or portion thereof. However, the band may have a mobility different than that expected as a result of modifications such as glycosylation, ubiquitination, or enzymatic cleavage.

The expressed protein or polypeptide may be purified, isolated or enriched using a variety of methods. In some methods, the protein or polypeptide may be secreted into the culture medium via a native signal peptide or a heterologous signal peptide operably linked thereto. In some methods, the protein or polypeptide may be linked to a heterologous polypeptide which facilitates its isolation, purification, or enrichment such as a nickel binding polypeptide. The protein or polypeptide may also be obtained by gel electrophoresis, ion exchange chromatography, size chromatography, hplc, salt precipitation, immunoprecipitation, a combination of any of the preceding methods, or any of the isolation, purification, or enrichment techniques familiar to those skilled in the art.

The protein encoded by the nucleic acid insert may also be purified using standard immunochromatography techniques using immunoaffinity chromatography with antibodies directed against the encoded protein or polypeptide as described in more detail below. If antibody production is not possible, the nucleic acid insert encoding the desired protein or polypeptide may be incorporated into expression vectors designed for use in purification schemes employing chimeric polypeptides. In such strategies, the coding sequence of the nucleic acid insert is ligated in frame with the gene encoding the other half of the chimera. The other half of the chimera may be β-globin or a nickel binding polypeptide. A chromatography matrix having antibody to β-globin or nickel attached thereto is then used to purify the chimeric protein. Protease cleavage sites may be engineered between the β-globin gene or the nickel binding polypeptide and the extended cDNA or portion thereof. Thus, the two polypeptides of the chimera may be separated from one another by protease digestion.

One useful expression vector for generating β-globin chimerics is pSG5 (Stratagene), which encodes rabbit β-globin. Intron II of the rabbit β-globin gene facilitates splicing of the expressed transcript, and the polyadenylation signal incorporated into the construct increases the level of

expression. These techniques as described are well known to those skilled in the art of molecular biology. Standard methods are published in methods texts such as Davis *et al.*, (*Basic Methods in Molecular Biology*, L.G. Davis, M.D. Dibner, and J.F. Battey, ed., Elsevier Press, NY, 1986) and many of the methods are available from Stratagene, Life Technologies, Inc., or Promega. Polypeptide may additionally be produced from the construct using *in vitro* translation systems such as the *In vitro* Express$^{TM}$ Translation Kit (Stratagene).

Following expression and purification of the proteins or polypeptides encoded by the nucleic acid inserts, the purified proteins may be tested for the ability to bind to the surface of various cell types as described in Example 23 below. It will be appreciated that a plurality of proteins expressed from these nucleic acid inserts may be included in a panel of proteins to be simultaneously evaluated for the activities specifically described below, as well as other biological roles for which assays for determining activity are available.

## EXAMPLE 23

Analysis of Secreted Proteins to Determine Whether they Bind to the Cell Surface

The EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids, fragments of positional segments of EST-related nucleic acids, nucleic acids encoding the EST-related polypeptides, nucleic acids encoding fragments of the EST-related polypeptides, nucleic acids encoding positional segments of EST-related polypeptides, or nucleic acids encoding fragments of positional segments of EST-related polypeptides are cloned into expression vectors such as those described in Example 22. The encoded proteins or polypeptides are purified, isolated, or enriched as described above. Following purification, isolation, or enrichment, the proteins or polypeptides are labeled using techniques known to those skilled in the art. The labeled proteins or polypeptides are incubated with cells or cell lines derived from a variety of organs or tissues to allow the proteins to bind to any receptor present on the cell surface. Following the incubation, the cells are washed to remove non-specifically bound proteins or polypeptides. The specifically bound labeled proteins or polypeptides are detected by autoradiography. Alternatively, unlabeled proteins or polypeptides may be incubated with the cells and detected with antibodies having a detectable label, such as a fluorescent molecule, attached thereto.

Specificity of cell surface binding may be analyzed by conducting a competition analysis in which various amounts of unlabeled protein or polypeptide are incubated along with the labeled protein or polypeptide. The amount of labeled protein or polypeptide bound to the cell surface decreases as the amount of competitive unlabeled protein or polypeptide increases. As a control, various amounts of an unlabeled protein or polypeptide unrelated to the labeled protein or polypeptide is included in some binding reactions. The amount of labeled protein or polypeptide bound to the cell surface does not decrease in binding reactions containing increasing amounts of unrelated unlabeled protein, indicating that the protein or polypeptide encoded by the nucleic acid binds specifically to the cell surface.

As discussed above, human proteins have been shown to have a number of important physiological effects and, consequently, represent a valuable therapeutic resource. The human proteins or polypeptides made as described above may be evaluated to determine their physiological activities as described below.

## EXAMPLE 24

### Assaying the Expressed Proteins or Polypeptides for Cytokine, Cell Proliferation or Cell Differentiation Activity

As discussed above, some human proteins act as cytokines or may affect cellular proliferation or differentiation. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein or polypeptide of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, $M^+$ (preB $M^+$), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7c and CMK. The proteins or polypeptides prepared as described above may be evaluated for their ability to regulate T cell or thymocyte proliferation in assays such as those described above or in the following references: *Current Protocols in Immunology*, Ed. by J.E. Coligan *et al.*, Greene Publishing Associates and Wiley-Interscience; Takai *et al. J. Immunol.* **137**:3494-3500, 1986., Bertagnolli *et al.* J. Immunol. **145**:1706-1712, 1990., Bertagnolli *et al.*, *Cellular Immunology* **133**:327-341, 1991. Bertagnolli, *et al. J. Immunol.* **149**:3778-3783, 1992; Bowman *et al., J. Immunol.* **152**:1756-1761, 1994.

In addition, numerous assays for cytokine production and/or the proliferation of spleen cells, lymph node cells and thymocytes are known. These include the techniques disclosed in *Current Protocols in Immunology*. J.E. Coligan *et al.* Eds., **1**:3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Schreiber, R.D. In *Current Protocols in Immunology., supra* **1** : 6.8.1-6.8.8.

The proteins or polypeptides prepared as described above may also be assayed for the ability to regulate the proliferation and differentiation of hematopoietic or lymphopoietic cells. Many assays for such activity are familiar to those skilled in the art, including the assays in the following references: Bottomly *et al.*, In *Current Protocols in Immunology., supra*. **1** : 6.3.1-6.3.12,; deVries *et al., J. Exp. Med.* **173**:1205-1211, 1991; Moreau *et al., Nature* **36**:690-692, 1988; Greenberger *et al., Proc. Natl. Acad. Sci. U.S.A.* **80**:2931-2938, 1983; Nordan, R., In *Current Protocols in Immunology., supra*. **1** : 6.6.1-6.6.5; Smith *et al., Proc. Natl. Acad. Sci. U.S.A.* **83**:1857-1861, 1986; Bennett *et al* in *Current Protocols in Immunology supra* **1** : 6.15.1; Ciarletta *et al* In *Current Protocols in Immunology. supra* **1** : 6.13.1.

The proteins or polypeptides prepared as described above may also be assayed for their ability to regulate T-cell responses to antigens. Many assays for such activity are familiar to those skilled in the art, including the assays described in the following references: Chapter 3 (*In vitro* Assays for Mouse

Lymphocyte Function), Chapter 6 (Cytokines and Their Cellular Receptors) and Chapter 7, (Immunologic Studies in Humans) in *Current Protocols in Immunology supra*; Weinberger *et al., Proc. Natl. Acad. Sci. USA* 77:6091-6095, 1980; Weinberger *et al., Eur. J. Immun.* 11:405-411, 1981; Takai *et al., J. Immunol.* 137:3494-3500, 1986; Takai *et al., J. Immunol.* 140:508-512, 1988.

Those proteins or polypeptides which exhibit cytokine, cell proliferation, or cell differentiation activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which induction of cell proliferation or differentiation is beneficial. Alternatively, as described in more detail below, nucleic acids encoding these proteins or polypeptides or nucleic acids regulating the expression of these proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 25

### Assaying the Expressed Proteins or Polypeptides for Activity as Immune System Regulators

The proteins or polypeptides prepared as described above may also be evaluated for their effects as immune regulators. For example, the proteins or polypeptides may be evaluated for their activity to influence thymocyte or splenocyte cytotoxicity. Numerous assays for such activity are familiar to those skilled in the art including the assays described in the following references: Chapter 3 (*In vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic studies in Humans) in *Current Protocols in Immunology* , J.E. Coligan *et al.* Eds, Greene Publishing Associates and Wiley-Interscience; Herrmann *et al., Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann *et al., J. Immunol.* 128:1968-1974, 1982; Handa *et al., J. Immunol.* 135:1564-1572, 1985; Takai *et al., J. Immunol.* 137:3494-3500, 1986; Takai *et al., J. Immunol.* 140:508-512, 1988; Bowman *et al., J. Virology* 61:1992-1998; Bertagnolli *et al. Cell. Immunol.* 133:327-341, 1991; Brown *et al., J. Immunol.* 153:3079-3092, 1994.

The proteins or polypeptides prepared as described above may also be evaluated for their effects on T-cell dependent immunoglobulin responses and isotype switching. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; Mond *et al.* in *Current Protocols in Immunology*, 1 : 3.8.1-3.8.16, *supra*.

The proteins or polypeptides prepared as described above may also be evaluated for their effect on immune effector cells, including their effect on Th1 cells and cytotoxic lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 3 (*In vitro* Assays for Mouse Lymphocyte Function 3.1-3.19) and Chapter 7 (Immunologic Studies in Humans) in *Current Protocols in Immunology, supra*; Takai *et al., J. Immunol.* 137:3494-3500, 1986; Takai *et al., J. Immunol.* 140:508-512, 1988; Bertagnolli *et al., J. Immunol.* 149:3778-3783, 1992.

The proteins or polypeptides prepared as described above may also be evaluated for their effect on dendritic cell mediated activation of naive T-cells. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Guery *et al.*, *J. Immunol.* 134:536-544, 1995; Inaba *et al.*, *J. Exp. Med.* 173:549-559, 1991; Macatonia *et al.*, *J. Immunol.* 154:5071-5079, 1995; Porgador *et al J. Exp. Med* 182:255-260, 1995; Nair *et al.*, *J. Virol.* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al J. Exp. Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba *et al.*, *J. Exp. Med* 172:631-640, 1990.

The proteins or polypeptides prepared as described above may also be evaluated for their influence on the lifetime of lymphocytes. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res.* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J. Immunol.* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Int. J. Oncol.* 1:639-648, 1992.

The proteins or polypeptides prepared as described above may also be evaluated for their influence on early steps of T-cell commitment and development. Numerous assays for such activity are familiar to those skilled in the art, including without limitation the assays disclosed in the following references: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell. Immunol.* 155:111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc. Nat. Acad Sci. USA* 88:7548-7551, 1991.

Those proteins or polypeptides which exhibit activity as immune system regulators activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of immune activity is beneficial. For example, the protein or polypeptide may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using the protein or polypeptide including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., plamodium. and various fungal infections such as candidiasis. Of course, in this regard, a protein or polypeptide may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Alternatively, the proteins or polypeptides prepared as described above may be used in treatment of autoimmune disorders including, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein or polypeptide may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic

asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using the protein or polypeptide.

Using the proteins or polypeptides of the invention it may also be possible to regulate immune responses either up or down. Down regulation may involve inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T-cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active non-antigen-specific process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after the end of exposure to the tolerizing agent. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions, such as, for example, B7 costimulation), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation, can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792 (1992) and Turka *et al.*, *Proc. Natl. Acad. Sci USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed.,

*Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor/ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which potentially involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/pr/pr mice or NZB hybrid mice, murine autoimmuno collagen arthritis, diabetes mellitus in OD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may involve either enhancing an existing immune response or eliciting an initial immune response as shown by the following examples. For instance, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory form of B lymphocyte antigens systemically.

Alternatively, antiviral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing the proteins or polypeptides described above or together with a stimulatory form of the protein or polypeptide and reintroducing the *in vitro* primed T cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to T cells *in vivo*, thereby activating the T cells.

In another application, upregulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with one of the above-described nucleic acids encoding a protein or polypeptide can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor

cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the protein or polypeptide encoded by the nucleic acids described above having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules can be transfected with nucleic acids encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I $\alpha$ chain and $\beta_2$ microglobulin or an MHC class II $\alpha$ chain and an MHC class II $\beta$ chain to thereby express MHC class I or MHC class II proteins on the cell surface, respectively. Expression of the appropriate MHC class I or class II molecules in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a nucleic acid encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a protein or polypeptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject. Alternatively, as described in more detail below, nucleic acids encoding these immune system regulator proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

## EXAMPLE 26

### Assaying the Expressed Proteins or Polypeptides for Hematopoiesis Regulating Activity

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their hematopoiesis regulating activity. For example, the effect of the proteins or polypeptides on embryonic stem cell differentiation may be evaluated. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Johansson *et al. Cell. Biol.* **15**:141-151, 1995; Keller *et al., Mol. Cell. Biol.* **13**:473-486, 1993; McClanahan *et al., Blood* 81:2903-2915, 1993.

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their influence on the lifetime of stem cells and stem cell differentiation. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Freshney, M.G. Methylcellulose Colony Forming Assays, in Culture of Hematopoietic Cells. R.I. Freshney, *et al.* Eds. pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama *et al., Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; McNiece, I.K. and Briddell, R.A. Primitive Hematopoietic Colony Forming Cells with High Proliferative Potential, in Culture of Hematopoietic Cells. *supra*;

Neben *et al.*, *Experimental Hematology* 22:353-359, 1994; Ploemacher, R.E. Cobblestone Area Forming Cell Assay, In Culture of Hematopoietic Cells. *supra*; Spooncer, E., Dexter, M. and Allen, T. Long Term Bone Marrow Cultures in the Presence of Stromal Cells, in Culture of Hematopoietic Cells *supra*; and Sutherland, H.J. Long Term Culture Initiating Cell Assay, in Culture of Hematopoietic Cells. *supra*..

Those proteins or polypeptides which exhibit hematopoiesis regulatory activity may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of hematopoeisis is beneficial. For example, a protein or polypeptide of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantion, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy. Alternatively, as described in more detail below, nucleic acids encoding these proteins or polypeptides or nucleic acids regulating the expression of these proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

## EXAMPLE 27

### Assaying the Expressed Proteins or Polypeptides for Regulation of Tissue Growth

The proteins or polypeptides encoded by the nucleic acids described above may also be evaluated for their effect on tissue growth. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in International Patent Publication No. WO95/16035, International Patent Publication No. WO95/05846 and International Patent Publication No. WO91/07491.

Assays for wound healing activity include, without limitation, those described in: Winter, *Epidermal Wound Healing*, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Those proteins or polypeptides which are involved in the regulation of tissue growth may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of tissue growth is beneficial. For example, a protein or polypeptide may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein or polypeptide encoded by the nucleic acids described above which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein or polypeptide of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone synthesis induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein or polypeptide of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the proteins or polypeptides encoded by the nucleic acids described above is tendon/ligament formation. A protein or polypeptide encoded by the nucleic acids described above, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a protein or polypeptide of the present invention contributes to the repair of tendon or ligaments defects of congenital, traumatic or other origin and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The proteins or polypeptides of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return *in vivo* to effect tissue repair. The proteins or polypeptides of the

invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The therapeutic compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The proteins or polypeptides of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.*, for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein or polypeptide may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein or polypeptide of the invention.

Proteins or polypeptides of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein or polypeptide of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium) muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to generate. A protein or polypeptide of the invention may also exhibit angiogenic activity.

A protein or polypeptide of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein or polypeptide of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

Alternatively, as described in more detail below, nucleic acids encoding tissue growth regulating activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins as desired.

## EXAMPLE 28

### Assaying the Expressed Proteins or Polypeptides for Regulation of Reproductive Hormones

The proteins or polypeptides of the present invention may also be evaluated for their ability to regulate reproductive hormones, such as follicle stimulating hormone. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Vale *et al., Endocrinol.* 91:562-572, 1972; Ling *et al., Nature* 321:779-782, 1986; Vale *et al., Nature* 321:776-779, 1986; Mason *et al., Nature* 318:659-663, 1985; Forage *et al., Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986. Chapter 6.12 in *Current Protocols in Immunology*, J.E. Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience ; Taub *et al. J. Clin. Invest.* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al. Eur. J. Immunol.* 25:1744-1748; Gruber *et al. J. Immunol.* 152:5860-5867, 1994; Johnston *et al., J Immunol.* 153:1762-1768, 1994.

Those proteins or polypeptides which exhibit activity as reproductive hormones or regulators of cell movement may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of reproductive hormones are beneficial. For example, a protein or polypeptide may exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of FSH. Thus, a protein or polypeptide of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein or polypeptide of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-B group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein or polypeptide of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

Alternatively, as described in more detail below, nucleic acids encoding reproductive hormone regulating activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 29

Assaying the Expressed Proteins or Polypeptides For Chemotactic/Chemokinetic Activity

The proteins or polypeptides of the present invention may also be evaluated for chemotactic/chemokinetic activity. For example, a protein or polypeptide of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins or polypeptides can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins or

polypeptides provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or polypeptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or polypeptide has the ability to directly stimulate directed movement of cells. Whether a particular protein or polypeptide has chemotactic activity for a population of cells can be readily determined by employing such protein or polypeptide in any known assay for cell chemotaxis.

The activity of a protein or polypeptide of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins or polypeptides that induce or prevent chemotaxis) consist of assays that measure the ability of a protein or polypeptide to induce the migration of cells across a membrane as well as the ability of a protein or polypeptide to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience,Chapter **6.12**: 6.12.1-6.12.28; Taub *et al. J. Clin. Invest.* 95:1370-1376, 1995; Lind *et al. APMIS* **103**:140-146, 1995; Mueller *et al., Eur. J. Immunol.* **25**:1744-1748; Gruber *et al. J. Immunol.* **152**:5860-5867, 1994; Johnston *et al. J. Immunol.*, **153**:1762-1768, 1994.

## EXAMPLE 30

Assaying the Expressed Proteins or Polypeptides for Regulation of Blood Clotting

The proteins or polypeptides of the present invention may also be evaluated for their effects on blood clotting. Numerous assays for such activity are familiar to those skilled in the art, including the assays disclosed in the following references: Linet *et al., J. Clin. Pharmacol.* **26**:131-140, 1986; Burdick *et al., Thrombosis Res.* **45**:413-419, 1987; Humphrey *et al., Fibrinolysis* **5**:71-79 (1991); Schaub, *Prostaglandins* **35**:467-474, 1988.

Those proteins or polypeptides which are involved in the regulation of blood clotting may then be formulated as pharmaceuticals and used to treat clinical conditions in which regulation of blood clotting is beneficial. For example, a protein or polypeptide of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein or polypeptide is expected to be useful in treatment of various coagulations disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein or polypeptide of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as infarction of cardiac and central nervous system vessels (e.g., stroke)). Alternatively, as described in

more detail below, nucleic acids encoding blood clotting activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 31

### Assaying the Expressed Proteins or Polypeptides for Involvement in Receptor/Ligand Interactions

The proteins or polypeptides of the present invention may also be evaluated for their involvement in receptor/ligand interactions. Numerous assays for such involvement are familiar to those skilled in the art, including the assays disclosed in the following references: Chapter 7. 7.28.1-7.28.22) in *Current Protocols in Immunology*, J.E. Coligan *et al.* Eds. Greene Publishing Associates and Wiley-Interscience; Takai *et al., Proc. Natl. Acad. Sci. USA* **84**:6864-6868, 1987; Bierer *et al., J. Exp. Med.* 168:1145-1156, 1988; Rosenstein *et al., J. Exp. Med.* 169:149-160, 1989; Stoltenborg *et al., J. Immunol. Methods* 175:59-68, 1994; Stitt *et al., Cell* 80:661-670, 1995; Gyuris *et al., Cell* 75:791-803, 1993.

For example, the proteins or polypeptides of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein or polypeptide of the present invention (including, without limitation, fragments of receptors and ligands) may be useful as inhibitors of receptor/ligand interactions. Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides involved in receptor/ligand interactions or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 32

### Assaying the Proteins or Polypeptides for Anti-Inflammatory Activity

The proteins or polypeptides of the present invention may also be evaluated for anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins or polypeptides exhibiting such activities can be used to treat inflammatory conditions

including chronic or acute conditions, including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome), ischemia-reperfusioninury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine- or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins or polypeptides of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material. Alternatively, as described in more detail below, nucleic acids encoding anti-inflammatory activity proteins or polypeptides or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 33

Assaying the Expressed Proteins or Polypeptides for Tumor Inhibition Activity

The proteins or polypeptides of the present invention may also be evaluated for tumor inhibition activity. In addition to the activities described above for immunological treatment or prevention of tumors, a protein or polypeptide of the invention may exhibit other anti-tumor activities. A protein or polypeptide may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein or polypeptide may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.. Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides with tumor inhibition activity or nucleic acids regulating the expression of such proteins or polypeptides may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

A protein or polypeptide of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or climination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem

cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein. Alternatively, as described in more detail below, nucleic acids encoding proteins or polypeptides involved in any of the above mentioned activities or nucleic acids regulating the expression of such proteins may be introduced into appropriate host cells to increase or decrease the expression of the proteins or polypeptides as desired.

## EXAMPLE 34

### Identification of Proteins or Polypeptides which Interact with Proteins or Polypeptides of the Present Invention

Proteins or polypeptides which interact with the proteins or polypeptides of the present invention, such as receptor proteins, may be identified using two hybrid systems such as the Matchmaker Two Hybrid System 2 (Catalog No. K1604-1, Clontech). As described in the manual accompanying the kit, nucleic acids encoding the proteins or polypeptides of the present invention, are inserted into an expression vector such that they are in frame with DNA encoding the DNA binding domain of the yeast transcriptional activator GAL4. cDNAs in a cDNA library which encode proteins or polypeptides which might interact with the proteins or polypeptides of the present invention are inserted into a second expression vector such that they are in frame with DNA encoding the activation domain of GAL4. The two expression plasmids are transformed into yeast and the yeast are plated on selection medium which selects for expression of selectable markers on each of the expression vectors as well as GAL4 dependent expression of the HIS3 gene. Transformants capable of growing on medium lacking histidine are screened for GAL4 dependent lacZ expression. Those cells which are positive in both the histidine selection and the lacZ assay contain plasmids encoding proteins or polypeptides which interact with the proteins or polypeptides of the present invention.

Alternatively, the system described in Lustig *et al.*, *Methods in Enzymology* **283**: 83-99 (1997) may be used for identifying molecules which interact with the proteins or polypeptides of the present invention. In such systems, *in vitro* transcription reactions are performed on a pool of vectors containing nucleic acid inserts which encode the proteins or polypeptides of the present invention. The nucleic acid inserts are cloned downstream of a promoter which drives *in vitro* transcription. The resulting pools of mRNAs are introduced into *Xenopus laevis* oocytes. The oocytes are then assayed for a desired activity.

Alternatively, the pooled *in vitro* transcription products produced as described above may be translated *in vitro*. The pooled *in vitro* translation products can be assayed for a desired activity or for interaction with a known protein or polypeptide.

Proteins, polypeptides or other molecules interacting with proteins or polypeptides of the present invention can be found by a variety of additional techniques. In one method, affinity columns containing the protein or polypeptide of the present invention can be constructed. In some versions, of this method the affinity column contains chimeric proteins in which the protein or polypeptide of the present invention is fused to glutathione S-transferase. A mixture of cellular proteins or pool of expressed proteins as described above and is applied to the affinity column. Molecules interacting with the protein or polypeptide attached to the column can then be isolated and analyzed on 2-D electrophoresis gel as described in Ramunsen *et al. Electrophoresis*, 18, 588-598 (1997). Alternatively, the molecules retained on the affinity column can be purified by electrophoresis based methods and sequenced. The same method can be used to isolate antibodies, to screen phage display products, or to screen phage display human antibodies.

Molecules interacting with the proteins or polypeptides of the present invention can also be screened by using an Optical Biosensor as described in Edwards & Leatherbarrow, *Analytical Biochemistry*, 246, 1-6 (1997). The main advantage of the method is that it allows the determination of the association rate between the protein or polypeptide and other interacting molecules. Thus, it is possible to specifically select interacting molecules with a high or low association rate. Typically a target molecule is linked to the sensor surface (through a carboxymethl dextran matrix) and a sample of test molecules is placed in contact with the target molecules. The binding of a test molecule to the target molecule causes a change in the refractive index and/ or thickness. This change is detected by the Biosensor provided it occurs in the evanescent field (which extends a few hundred nanometers from the sensor surface). In these screening assays, the target molecule can be one of the proteins or polypeptides of the present invention and the test sample can be a collection of proteins, polypeptides or other molecules extracted from tissues or cells, a pool of expressed proteins, combinatorial peptide and/ or chemical libraries, or phage displayed peptides. The tissues or cells from which the test molecules are extracted can originate from any species.

In other methods, a target protein or polypeptide is immobilized and the test population is a collection of unique proteins or polypeptides of the present invention.

To study the interaction of the proteins or polypeptides of the present invention with drugs, the microdialysis coupled to HPLC method described by Wang *et al.*, *Chromatographia*, 44, 205-208(1997) or the affinity capillary electrophoresis method described by Busch *et al.*, *J. Chromatogr.* 777:311-328 (1997)can be used.

The system described in U.S. Patent No. 5,654,150 may also be used to identify molecules which interact with the proteins or polypeptides of the present invention. In this system, pools of nucleic acids encoding the proteins or polypeptides of the present invention are transcribed and translated *in vitro* and the reaction products are assayed for interaction with a known polypeptide or antibody.

It will be appreciated by those skilled in the art that the proteins or polypeptides of the present invention may be assayed for numerous activities in addition to those specifically enumerated above.

For example, the expressed proteins or polypeptides may be evaluated for applications involving control and regulation of inflammation, tumor proliferation or metastasis, infection, or other clinical conditions. In addition, the proteins or polypeptides may be useful as nutritional agents or cosmetic agents.

The proteins or polypeptides of the present invention may be used to generate antibodies capable of specifically binding to the proteins or polypeptides of the present invention. The antibodies may be monoclonal antibodies or polyclonal antibodies. As used herein, "antibody" refers to a polypeptide or group of polypeptides which are comprised of at least one binding domain, where a binding domain is formed from the folding of variable domains of an antibody molecule to form three-dimensional binding spaces with an internal surface shape and charge distribution complementary to the features of an antigenic determinant of an antigen., which allows an immunological reaction with the antigen. Antibodies include recombinant proteins comprising the binding domains, as wells as fragments, including Fab, Fab', $F(ab)_2$, and $F(ab')_2$ fragments.

As used herein, an "antigenic determinant" is the portion of an antigen molecule, that determines the specificity of the antigen-antibody reaction. An "epitope" refers to an antigenic determinant of a polypeptide. An epitope can comprise as few as 3 amino acids in a spatial conformation which is unique to the epitope. Generally an epitope consists of at least 6 such amino acids, and more usually at least 8-10 such amino acids. Methods for determining the amino acids which make up an epitope include x-ray crystallography, 2-dimensional nuclear magnetic resonance, and epitope mapping e.g. the Pepscan method described by H. Mario Geysen *et al.* 1984. Proc. Natl. Acad. Sci. U.S.A. 81:3998-4002; PCT Publication No. WO 84/03564; and PCT Publication No. WO 84/03506.

In some embodiments, the antibodies may be capable of specifically binding to a protein or polypeptide encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In some embodiments, the antibody may be capable of binding an antigenic determinant or an epitope in a protein or polypeptide encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

In other embodiments, the antibodies may be capable of specifically binding to an EST-related polypeptide, fragment of an EST-related polypeptide, positional segment of an EST-related polypeptide or fragment of a positional segment of an EST-related polypeptide. In some embodiments, the antibody may be capable of binding an antigenic determinant or an epitope in an EST-related polypeptide, fragment of an EST-related polypeptide, positional segment of an EST-related polypeptide or fragment of a positional segment of an EST-related polypeptide.

In the case of secreted proteins, the antibodies may be capable of binding a full-length protein encoded by a nucleic acid of the present invention, a mature protein (*i.e.* the protein generated by

cleavage of the signal peptide) encoded by a nucleic acid of the present invention, or a signal peptide encoded by a nucleic acid of the present invention.

## EXAMPLE 35

Production of an Antibody to a Human Polypeptide or Protein

The above described EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or nucleic acids encoding EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides are operably linked to promoters and introduced into cells as described above.

In the case of secreted proteins, nucleic acids encoding the full protein (*i.e.* the mature protein and the signal peptide), nucleic acids encoding the mature protein (*i.e.* the protein generated by cleavage of the signal peptide), or nucleic acids encoding the signal peptide are operably linked to promoters and introduced into cells as described above.

The encoded proteins or polypeptides are then substantially purified or isolated as described above. The concentration of protein in the final preparation is adjusted, for example, by concentration on an Amicon filter device, to the level of a few μg/ml. Monoclonal or polyclonal antibody to the protein or polypeptide can then be prepared as follows:

1. Monoclonal Antibody Production by Hybridoma Fusion

Monoclonal antibody to epitopes of any of the proteins or polypeptides identified and isolated as described can be prepared from murine hybridomas according to the classical method of Kohler, and Milstein, *Nature* 256:495 (1975) or derivative methods thereof. Briefly, a mouse is repetitively inoculated with a few micrograms of the selected protein or peptides derived therefrom over a period of a few weeks. The mouse is then sacrificed, and the antibody producing cells of the spleen isolated. The spleen cells are fused by means of polyethylene glycol with mouse myeloma cells, and the excess unfused cells destroyed by growth of the system on selective media comprising aminopterin (HAT media). The successfully fused cells are diluted and aliquots of the dilution placed in wells of a microtiter plate where growth of the culture is continued. Antibody-producing clones are identified by detection of antibody in the supernatant fluid of the wells by immunoassay procedures, such as Elisa, as originally described by Engvall, *Meth. Enzymol.* 70:419 (1980). Selected positive clones can be expanded and their monoclonal antibody product harvested for use. Detailed procedures for monoclonal antibody production are described in Davis, L. *et al.* in *Basic Methods in Molecular Biology* Elsevier, New York. Section 21-2.

2. Polyclonal Antibody Production by Immunization

Polyclonal antiserum containing antibodies to heterogenous epitopes of a single protein or polypeptide can be prepared by immunizing suitable animals with the expressed protein or peptides derived therefrom, which can be unmodified or modified to enhance immunogenicity. Effective

polyclonal antibody production is affected by many factors related both to the antigen and the host species. For example, small molecules tend to be less immunogenic than others and may require the use of carriers and adjuvant. Also, host animals response vary depending on site of inoculations and doses, with both inadequate or excessive doses of antigen resulting in low titer antisera. Small doses (ng level) of antigen administered at multiple intradermal sites appears to be most reliable. An effective immunization protocol for rabbits can be found in Vaitukaitis. *et al.J. Clin. Endocrinol. Metab.* 33:988-991 (1971).

Booster injections can be given at regular intervals, and antiserum harvested when antibody titer thereof, as determined semi-quantitatively, for example, by double immunodiffusion in agar against known concentrations of the antigen, begins to fall. See, for example, Ouchterlony, *et al.*, Chap. 19 in: *Handbook of Experimental Immunology* D. Wier (ed) Blackwell (1973). Plateau concentration of antibody is usually in the range of 0.1 to 0.2 mg/ml of serum (about 12 μM). Affinity of the antisera for the antigen is determined by preparing competitive binding curves, as described, for example, by Fisher, D., Chap. 42 in: *Manual of Clinical Immunology*, 2d Ed. (Rose and Friedman, Eds.) Amer. Soc. For Microbiol., Washington, D.C. (1980).

Antibody preparations prepared according to either of the above protocols are useful in a variety of contexts. In particular, the antibodies may be used in immunoaffinity chromatography techniques such as those described below to facilitate large scale isolation, purification, or enrichment of the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or for the isolation, purification or enrichment of EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

In the case of secreted proteins, the antibodies may be used for the isolation, purification, or enrichment of the full protein (*i.e.* the mature protein and the signal peptide), the mature protein (*i.e.* the protein generated by cleavage of the signal peptide), or the signal peptide are operably linked to promoters and introduced into cells as described above.

Additionally, the antibodies may be used in immunoaffinity chromatography techniques such as those described below to isolate, purify, or enrich polypeptides which have been linked to the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or to isolate, purify, or enrich EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

The antibodies may also be used to determine the cellular localization of polypeptides encoded by the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the cellular

localization of EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

In addition, the antibodies may also be used to determine the cellular localization of polypeptides which have been linked to the proteins or polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or polypeptides which have been linked to EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides.

The antibodies may also be used in quantitative immunoassays which determine concentrations of antigen-bearing substances in biological samples; they may also used semi-quantitatively or qualitatively to identify the presence of antigen in a biological sample or to identify the type of tissue present in a biological sample. The antibodies may also be used in therapeutic compositions for killing cells expressing the protein or reducing the levels of the protein in the body.

**VI. Use of 5'ESTs or Consensus Contigated 5' ESTs or Sequences Obtainable Therefrom or Portions Thereof as Reagents**

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used as reagents in isolation procedures, diagnostic assays, and forensic procedures. For example, sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids, may be detectably labeled and used as probes to isolate other sequences capable of hybridizing to them. In addition, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to design PCR primers to be used in isolation, diagnostic, or forensic procedures.

1. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in isolation, diagnostic and forensic procedures

**EXAMPLE 36**

Preparation of PCR Primers and Amplification of DNA

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to prepare PCR primers for a variety of applications, including isolation procedures for cloning nucleic acids capable of hybridizing to such sequences, diagnostic techniques and forensic techniques. In some embodiments, the PCR primers at least 10, 15, 18, 20, 23, 25, 28, 30, 40, or 50 nucleotides in length. In some embodiments, the PCR primers may be more than 30 bases in length. It is preferred that the primer pairs have approximately the same G/C ratio, so that melting temperatures are approximately the same. A variety of PCR techniques are familiar to those skilled in the art. For a review of PCR technology, see Molecular Cloning to

Genetic Engineering White, B.A. Ed. *in Methods in Molecular Biology* 67: Humana Press, Totowa 1997. In each of these PCR procedures, PCR primers on either side of the nucleic acid sequences to be amplified are added to a suitably prepared nucleic acid sample along with dNTPs and a thermostable polymerase such as Taq polymerase, Pfu polymerase, or Vent polymerase. The nucleic acid in the sample is denatured and the PCR primers are specifically hybridized to complementary nucleic acid sequences in the sample. The hybridized primers are extended. Thereafter, another cycle of denaturation, hybridization, and extension is initiated. The cycles are repeated multiple times to produce an amplified fragment containing the nucleic acid sequence between the primer sites.

## EXAMPLE 37

### Use of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids as probes

Probes derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be labeled with detectable labels familiar to those skilled in the art, including radioisotopes and non-radioactive labels, to provide a detectable probe. The detectable probe may be single stranded or double stranded and may be made using techniques known in the art, including *in vitro* transcription, nick translation, or kinase reactions. A nucleic acid sample containing a sequence capable of hybridizing to the labeled probe is contacted with the labeled probe. If the nucleic acid in the sample is double stranded, it may be denatured prior to contacting the probe. In some applications, the nucleic acid sample may be immobilized on a surface such as a nitrocellulose or nylon membrane. The nucleic acid sample may comprise nucleic acids obtained from a variety of sources, including genomic DNA, cDNA libraries, RNA, or tissue samples.

Procedures used to detect the presence of nucleic acids capable of hybridizing to the detectable probe include well known techniques such as Southern blotting, Northern blotting, dot blotting, colony hybridization, and plaque hybridization. In some applications, the nucleic acid capable of hybridizing to the labeled probe may be cloned into vectors such as expression vectors, sequencing vectors, or *in vitro* transcription vectors to facilitate the characterization and expression of the hybridizing nucleic acids in the sample. For example, such techniques may be used to isolate and clone sequences in a genomic library or cDNA library which are capable of hybridizing to the detectable probe as described in Example 20 above.

PCR primers made as described in Example 36 above may be used in forensic analyses, such as the DNA fingerprinting techniques described in Examples 38-42 below. Such analyses may utilize detectable probes or primers based on the sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

## EXAMPLE 38

### Forensic Matching by DNA Sequencing

In one exemplary method, DNA samples are isolated from forensic specimens of, for example, hair, semen, blood or skin cells by conventional methods. A panel of PCR primers based on a number of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is then utilized in accordance with Example 36 to amplify DNA of approximately 100-200 bases in length from the forensic specimen. Corresponding sequences are obtained from a test subject. Each of these identification DNAs is then sequenced using standard techniques, and a simple database comparison determines the differences, if any, between the sequences from the subject and those from the sample. Statistically significant differences between the suspect's DNA sequences and those from the sample conclusively prove a lack of identity. This lack of identity can be proven, for example, with only one sequence. Identity, on the other hand, should be demonstrated with a large number of sequences, all matching. Preferably, a minimum of 50 statistically identical sequences of 100 bases in length are used to prove identity between the suspect and the sample.

## EXAMPLE 39

### Positive Identification by DNA Sequencing

The technique outlined in the previous example may also be used on a larger scale to provide a unique fingerprint-type identification of any individual. In this technique, primers are prepared from a large number of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Preferably, 20 to 50 different primers are used. These primers are used to obtain a corresponding number of PCR-generated DNA segments from the individual in question in accordance with Example 34. Each of these DNA segments is sequenced, using the methods set forth in Example 36. The database of sequences generated through this procedure uniquely identifies the individual from whom the sequences were obtained. The same panel of primers may then be used at any later time to absolutely correlate tissue or other biological specimen with that individual.

## EXAMPLE 40

### Southern Blot Forensic Identification

The procedure of Example 38 is repeated to obtain a panel of at least 10 amplified sequences from an individual and a specimen. Preferably, the panel contains at least 50 amplified sequences. More preferably, the panel contains 100 amplified sequences. In some embodiments, the panel contains 200 amplified sequences. This PCR-generated DNA is then digested with one or a combination of, preferably, four base specific restriction enzymes. Such enzymes are commercially available and known to those of skill in the art. After digestion, the resultant gene fragments are size separated in multiple duplicate wells on an agarose gel and transferred to nitrocellulose using Southern blotting techniques well known to those with skill in the art. For a review of Southern blotting see Davis *et al.* (Basic Methods in Molecular Biology, 1986, Elsevier Press. pp 62-65).

A panel of probes based on the sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are radioactively or colorimetrically labeled using methods known in the art, such as nick translation or end labeling, and hybridized to the Southern blot using techniques known in the art (Davis *et al.*, supra). Preferably, the probe is at least 10, 12, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 nucleotides in length. Preferably, the probes are at least 10, 12, 15, 18, 20, 25, 28, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400 or 500 nucleotides in length. In some embodiments, the probes are oligonucleotides which are 40 nucleotides in length or less.

Preferably, at least 5 to 10 of these labeled probes are used, and more preferably at least about 20 or 30 are used to provide a unique pattern. The resultant bands appearing from the hybridization of a large sample of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids will be a unique identifier. Since the restriction enzyme cleavage will be different for every individual, the band pattern on the Southern blot will also be unique. Increasing the number of probes will provide a statistically higher level of confidence in the identification since there will be an increased number of sets of bands used for identification.

## EXAMPLE 41

### Dot Blot Identification Procedure

Another technique for identifying individuals using the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids disclosed herein utilizes a dot blot hybridization technique.

Genomic DNA is isolated from nuclei of subject to be identified. Probes are prepared that correspond to at least 10, preferably 50 sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The probes are used to hybridize to the genomic DNA through conditions known to those in the art. The oligonucleotides are end labeled with $P^{32}$ using polynucleotide kinase (Pharmacia). Dot Blots are created by spotting the genomic DNA onto nitrocellulose or the like using a vacuum dot blot manifold (BioRad, Richmond California). The nitrocellulose filter containing the genomic sequences is baked or UV linked to the filter, prehybridized and hybridized with labeled probe using techniques known in the art (Davis *et al.*, *supra*). The $^{32}P$ labeled DNA fragments are sequentially hybridized with successively stringent conditions to detect minimal differences between the 30 bp sequence and the DNA. Tetramethylammonium chloride is useful for identifying clones containing small numbers of nucleotide mismatches (Wood *et al., Proc. Natl. Acad. Sci. USA* 82(6):1585-1588 (1985)). A unique pattern of dots distinguishes one individual from another individual.

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids can be used as probes in the following alternative

fingerprinting technique. In some embodiments, the probes are oligonucleotides which are 40 nucleotides in length or less.

Preferably, a plurality of probes having sequences from different EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are used in the alternative fingerprinting technique. Example 42 below provides a representative alternative fingerprinting procedure in which the probes are derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

## EXAMPLE 42

Alternative "Fingerprint" Identification Technique

Oligonucleotides are prepared from a large number, e.g. 50, 100, or 200, EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids using commercially available oligonucleotide services such as Genset, Paris, France. Preferably, the oligonucleotides are at least 10, 15, 18, 20, 23, 25 28, or 30 nucleotides in length. However, in some embodiments, the oligonucleotides may be more than 40, 50, 60 or 70 nucleotides in length.

Cell samples from the test subject are processed for DNA using techniques well known to those with skill in the art. The nucleic acid is digested with restriction enzymes such as EcoRI and XbaI. Following digestion, samples are applied to wells for electrophoresis. The procedure, as known in the art, may be modified to accommodate polyacrylamide electrophoresis, however in this example, samples containing 5 ug of DNA are loaded into wells and separated on 0.8% agarose gels. The gels are transferred onto nitrocellulose using standard Southern blotting techniques.

10 ng of each of the oligonucleotides are pooled and end-labeled with $P^{32}$. The nitrocellulose is prehybridized with blocking solution and hybridized with the labeled probes. Following hybridization and washing, the nitrocellulose filter is exposed to X-Omat AR X-ray film. The resulting hybridization pattern will be unique for each individual.

It is additionally contemplated within this example that the number of probe sequences used can be varied for additional accuracy or clarity.

In addition to their applications in forensics and identification, EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be mapped to their chromosomal locations. Example 41 below describes radiation hybrid (RH) mapping of human chromosomal regions using EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Example 42 below describes a representative procedure for mapping EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to their locations on human chromosomes. Example 43 below describes mapping of

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids on metaphase chromosomes by Fluorescence In Situ Hybridization (FISH).

2. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in Chromosome Mapping

**EXAMPLE 43**

Radiation hybrid mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to the human genome

Radiation hybrid (RH) mapping is a somatic cell genetic approach that can be used for high resolution mapping of the human genome. In this approach, cell lines containing one or more human chromosomes are lethally irradiated, breaking each chromosome into fragments whose size depends on the radiation dose. These fragments are rescued by fusion with cultured rodent cells, yielding subclones containing different portions of the human genome. This technique is described by Benham *et al.* (*Genomics* 4:509-517, 1989) and Cox *et al.*; (*Science* 250:245-250, 1990). The random and independent nature of the subclones permits efficient mapping of any human genome marker. Human DNA isolated from a panel of 80-100 cell lines provides a mapping reagent for ordering EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In this approach, the frequency of breakage between markers is used to measure distance, allowing construction of fine resolution maps as has been done using conventional ESTs (Schuler *et al.*, *Science* 274:540-546, 1996).

RH mapping has been used to generate a high-resolution whole genome radiation hybrid map of human chromosome 17q22-q25.3 across the genes for growth hormone (GH) and thymidine kinase (TK) (Foster *et al.*, *Genomics* 33:185-192, 1996), the region surrounding the Gorlin syndrome gene (Obermayr *et al.*, *Eur. J. Hum. Genet.* 4:242-245, 1996), 60 loci covering the entire short arm of chromosome 12 (Raeymaekers *et al.*, *Genomics* 29:170-178, 1995), the region of human chromosome 22 containing the neurofibromatosis type 2 locus (Frazer *et al.*, *Genomics* 14:574-584, 1992) and 13 loci on the long arm of chromosome 5 (Warrington *et al.*, *Genomics* 11:701-708, 1991).

**EXAMPLE 44**

Mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Human Chromosomes using PCR techniques

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be assigned to human chromosomes using PCR based methodologies. In such approaches, oligonucleotide primer pairs are designed from EST-related

nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to minimize the chance of amplifying through an intron. Preferably, the oligonucleotide primers are 18-23 bp in length and are designed for PCR amplification. The creation of PCR primers from known sequences is well known to those with skill in the art. For a review of PCR technology see Erlich. in PCR Technology; Principles and Applications for DNA Amplification. 1992. W.H. Freeman and Co., New York.

The primers are used in polymerase chain reactions (PCR) to amplify templates from total human genomic DNA. PCR conditions are as follows: 60 ng of genomic DNA is used as a template for PCR with 80 ng of each oligonucleotide primer, 0.6 unit of Taq polymerase, and 1 μCu of a 32P-labeled deoxycytidine triphosphate. The PCR is performed in a microplate thermocycler (Techne) under the following conditions: 30 cycles of 94°C, 1.4 min; 55°C, 2 min; and 72°C, 2 min; with a final extension at 72°C for 10 min. The amplified products are analyzed on a 6% polyacrylamide sequencing gel and visualized by autoradiography. If the length of the resulting PCR product is identical to the distance between the ends of the primer sequences in the 5'EST from which the primers are derived, then the PCR reaction is repeated with DNA templates from two panels of human-rodent somatic cell hybrids, BIOS PCRable DNA (BIOS Corporation) and NIGMS Human-Rodent Somatic Cell Hybrid Mapping Panel Number 1 (NIGMS, Camden, NJ).

PCR is used to screen a series of somatic cell hybrid cell lines containing defined sets of human chromosomes for the presence of a given 5'EST. DNA is isolated from the somatic hybrids and used as starting templates for PCR reactions using the primer pairs from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Only those somatic cell hybrids with chromosomes containing the human gene corresponding to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids will yield an amplified fragment. The 5'ESTs are assigned to a chromosome by analysis of the segregation pattern of PCR products from the somatic hybrid DNA templates. The single human chromosome present in all cell hybrids that give rise to an amplified fragment is the chromosome containing that EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. For a review of techniques and analysis of results from somatic cell gene mapping experiments. (See Ledbetter *et al.*, Genomics 6:475-481 (1990)).

Alternatively, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be mapped to individual chromosomes using FISH as described in Example 45 below.

## EXAMPLE 45

Mapping of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of

EST-related nucleic acids to Chromosomes Using Fluorescence *In Situ* Hybridization

Fluorescence in situ hybridization allows the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to be mapped to a particular location on a given chromosome. The chromosomes to be used for fluorescence in situ hybridization techniques may be obtained from a variety of sources including cell cultures, tissues, or whole blood.

In a preferred embodiment, chromosomal localization of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are obtained by FISH as described by Cherif *et al.* (*Proc. Natl. Acad. Sci. U.S.A.*, 87:6639-6643, 1990). Metaphase chromosomes are prepared from phytohemagglutinin (PHA)-stimulated blood cell donors. PHA-stimulated lymphocytes from healthy males are cultured for 72 h in RPMI-1640 medium. For synchronization, methotrexate (10 μM) is added for 17 h, followed by addition of 5-bromodeoxyuridine (5-BrdU, 0.1 mM) for 6 h. Colcemid (1 μg/ml) is added for the last 15 min before harvesting the cells. Cells are collected, washed in RPMI, incubated with a hypotonic solution of KCl (75 mM) at 37°C for 15 min and fixed in three changes of methanol:acetic acid (3:1). The cell suspension is dropped onto a glass slide and air dried. The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is labeled with biotin-16 dUTP by nick translation according to the manufacturer's instructions (Bethesda Research Laboratories, Bethesda, MD), purified using a Sephadex G-50 column (Pharmacia, Upsala, Sweden) and precipitated. Just prior to hybridization, the DNA pellet is dissolved in hybridization buffer (50% formamide, 2 X SSC, 10% dextran sulfate, 1 mg/ml sonicated salmon sperm DNA, pH 7) and the probe is denatured at 70°C for 5-10 min.

Slides kept at -20°C are treated for 1 h at 37°C with RNase A (100 μg/ml), rinsed three times in 2 X SSC and dehydrated in an ethanol series. Chromosome preparations are denatured in 70% formamide, 2 X SSC for 2 min at 70°C, then dehydrated at 4°C. The slides are treated with proteinase K (10 μg/100 ml in 20 mM Tris-HCl, 2 mM $CaCl_2$) at 37°C for 8 min and dehydrated. The hybridization mixture containing the probe is placed on the slide, covered with a coverslip, sealed with rubber cement and incubated overnight in a humid chamber at 37°C. After hybridization and post-hybridization washes, the biotinylated probe is detected by avidin-FITC and amplified with additional layers of biotinylated goat anti-avidin and avidin-FITC. For chromosomal localization, fluorescent R-bands are obtained as previously described (Cherif *et al.*, *supra.*). The slides are observed under a LEICA fluorescence microscope (DMRXA). Chromosomes are counterstained with propidium iodide and the fluorescent signal of the probe appears as two symmetrical yellow-green spots on both chromatids of the fluorescent R-band chromosome (red). Thus, a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be localized to a particular cytogenetic R-band on a given chromosome.

Once the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids have been assigned to particular chromosomes using the techniques described in Examples 42-44 above, they may be utilized to construct a high resolution map of the chromosomes on which they are located or to identify the chromosomes in a sample.

## EXAMPLE 46

Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Construct or Expand Chromosome Maps

Chromosome mapping involves assigning a given unique sequence to a particular chromosome as described above. Once the unique sequence has been mapped to a given chromosome, it is ordered relative to other unique sequences located on the same chromosome. One approach to chromosome mapping utilizes a series of yeast artificial chromosomes (YACs) bearing several thousand long inserts derived from the chromosomes of the organism from which the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are obtained. This approach is described in Ramaiah Nagaraja *et al., Genome Research* 7:210-222, March 1997. Briefly, in this approach each chromosome is broken into overlapping pieces which are inserted into the YAC vector. The YAC inserts are screened using PCR or other methods to determine whether they include the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids whose position is to be determined. Once an insert has been found which includes the 5'EST, the insert can be analyzed by PCR or other methods to determine whether the insert also contains other sequences known to be on the chromosome or in the region from which the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids was derived. This process can be repeated for each insert in the YAC library to determine the location of each of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids relative to one another and to other known chromosomal markers. In this way, a high resolution map of the distribution of numerous unique markers along each of the organisms chromosomes may be obtained.

As described in Example 47 below EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to identify genes associated with a particular phenotype, such as hereditary disease or drug response.

3. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids Gene Identification

## EXAMPLE 47

Identification of genes associated with hereditary diseases or drug response

This example illustrates an approach useful for the association of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with particular phenotypic characteristics. In this example, a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is used as a test probe to associate that EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with a particular phenotypic characteristic.

EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are mapped to a particular location on a human chromosome using techniques such as those described in Examples 41 and 42 or other techniques known in the art. A search of Mendelian Inheritance in Man (V. McKusick, *Mendelian Inheritance in Man* (available on line through Johns Hopkins University Welch Medical Library) reveals the region of the human chromosome which contains the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to be a very gene rich region containing several known genes and several diseases or phenotypes for which genes have not been identified. The gene corresponding to this EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids thus becomes an immediate candidate for each of these genetic diseases.

Cells from patients with these diseases or phenotypes are isolated and expanded in culture. PCR primers from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are used to screen genomic DNA, mRNA or cDNA obtained from the patients. EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids that are not amplified in the patients can be positively associated with a particular disease by further analysis. Alternatively, the PCR analysis may yield fragments of different lengths when the samples are derived from an individual having the phenotype associated with the disease than when the sample is derived from a healthy individual, indicating that the gene containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be responsible for the genetic disease.

**VII. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Construct Vectors**

The present EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to construct secretion vectors capable of directing the secretion of the proteins encoded by genes therein. Such secretion vectors may facilitate the purification or enrichment of the proteins encoded by genes inserted therein by

reducing the number of background proteins from which the desired protein must be purified or enriched. Exemplary secretion vectors are described in Example 48 below.

1. Construction of secretion vectors

## EXAMPLE 48

### Construction of Secretion Vectors

The secretion vectors of the present invention include a promoter capable of directing gene expression in the host cell, tissue, or organism of interest. Such promoters include the Rous Sarcoma Virus promoter, the SV40 promoter, the human cytomegalovirus promoter, and other promoters familiar to those skilled in the art.

A signal sequence from one of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is operably linked to the promoter such that the mRNA transcribed from the promoter will direct the translation of the signal peptide. Preferably, the signal sequence is from one of the nucleic acids of SEQ ID NOs.24-811. The host cell, tissue, or organism may be any cell, tissue, or organism which recognizes the signal peptide encoded by the signal sequence in the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. Suitable hosts include mammalian cells, tissues or organisms, avian cells, tissues, or organisms, insect cells, tissues or organisms, or yeast.

In addition, the secretion vector contains cloning sites for inserting genes encoding the proteins which are to be secreted. The cloning sites facilitate the cloning of the insert gene in frame with the signal sequence such that a fusion protein in which the signal peptide is fused to the protein encoded by the inserted gene is expressed from the mRNA transcribed from the promoter. The signal peptide directs the extracellular secretion of the fusion protein.

The secretion vector may be DNA or RNA and may integrate into the chromosome of the host, be stably maintained as an extrachromosomal replicon in the host, be an artificial chromosome, or be transiently present in the host. Preferably, the secretion vector is maintained in multiple copies in each host cell. As used herein, multiple copies means at least 2, 5, 10, 20, 25, 50 or more than 50 copies per cell. In some embodiments, the multiple copies are maintained extrachromosomally. In other embodiments, the multiple copies result from amplification of a chromosomal sequence.

Many nucleic acid backbones suitable for use as secretion vectors are known to those skilled in the art, including retroviral vectors, SV40 vectors, Bovine Papilloma Virus vectors, yeast integrating plasmids, yeast episomal plasmids, yeast artificial chromosomes, human artificial chromosomes, P element vectors, baculovirus vectors, or bacterial plasmids capable of being transiently introduced into the host.

The secretion vector may also contain a polyA signal such that the polyA signal is located downstream of the gene inserted into the secretion vector.

After the gene encoding the protein for which secretion is desired is inserted into the secretion vector, the secretion vector is introduced into the host cell, tissue, or organism using calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection, viral particles or as naked DNA. The protein encoded by the inserted gene is then purified or enriched from the supernatant using conventional techniques such as ammonium sulfate precipitation, immunoprecipitation, immunoaffinitychromatography, size exclusion chromatography, ion exchange chromatography, and HPLC. Alternatively, the secreted protein may be in a sufficiently enriched or pure state in the supernatant or growth media of the host to permit it to be used for its intended purpose without further enrichment.

The signal sequences may also be inserted into vectors designed for gene therapy. In such vectors, the signal sequence is operably linked to a promoter such that mRNA transcribed from the promoter encodes the signal peptide. A cloning site is located downstream of the signal sequence such that a gene encoding a protein whose secretion is desired may readily be inserted into the vector and fused to the signal sequence. The vector is introduced into an appropriate host cell. The protein expressed from the promoter is secreted extracellularly, thereby producing a therapeutic effect.

## EXAMPLE 49

### Fusion Vectors

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to construct fusion vectors for the expression of chimeric polypeptides. The chimeric polypeptides comprise a first polypeptide portion and a second polypeptide portion. In the fusion vectors of the present invention, nucleic acids encoding the first polypeptide portion and the second polypeptide portion are joined in frame with one another so as to generate a nucleic acid encoding the chimeric polypeptide. The nucleic acid encoding the chimeric polypeptide is operably linked to a promoter which directs the expression of an mRNA encoding the chimeric polypeptide. The promoter may be in any of the expression vectors described herein including those described in Examples 21 and 48.

Preferably, the fusion vector is maintained in multiple copies in each host cell. In some embodiments, the multiple copies are maintained extrachromosomally. In other embodiments, the multiple copies result from amplification of a chromosomal sequence.

The first polypeptide portion may comprise any of the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. In some embodiments, the first polypeptide portion may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides.

The second polypeptide portion may comprise any polypeptide of interest. In some embodiments, the second polypeptide portion may comprise a polypeptide having a detectable

enzymatic activity such as green fluorescent protein or β galactosidase. Chimeric polypeptides in which the second polypeptide portion comprises a detectable polypeptide may be used to determine the intracellular localization of the first polypeptide portion. In such procedures, the fusion vector encoding the chimeric polypeptide is introduced into a host cell under conditions which facilitate the expression of the chimeric polypeptide. Where appropriate, the cells are treated with a detection reagent which is visible under the microscope following a catalytic reaction with the detectable polypeptide and the cellular location of the detection reagent is determined. For example, if the polypeptide having a detectable enzymatic activity is β galactosidase, the cells may be treated with Xgal. Alternatively, where the detectable polypeptide is directly detectable without the addition of a detection reagent, the intracellular location of the chimeric polypeptide is determined by performing microscopy under conditions in which the dectable polypeptide is visible. For example, if the detectable polypeptide is green fluorescent protein or a modified version thereof, microscopy is performed by exposing the host cells to light having an appropriate wavelength to cause the green fluorescent protein or modified version thereof to fluoresce.

Alternatively, the second polypeptide portion may comprise a polypeptide whose isolation, purification, or enrichment is desired. In such embodiments, the isolation, purification, or enrichment of the second polypeptide portion may be achieved by performing the immunoaffinity chromatography procedures described below using an immunoaffinity column having an antibody directed against the first polypeptide portion coupled thereto.

The proteins encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides may also be used to generate antibodies as explained herein in order to identify the tissue type or cell species from which a sample is derived as described in Example 50.

## EXAMPLE 50

### Identification of Tissue Types or Cell Species by Means of Labeled Tissue Specific Antibodies

Identification of specific tissues is accomplished by the visualization of tissue specific antigens by means of antibody preparations as described herein which are conjugated, directly or indirectly to a detectable marker. Selected labeled antibody species bind to their specific antigen binding partner in tissue sections, cell suspensions, or in extracts of soluble proteins from a tissue sample to provide a pattern for qualitative or semi-qualitative interpretation.

Antisera for these procedures must have a potency exceeding that of the native preparation, and for that reason, antibodies are concentrated to a mg/ml level by isolation of the gamma globulin fraction, for example, by ion-exchange chromatography or by ammonium sulfate fractionation. Also, to provide

the most specific antisera, unwanted antibodies, for example to common proteins, must be removed from the gamma globulin fraction, for example by means of insoluble immunoabsorbents, before the antibodies are labeled with the marker. Either monoclonal or heterologous antisera is suitable for either procedure.

*1. Immunohistochemical Techniques*

Purified, high-titer antibodies, prepared as described above, are conjugated to a detectable marker, as described, for example, by Fudenberg, H., Chap. 26 in: *Basic 503 Clinical Immunology*, 3rd Ed. Lange, Los Altos, California (1980) or Rose,. *et al.*, Chap. 12 in: *Methods in Immunodiagnosis*, 2d Ed. John Wiley and Sons, New York (1980).

A fluorescent marker, either fluorescein or rhodamine, is preferred, but antibodies can also be labeled with an enzyme that supports a color producing reaction with a substrate, such as horseradish peroxidase. Markers can be added to tissue-bound antibody in a second step, as described below. Alternatively, the specific antitissue antibodies can be labeled with ferritin or other electron dense particles, and localization of the ferritin coupled antigen-antibody complexes achieved by means of an electron microscope. In yet another approach, the antibodies are radiolabeled, with, for example $^{125}I$, and detected by overlaying the antibody treated preparation with photographic emulsion.

Preparations to carry out the procedures can comprise monoclonal or polyclonal antibodies to a single protein or peptide identified as specific to a tissue type, for example, brain tissue, or antibody preparations to several antigenically distinct tissue specific antigens can be used in panels, independently or in mixtures, as required.

Tissue sections and cell suspensions are prepared for immunohistochemical examination according to common histological techniques. Multiple cryostat sections (about 4 µm, unfixed) of the unknown tissue and known control, are mounted and each slide covered with different dilutions of the antibody preparation. Sections of known and unknown tissues should also be treated with preparations to provide a positive control, a negative control, for example, pre-immune sera, and a control for non-specific staining, for example, buffer.

Treated sections are incubated in a humid chamber for 30 min at room temperature, rinsed, then washed in buffer for 30-45 min. Excess fluid is blotted away, and the marker developed.

If the tissue specific antibody was not labeled in the first incubation, it can be labeled at this time in a second antibody-antibody reaction, for example, by adding fluorescein- or enzyme-conjugated antibody against the immunoglobulin class of the antiserum-producing species, for example, fluorescein labeled antibody to mouse IgG. Such labeled sera are commercially available.

The antigen found in the tissues by the above procedure can be quantified by measuring the intensity of color or fluorescence on the tissue section, and calibrating that signal using appropriate standards.

*2. Identification of Tissue Specific Soluble Proteins*

The visualization of tissue specific proteins and identification of unknown tissues from that procedure is carried out using the labeled antibody reagents and detection strategy as described for immunohistochemistry; however the sample is prepared according to an electrophoretic technique to distribute the proteins extracted from the tissue in an orderly array on the basis of molecular weight for detection.

A tissue sample is homogenized using a Virtis apparatus; cell suspensions are disrupted by Dounce homogenization or osmotic lysis, using detergents in either case as required to disrupt cell membranes, as is the practice in the art. Insoluble cell components such as nuclei, microsomes, and membrane fragments are removed by ultracentrifugation, and the soluble protein-containing fraction concentrated if necessary and reserved for analysis.

A sample of the soluble protein solution is resolved into individual protein species by conventional SDS polyacrylamide electrophoresis as described, for example, by Davis,L. *et al.*, Section 19-2 in: *Basic Methods in Molecular Biology* (P. Leder, ed), Elsevier, New York (1986), using a range of amounts of polyacrylamide in a set of gels to resolve the entire molecular weight range of proteins to be detected in the sample. A size marker is run in parallel for purposes of estimating molecular weights of the constituent proteins. Sample size for analysis is a convenient volume of from 5 to 55 μl, and containing from about 1 to 100 μg protein. An aliquot of each of the resolved proteins is transferred by blotting to a nitrocellulose filter paper, a process that maintains the pattern of resolution. Multiple copies are prepared. The procedure, known as Western Blot Analysis, is well described in Davis, L. *et al.*, *supra* Section 19-3. One set of nitrocellulose blots is stained with Coomassie Blue dye to visualize the entire set of proteins for comparison with the antibody bound proteins. The remaining nitrocellulose filters are then incubated with a solution of one or more specific antisera to tissue specific proteins prepared as described in Examples 20 and 33. In this procedure, as in procedure A above, appropriate positive and negative sample and reagent controls are run.

In either procedure described above a detectable label can be attached to the primary tissue antigen-primary antibody complex according to various strategies and permutations thereof. In a straightforward approach, the primary specific antibody can be labeled; alternatively, the unlabeled complex can be bound by a labeled secondary anti-IgG antibody. In other approaches, either the primary or secondary antibody is conjugated to a biotin molecule, which can, in a subsequent step, bind an avidin conjugated marker. According to yet another strategy, enzyme labeled or radioactive protein A, which has the property of binding to any IgG, is bound in a final step to either the primary or secondary antibody.

## EXAMPLE 51

### Immunohistochemical Localization of Polypeptides

The antibodies prepared as described herein above may be utilized to determine the cellular location of a polypeptide. The polypeptide may be any of the polypeptides encoded by EST-related

nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the polypeptide may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. In some embodiments, the polypeptide may be a chimeric polypeptide such as those encoded by the fusion vectors of Example 49.

Cells expressing the polypeptide to be localized are applied to a microscope slide and fixed using any of the procedures typically employed in immunohistochemical localization techniques, including the methods described in *Current Protocols in Molecular Biology*, John Wiley and Sons, Inc. 1997. Following a washing step, the cells are contacted with the antibody. In some embodiments, the antibody is conjugated to a detectable marker as described above to facilitate detection. Alternatively, in some embodiments, after the cells have been contacted with an antibody to the polypeptide to be localized, a secondary antibody which has been conjugated to a detectable marker is placed in contact with the antibody against the polypeptide to be localized.

Thereafter, microscopy is performed under conditions suitable for visualizing the cellular location of the polypeptide.

The visualization of tissue specific antigen binding at levels above those seen in control tissues to one or more tissue specific antibodies, directed against the polypeptides encoded by EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or antibodies against the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides, can identify tissues of unknown origin, for example, forensic samples, or differentiated tumor tissue that has metastasized to foreign bodily sites.

The antibodies described herein may also be used in the immunoaffinity chromatography techniques described below to isolate, purify or enrich the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or to isolate, purify or enrich EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. The immunoaffinity chromatography techniques described below may also be used to isolate, purify or enrich polypeptides which have been linked to the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or to isolate, purify or enrich polypeptides which have been linked to EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides.

## EXAMPLE 52

Immunoaffinity Chromatography

Antibodies prepared as described above are coupled to a support. Preferably, the antibodies are monoclonal antibodies, but polyclonal antibodies may also be used. The support may be any of those typically employed in immunoaffinity chromatography, including Sepharose CL-4B (Pharmacia, Piscataway, NJ), Sepharose CL-2B (Pharmacia, Piscataway, NJ), Affi-gel 10 (Biorad, Richmond, CA), or glass beads.

The antibodies may be coupled to the support using any of the coupling reagents typically used in immunoaffinity chromatography, including cyanogen bromide. After coupling the antibody to the support, the support is contacted with a sample which contains a target polypeptide whose isolation, purification or enrichment is desired. The target polypeptide may be a polypeptide encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the target polypeptide may be one of the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides. The target polypeptides may also be polypeptides which have been linked to the polypeptides encoded by the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or the target polypeptides may be polypeptides which have been linked to EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of positional segments of EST-related polypeptides using the fusion vectors described above.

Preferably, the sample is placed in contact with the support for a sufficient amount of time and under appropriate conditions to allow at least 50% of the target polypeptide to specifically bind to the antibody coupled to the support.

Thereafter, the support is washed with an appropriate wash solution to remove polypeptides which have non-specifically adhered to the support. The wash solution may be any of those typically employed in immunoaffinity chromatography, including PBS, Tris-lithium chloride buffer (0.1M lysine base and 0.5M lithium chloride, pH 8.0), Tris-hydrochloride buffer (0.05M Tris-hydrochloride, pH 8.0), or Tris/Triton/NaCl buffer (50mM Tris.cl, pH 8.0 or 9.0, 0.1% Triton X-100, and 0.5MNaCl).

After washing, the specifically bound target polypeptide is eluted from the support using the high pH or low pH elution solutions typically employed in immunoaffinity chromatography. In particular, the elution solutions may contain an eluant such as triethanolamine, diethylamine, calcium chloride, sodium thiocyanate, potasssium bromide, acetic acid, or glycine. In some embodiments, the elution solution may also contain a detergent such as Triton X-100 or octyl-β-D-glucoside.

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to clone sequences located upstream of the 5'ESTs which are capable of regulating gene expression, including promoter sequences, enhancer

sequences, and other upstream sequences which influence transcription or translation levels. Once identified and cloned, these upstream regulatory sequences may be used in expression vectors designed to direct the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative fashion. Example 51 describes a method for cloning sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids.

2. Identification of upstream sequences with promoting or regulatory activities

**EXAMPLE 53**

Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to Clone Upstream Sequences from Genomic DNA

Sequences derived from EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to isolate the promoters of the corresponding genes using chromosome walking techniques. In one chromosome walking technique, which utilizes the GenomeWalker™ kit available from Clontech, five complete genomic DNA samples are each digested with a different restriction enzyme which has a 6 base recognition site and leaves a blunt end. Following digestion, oligonucleotide adapters are ligated to each end of the resulting genomic DNA fragments.

For each of the five genomic DNA libraries, a first PCR reaction is performed according to the manufacturer's instructions using an outer adapter primer provided in the kit and an outer gene specific primer. The gene specific primer should be selected to be specific for 5' EST of interest and should have a melting temperature, length, and location in the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids which is consistent with its use in PCR reactions. Each first PCR reaction contains 5ng of genomic DNA, 5 μl of 10X Tth reaction buffer, 0.2 mM of each dNTP, 0.2 μM each of outer adapter primer and outer gene specific primer, 1.1 mM of $Mg(OAc)_2$, and 1 μl of the Tth polymerase 50X mix in a total volume of 50 μl. The reaction cycle for the first PCR reaction is as follows: 1 min at 94°C / 2 sec at 94°C, 3 min at 72°C (7 cycles) / 2 sec at 94°C, 3 min at 67°C (32 cycles) / 5 min at 67°C.

The product of the first PCR reaction is diluted and used as a template for a second PCR reaction according to the manufacturer's instructions using a pair of nested primers which are located internally on the amplicon resulting from the first PCR reaction. For example, 5 μl of the reaction product of the first PCR reaction mixture may be diluted 180 times. Reactions are made in a 50 μl volume having a composition identical to that of the first PCR reaction except the nested primers are used. The first nested primer is specific for the adapter, and is provided with the GenomeWalker™ kit. The second nested primer is specific for the particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids for which the promoter is to be cloned and should have a melting temperature, length, and location in

the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids which is consistent with its use in PCR reactions. The reaction parameters of the second PCR reaction are as follows: 1 min at 94°C / 2 sec at 94°C, 3 min at 72°C (6 cycles) / 2 sec at 94°C, 3 min at 67°C (25 cycles) / 5 min at 67°C. The product of the second PCR reaction is purified, cloned, and sequenced using standard techniques.

Alternatively, two or more human genomic DNA libraries can be constructed by using two or more restriction enzymes. The digested genomic DNA is cloned into vectors which can be converted into single stranded, circular, or linear DNA. A biotinylated oligonucleotide comprising at least 10, 12, 15, 18, 20, 23, 25, 27, 30, 35, 40, or 50 nucleotides from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids sequence is hybridized to the single stranded DNA. Hybrids between the biotinylated oligonucleotide and the single stranded DNA containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are isolated as described above. Thereafter, the single stranded DNA containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is released from the beads and converted into double stranded DNA using a primer specific for the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids or a primer corresponding to a sequence included in the cloning vector. The resulting double stranded DNA is transformed into bacteria. cDNAs containing the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are identified by colony PCR or colony hybridization.

Once the upstream genomic sequences have been cloned and sequenced as described above, prospective promoters and transcription start sites within the upstream sequences may be identified by comparing the sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids with databases containing known transcription start sites, transcription factor binding sites, or promoter sequences.

In addition, promoters in the upstream sequences may be identified using promoter reporter vectors as described in Example 54.

## EXAMPLE 54

### Identification of Promoters in Cloned Upstream Sequences

The genomic sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are cloned into a suitable promoter reporter vector, such as the pSEAP-Basic, pSEAP-Enhancer, pβ-gal-Basic, pβ-gal-Enhancer, or pEGFP-1 Promoter Reporter vectors available from Clontech. Briefly, each of these promoter reporter vectors include multiple cloning sites positioned upstream of a reporter gene encoding a readily assayable protein such as secreted alkaline phosphatase, β-galactosidase, or green fluorescent

protein. The sequences upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are inserted into the cloning sites upstream of the reporter gene in both orientations and introduced into an appropriate host cell. The level of reporter protein is assayed and compared to the level obtained from a vector which lacks an insert in the cloning site. The presence of an elevated expression level in the vector containing the insert with respect to the control vector indicates the presence of a promoter in the insert. If necessary, the upstream sequences can be cloned into vectors which contain an enhancer for augmenting transcription levels from weak promoter sequences. A significant level of expression above that observed with the vector lacking an insert indicates that a promoter sequence is present in the inserted upstream sequence.

Appropriate host cells for the promoter reporter vectors may be chosen based on the results of the above described determination of expression patterns of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. For example, if the expression pattern analysis indicates that the mRNA corresponding to a particular EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids is expressed in fibroblasts, the promoter reporter vector may be introduced into a human fibroblast cell line.

Promoter sequences within the upstream genomic DNA may be further defined by constructing nested deletions in the upstream DNA using conventional techniques such as Exonuclease III digestion. The resulting deletion fragments can be inserted into the promoter reporter vector to determine whether the deletion has reduced or obliterated promoter activity. In this way, the boundaries of the promoters may be defined. If desired, potential individual regulatory sites within the promoter may be identified using site directed mutagenesis or linker scanning to obliterate potential transcription factor binding sites within the promoter individually or in combination. The effects of these mutations on transcription levels may be determined by inserting the mutations into the cloning sites in the promoter reporter vectors.

## EXAMPLE 55

### Cloning and Identification of Promoters

Using the method described in Example 54 above with 5' ESTs, sequences upstream of several genes were obtained. Using the primer pairs GGG AAG ATG GAG ATA GTA TTG CCT G (SEQ ID NO:15) and CTG CCA TGT ACA TGA TAG AGA GAT TC (SEQ ID NO:16), the promoter having the internal designation P13H2 (SEQ ID NO:17) was obtained.

Using the primer pairs GTA CCA GGGG ACT GTG ACC ATT GC (SEQ ID NO:18) and CTG TGA CCA TTG CTC CCA AGA GAG (SEQ ID NO:19), the promoter having the internal designation P15B4 (SEQ ID NO:20) was obtained.

Using the primer pairs CTG GGA TGG AAG GCA CGG TA (SEQ ID NO:21) and GAG ACC ACA CAG CTA GAC AA (SEQ ID NO:22), the promoter having the internal designation P29B6 (SEQ ID NO:23) was obtained.

Figure 4 provides a schematic description of the promoters isolated and the way they are assembled with the corresponding 5' tags. The upstream sequences were screened for the presence of motifs resembling transcription factor binding sites or known transcription start sites using the computer program MatInspector release 2.0, August 1996.

Figure 5 describes the transcription factor binding sites present in each of these promoters. The columns labeled matrice provides the name of the MatInspector matrix used. The column labeled position provides the 5' position of the promoter site. Numeration of the sequence starts from the transcription site as determined by matching the genomic sequence with the 5' EST sequence. The column labeled "orientation" indicates the DNA strand on which the site is found, with the + strand being the coding strand as determined by matching the genomic sequence with the sequence of the 5' EST. The column labeled "score" provides the MatInspector score found for this site. The column labeled "length" provides the length of the site in nucleotides. The column labeled "sequence" provides the sequence of the site found.

Bacterial clones containing plasmids containing the promoter sequences described above described above are presently stored in the inventor's laboratories under the internal identification numbers provided above. The inserts may be recovered from the deposited materials by growing an aliquot of the appropriate bacterial clone in the appropriate medium. The plasmid DNA can then be isolated using plasmid isolation procedures familiar to those skilled in the art such as alkaline lysis minipreps or large scale alkaline lysis plasmid isolation procedures. If desired the plasmid DNA may be further enriched by centrifugation on a cesium chloride gradient, size exclusion chromatography, or anion exchange chromatography. The plasmid DNA obtained using these procedures may then be manipulated using standard cloning techniques familiar to those skilled in the art. Alternatively, a PCR can be done with primers designed at both ends of the inserted EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The PCR product which corresponds to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids can then be manipulated using standard cloning techniques familiar to those skilled in the art.

The promoters and other regulatory sequences located upstream of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used to design expression vectors capable of directing the expression of an inserted gene in a desired spatial, temporal, developmental, or quantitative manner. A promoter capable of directing the desired spatial, temporal, developmental, and quantitative patterns may be selected using the results of the expression analysis described above. For example, if a promoter which confers a high level of expression in muscle is desired, the promoter sequence upstream of EST-related nucleic acids,

positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids derived from an mRNA which are expressed at a high level in muscle, as determined by the methods above, may be used in the expression vector.

Preferably, the desired promoter is placed near multiple restriction sites to facilitate the cloning of the desired insert downstream of the promoter, such that the promoter is able to drive expression of the inserted gene. The promoter may be inserted in conventional nucleic acid backbones designed for extrachromosomal replication, integration into the host chromosomes or transient expression. Suitable backbones for the present expression vectors include retroviral backbones, backbones from eukaryotic episomes such as SV40 or Bovine Papilloma Virus, backbones from bacterial episomes, or artificial chromosomes.

Preferably, the expression vectors also include a polyA signal downstream of the multiple restriction sites for directing the polyadenylation of mRNA transcribed from the gene inserted into the expression vector.

Following the identification of promoter sequences, proteins which interact with the promoter may be identified as described in Example 56 below.

**EXAMPLE 56**

Identification of Proteins Which Interact with Promoter Sequences, Upstream Regulatory Sequences, or mRNA

Sequences within the promoter region which are likely to bind transcription factors may be identified by homology to known transcription factor binding sites or through conventional mutagenesis or deletion analyses of reporter plasmids containing the promoter sequence. For example, deletions may be made in a reporter plasmid containing the promoter sequence of interest operably linked to an assayable reporter gene. The reporter plasmids carrying various deletions within the promoter region are transfected into an appropriate host cell and the effects of the deletions on expression levels is assessed. Transcription factor binding sites within the regions in which deletions reduce expression levels may be further localized using site directed mutagenesis, linker scanning analysis, or other techniques familiar to those skilled in the art.

Nucleic acids encoding proteins which interact with sequences in the promoter may be identified using one-hybrid systems such as those described in the manual accompanying the Matchmaker One-Hybrid System kit available from Clontech (Catalog No. K1603-1). Briefly, the Matchmaker One-hybrid system is used as follows. The target sequence for which it is desired to identify binding proteins is cloned upstream of a selectable reporter gene and integrated into the yeast genome. Preferably, multiple copies of the target sequences are inserted into the reporter plasmid in tandem. A library comprised of fusions between cDNAs to be evaluated for the ability to bind to the promoter and the activation domain of a yeast transcription factor, such as GAL4, is transformed into the yeast strain containing the integrated reporter sequence. The yeast are plated on selective media to select cells

expressing the selectable marker linked to the promoter sequence. The colonies which grow on the selective media contain genes encoding proteins which bind the target sequence. The inserts in the genes encoding the fusion proteins are further characterized by sequencing. In addition, the inserts may be inserted into expression vectors or *in vitro* transcription vectors. Binding of the polypeptides encoded by the inserts to the promoter DNA may be confirmed by techniques familiar to those skilled in the art, such as gel shift analysis or DNAse protection analysis.

**VIII. Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in Gene Therapy**

The present invention also comprises the use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids in gene therapy strategies, including antisense and triple helix strategies as described in Examples 57 and 58 below. In antisense approaches, nucleic acid sequences complementary to an mRNA are hybridized to the mRNA intracellularly, thereby blocking the expression of the protein encoded by the mRNA. The antisense sequences may prevent gene expression through a variety of mechanisms. For example, the antisense sequences may inhibit the ability of ribosomes to translate the mRNA. Alternatively, the antisense sequences may block transport of the mRNA from the nucleus to the cytoplasm, thereby limiting the amount of mRNA available for translation. Another mechanism through which antisense sequences may inhibit gene expression is by interfering with mRNA splicing. In yet another strategy, the antisense nucleic acid may be incorporated in a ribozyme capable of specifically cleaving the target mRNA.

**EXAMPLE 57**

Preparation and Use of Antisense Oligonucleotides

The antisense nucleic acid molecules to be used in gene therapy may be either DNA or RNA sequences. They may comprise a sequence complementary to the sequence of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids. The antisense nucleic acids should have a length and melting temperature sufficient to permit formation of an intracellular duplex with sufficient stability to inhibit the expression of the mRNA in the duplex. Strategies for designing antisense nucleic acids suitable for use in gene therapy are disclosed in Green *et al., Ann. Rev. Biochem.* 55:569-597 (1986) and Izant and Weintraub, *Cell* 36:1007-1015 (1984).

In some strategies, antisense molecules are obtained from a nucleotide sequence encoding a protein by reversing the orientation of the coding region with respect to a promoter so as to transcribe the opposite strand from that which is normally transcribed in the cell. The antisense molecules may be transcribed using *in vitro* transcription systems such as those which employ T7 or SP6 polymerase to

generate the transcript. Another approach involves transcription of the antisense nucleic acids *in vivo* by operably linking DNA containing the antisense sequence to a promoter in an expression vector.

Alternatively, oligonucleotides which are complementary to the strand normally transcribed in the cell may be synthesized *in vitro*. Thus, the antisense nucleic acids are complementary to the corresponding mRNA and are capable of hybridizing to the mRNA to create a duplex. In some embodiments, the antisense sequences may contain modified sugar phosphate backbones to increase stability and make them less sensitive to RNase activity. Examples of modifications suitable for use in antisense strategies are described by Rossi *et al.*, *Pharmacol. Ther.* 50(2):245-254, (1991).

Various types of antisense oligonucleotides complementary to the sequence of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may be used. In one preferred embodiment, stable and semi-stable antisense oligonucleotides described in International Application No. PCT WO94/23026 are used. In these molecules, the 3' end or both the 3' and 5' ends are engaged in intramolecular hydrogen bonding between complementary base pairs. These molecules are better able to withstand exonuclease attacks and exhibit increased stability compared to conventional antisense oligonucleotides.

In another preferred embodiment, the antisense oligodeoxynucleotides against herpes simplex virus types 1 and 2 described in International Application No. WO 95/04141 are used.

In yet another preferred embodiment, the covalently cross-linked antisense oligonucleotides described in International Application No. WO 96/31523 are used. These double- or single-stranded oligonucleotides comprise one or more, respectively, inter- or intra-oligonucleotide covalent cross-linkages, wherein the linkage consists of an amide bond between a primary amine group of one strand and a carboxyl group of the other strand or of the same strand, respectively, the primary amine group being directly substituted in the 2' position of the strand nucleotide monosaccharide ring, and the carboxyl group being carried by an aliphatic spacer group substituted on a nucleotide or nucleotide analog of the other strand or the same strand, respectively.

The antisense oligodeoxynucleotides and oligonucleotides disclosed in International Application No. WO 92/18522 may also be used. These molecules are stable to degradation and contain at least one transcription control recognition sequence which binds to control proteins and are effective as decoys therefor. These molecules may contain "hairpin" structures, "dumbbell" structures, "modified dumbbell" structures, "cross-linked" decoy structures and "loop" structures.

In another preferred embodiment, the cyclic double-stranded oligonucleotides described in European Patent Application No. 0 572 287 A2. These ligated oligonucleotide "dumbbells" contain the binding site for a transcription factor and inhibit expression of the gene under control of the transcription factor by sequestering the factor.

Use of the closed antisense oligonucleotides disclosed in International Application No. WO 92/19732 is also contemplated. Because these molecules have no free ends, they are more resistant to

degradation by exonucleases than are conventional oligonucleotides. These oligonucleotides may be multifunctional, interacting with several regions which are not adjacent to the target mRNA.

The appropriate level of antisense nucleic acids required to inhibit gene expression may be determined using *in vitro* expression analysis. The antisense molecule may be introduced into the cells by diffusion, injection, infection or transfection using procedures known in the art. For example, the antisense nucleic acids can be introduced into the body as a bare or naked oligonucleotide, oligonucleotide encapsulated in lipid, oligonucleotide sequence encapsidated by viral protein, or as an oligonucleotide operably linked to a promoter contained in an expression vector. The expression vector may be any of a variety of expression vectors known in the art, including retroviral or viral vectors, vectors capable of extrachromosomal replication, or integrating vectors. The vectors may be DNA or RNA.

The antisense molecules are introduced onto cell samples at a number of different concentrations preferably between $1x10^{-10}M$ to $1x10^{-4}M$. Once the minimum concentration that can adequately control gene expression is identified, the optimized dose is translated into a dosage suitable for use *in vivo*. For example, an inhibiting concentration in culture of $1x10^{-7}$ translates into a dose of approximately 0.6 mg/kg bodyweight. Levels of oligonucleotide approaching 100 mg/kg bodyweight or higher may be possible after testing the toxicity of the oligonucleotide in laboratory animals. It is additionally contemplated that cells from the vertebrate are removed, treated with the antisense oligonucleotide, and reintroduced into the vertebrate.

It is further contemplated that the antisense oligonucleotide sequence is incorporated into a ribozyme sequence to enable the antisense to specifically bind and cleave its target mRNA. For technical applications of ribozyme and antisense oligonucleotides see Rossi *et al., supra*.

In a preferred application of this invention, the polypeptide encoded by the gene is first identified, so that the effectiveness of antisense inhibition on translation can be monitored using techniques that include but are not limited to antibody-mediated tests such as RIAs and ELISA, functional assays, or radiolabeling.

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used in gene therapy approaches based on intracellular triple helix formation. Triple helix oligonucleotides are used to inhibit transcription from a genome. They are particularly useful for studying alterations in cell activity as it is associated with a particular gene. The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids of the present invention or, more preferably, a portion of those sequences, can be used to inhibit gene expression in individuals having diseases associated with expression of a particular gene. Similarly, the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids can be used to study the effect of inhibiting transcription of a particular gene within a cell. Traditionally, homopurine sequences were considered the most useful for triple helix strategies.

However, homopyrimidine sequences can also inhibit gene expression. Such homopyrimidine oligonucleotides bind to the major groove at homopurine:homopyrimidine sequences. Thus, both types of sequences from the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are contemplated within the scope of this invention.

## EXAMPLE 58

Preparation and use of Triple Helix Probes

The sequences of the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are scanned to identify 10-mer to 20-mer homopyrimidine or homopurine stretches which could be used in triple-helix based strategies for inhibiting gene expression. Following identification of candidate homopyrimidine or homopurine stretches, their efficiency in inhibiting gene expression is assessed by introducing varying amounts of oligonucleotides containing the candidate sequences into tissue culture cells which normally express the target gene. The oligonucleotides may be prepared on an oligonucleotide synthesizer or they may be purchased commercially from a company specializing in custom oligonucleotide synthesis, such as GENSET, Paris, France.

The oligonucleotides may be introduced into the cells using a variety of methods known to those skilled in the art, including but not limited to calcium phosphate precipitation, DEAE-Dextran, electroporation, liposome-mediated transfection or native uptake.

Treated cells are monitored for altered cell function or reduced gene expression using techniques such as Northern blotting, RNase protection assays, or PCR based strategies to monitor the transcription levels of the target gene in cells which have been treated with the oligonucleotide. The cell functions to be monitored are predicted based upon the homologies of the target genes corresponding to the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids from which the oligonucleotide were derived with known gene sequences that have been associated with a particular function. The cell functions can also be predicted based on the presence of abnormal physiologies within cells derived from individuals with a particular inherited disease, particularly when the EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids are associated with the disease using techniques described herein.

The oligonucleotides which are effective in inhibiting gene expression in tissue culture cells may then be introduced *in vivo* using the techniques described above and in Example 56 at a dosage calculated based on the *in vitro* results, as described in Example 57.

In some embodiments, the natural (beta) anomers of the oligonucleotide units can be replaced with alpha anomers to render the oligonucleotide more resistant to nucleases. Further, an intercalating agent such as ethidium bromide, or the like, can be attached to the 3' end of the alpha oligonucleotide to

stabilize the triple helix. For information on the generation of oligonucleotides suitable for triple helix formation see Griffin *et al.* (*Science* 245:967-971 (1989)).

## EXAMPLE 59

Use of EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids to express an Encoded Protein in a Host Organism

The EST-related nucleic acids, positional segments of EST-related nucleic acids or fragments of positional segments of EST-related nucleic acids may also be used to express an encoded protein or polypeptide in a host organism to produce a beneficial effect. In addition, nucleic acids encoding the EST-related polypeptides, positional segments of EST-related polypeptides or fragments of positional segments of EST-related polypeptides may be used to express the encoded protein or polypeptide in a host organism to produce a beneficial effect.

In such procedures, the encoded protein or polypeptide may be transiently expressed in the host organism or stably expressed in the host organism. The encoded protein or polypeptide may have any of the activities described above. The encoded protein or polypeptide may be a protein or polypeptide which the host organism lacks or, alternatively, the encoded protein may augment the existing levels of the protein in the host organism.

In some embodiments in which the protein or polypeptide is secreted, nucleic acids encoding the full length protein (*i.e.* the signal peptide and the mature protein), or nucleic acids encoding only the mature protein (*i.e.* the protein generated when the signal peptide is cleaved off) is introduced into the host organism.

The nucleic acids encoding the proteins or polypeptides may be introduced into the host organism using a variety of techniques known to those of skill in the art. For example, the extended cDNA may be injected into the host organism as naked DNA such that the encoded protein is expressed in the host organism, thereby producing a beneficial effect.

Alternatively, the nucleic acids encoding the protein or polypeptide may be cloned into an expression vector downstream of a promoter which is active in the host organism. The expression vector may be any of the expression vectors designed for use in gene therapy, including viral or retroviral vectors. The expression vector may be directly introduced into the host organism such that the encoded protein is expressed in the host organism to produce a beneficial effect. In another approach, the expression vector may be introduced into cells *in vitro*. Cells containing the expression vector are thereafter selected and introduced into the host organism, where they express the encoded protein or polypeptide to produce a beneficial effect.

## EXAMPLE 60

Use of Signal Peptides To Import Proteins Into Cells

The short core hydrophobic region (h) of signal peptides encoded by the sequences of SEQ ID NOs. 24-728 and 766-792 may also be used as a carrier to import a peptide or a protein of interest, so-called cargo, into tissue culture cells (Lin *et al., J. Biol. Chem.*, 270: 14225-14258 (1995); Du *et al., J. Peptide Res.*, 51: 235-243 (1998); Rojas *et al., Nature Biotech.*, 16: 370-375 (1998)).

When cell permeable peptides of limited size (approximately up to 25 amino acids) are to be translocated across cell membrane, chemical synthesis may be used in order to add the h region to either the C-terminus or the N-terminus to the cargo peptide of interest. Alternatively, when longer peptides or proteins are to be imported into cells, nucleic acids can be genetically engineered, using techniques familiar to those skilled in the art, in order to link the extended cDNA sequence encoding the h region to the 5' or the 3' end of a DNA sequence coding for a cargo polypeptide. Such genetically engineered nucleic acids are then translated either *in vitro* or *in vivo* after transfection into appropriate cells, using conventional techniques to produce the resulting cell permeable polypeptide. Suitable hosts cells are then simply incubated with the cell permeable polypeptide which is then translocated across the membrane.

This method may be applied to study diverse intracellular functions and cellular processes. For instance, it has been used to probe functionally relevant domains of intracellular proteins and to examine protein-protein interactions involved in signal transduction pathways (Lin *et al., supra*; Lin *et al., J. Biol. Chem.*, 271: 5305-5308 (1996); Rojas *et al., J. Biol. Chem.*, 271: 27456-27461 (1996); Liu *et al., Proc. Natl. Acad. Sci. USA*, 93: 11819-11824 (1996); Rojas *et al., Bioch. Biophys. Res. Commun.*, 234: 675-680 (1997)).

Such techniques may be used in cellular therapy to import proteins producing therapeutic effects. For instance, cells isolated from a patient may be treated with imported therapeutic proteins and then re-introduced into the host organism.

Alternatively, the h region of signal peptides of the present invention could be used in combination with a nuclear localization signal to deliver nucleic acids into cell nucleus. Such oligonucleotides may be antisense oligonucleotides or oligonucleotides designed to form triple helixes, as describedabove, in order to inhibit processing and maturation of a target cellular RNA.

## EXAMPLE 61

### Computer Embodiments

As used herein the term "nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622" encompasses the nucleotide sequences of SEQ ID NOs. 24-811 and 1600-1622, fragments of SEQ ID NOs. 24-811 and 1600-1622, nucleotide sequences homologous to SEQ ID NOs. 24-811 and 1600-1622 or homologous to fragments of SEQ ID NOs. 24-811 and 1600-1622, and sequences complementary to all of the preceding sequences. The fragments include portions of SEQ ID NOs. 24-811 and 1600-1622 comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of SEQ ID NOs. 24-811 and 1600-1622. Preferably, the fragments are novel

fragments. Preferably the fragments include polynucleotides described in Table II, polynucleotides described in Table III, polynucleotides described in Table IV or portions thereof comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the polynucleotides described in Tables II, III, or IV. Homologous sequences and fragments of SEQ ID NOs. 24-811 and 1600-1622 refer to a sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, or 75% homology to these sequences. Homology may be determined using any of the computer programs and parameters described in Example 18, including BLAST2N with the default parameters or with any modified parameters. Homologous sequences also include RNA sequences in which uridines replace the thymines in the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error as described above. Preferably the homologous sequences and fragments of SEQ ID NOs. 24-811 and 1600-1622 include polynucleotides described in Table II, polynucleotides described in Table III, polynucleotides described in Table IV or portions thereof comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the polynucleotides described in Tables II, III, or IV. It will be appreciated that the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 can be represented in the traditional single character format (See the inside back cover of Styer, Lubert. *Biochemistry*, 3rd edition. W. H Freeman & Co., New York.) or in any other format which records the identity of the nucleotides in a sequence.

As used herein the term "polypeptide codes of SEQ ID NOS. 812-1599" encompasses the polypeptide sequence of SEQ ID NOs. 812-1599 which are encoded by the 5' EST s of SEQ ID NOs. 24-811 and 1600-1622, polypeptide sequences homologous to the polypeptides of SEQ ID NOS. 812-1599, or fragments of any of the preceding sequences. Homologous polypeptide sequences refer to a polypeptide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, 80%, 75% homology to one of the polypeptide sequences of SEQ ID NOS. 812-1599. Homology may be determined using any of the computer programs and parameters described herein, including FASTA with the default parameters or with any modified parameters. The homologous sequences may be obtained using any of the procedures described herein or may result from the correction of a sequencing error as described above. The polypeptide fragments comprise at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of the polypeptides of SEQ ID NOS. 812-1599. Preferably, the fragments are novel fragments. Preferably, the fragments include polypeptides encoded by the polynucleotides described in Table II, or portions thereof comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of the polypeptides encoded by the polynucleotides described in Table II. It will be appreciated that the polypeptide codes of the SEQ ID NOS. 812-1599 can be represented in the traditional single character format or three letter format (See the inside back cover of Starrier, Lubert. *Biochemistry*, 3rd edition. W. H Freeman & Co., New York.) or in any other format which relates the identity of the polypeptides in a sequence.

It will be appreciated by those skilled in the art that the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 and polypeptide codes of SEQ ID NOS. 812-1599 can be stored, recorded, and manipulated on any medium which can be read and accessed by a computer. As used herein, the words "recorded" and "stored" refer to a process for storing information on a computer medium. A skilled artisan can readily adopt any of the presently known methods for recording information on a computer readable medium to generate manufactures comprising one or more of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622, one or more of the polypeptide codes of SEQ ID NOS. 812-1599. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622. Another aspect of the present invention is a computer readable medium having recorded thereon at least 2, 5, 10, 15, 20, 25, 30, or 50 polypeptide codes of SEQ ID NOS. 812-1599.

Computer readable media include magnetically readable media, optically readable media, electronically readable media and magnetic/optical media. For example, the computer readable media may be a hard disk, a floppy disk, a magnetic tape, CD-ROM, Digital Versatile Disk (DVD), Random Access Memory (RAM), or Read Only Memory (ROM) as well as other types of other media known to those skilled in the art.

Embodiments of the present invention include systems, particularly computer systems which store and manipulate the sequence information described herein. One example of a computer system 100 is illustrated in block diagram form in Figure 6. As used herein, "a computer system" refers to the hardware components, software components, and data storage components used to analyze the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599. In one embodiment, the computer system 100 is a Sun Enterprise 1000 server (Sun Microsystems, Palo Alto, CA). The computer system 100 preferably includes a processor for processing, accessing and manipulating the sequence data. The processor 105 can be any well-known type of central processing unit, such as the Pentium III from Intel Corporation, or similar processor from Sun, Motorola, Compaq or International Business Machines.

Preferably, the computer system 100 is a general purpose system that comprises the processor 105 and one or more internal data storage components 110 for storing data, and one or more data retrieving devices for retrieving the data stored on the data storage components. A skilled artisan can readily appreciate that any one of the currently available computer systems are suitable.

In one particular embodiment, the computer system 100 includes a processor 105 connected to a bus which is connected to a main memory 115 (preferably implemented as RAM) and one or more internal data storage devices 110, such as a hard drive and/or other computer readable media having data recorded thereon. In some embodiments, the computer system 100 further includes one or more data retrieving device 118 for reading the data stored on the internal data storage devices 110.

The data retrieving device 118 may represent, for example, a floppy disk drive, a compact disk drive, a magnetic tape drive, etc. In some embodiments, the internal data storage device 110 is a

removable computer readable medium such as a floppy disk, a compact disk, a magnetic tape, etc. containing control logic and/or data recorded thereon. The computer system 100 may advantageously include or be programmed by appropriate software for reading the control logic and/or the data from the data storage component once inserted in the data retrieving device.

The computer system 100 includes a display 120 which is used to display output to a computer user. It should also be noted that the computer system 100 can be linked to other computer systems 125a-c in a network or wide area network to provide centralized access to the computer system 100.

Software for accessing and processing the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599 (such as search tools, compare tools, and modeling tools etc.) may reside in main memory 115 during execution.

In some embodiments, the computer system 100 may further comprise a sequence comparer for comparing the above-described nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide codes of SEQ ID NOS. 812-1599 stored on a computer readable medium to reference nucleotide or polypeptide sequences stored on a computer readable medium. A "sequence comparer" refers to one or more programs which are implemented on the computer system 100 to compare a nucleotide or polypeptide sequence with other nucleotide or polypeptide sequences and/or compounds including but not limited to peptides, peptidomimetics, and chemicals stored within the data storage means. For example, the sequence comparer may compare the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622, or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599 stored on a computer readable medium to reference sequences stored on a computer readable medium to identify homologies, motifs implicated in biological function, or structural motifs. The various sequence comparer programs identified elsewhere in this patent specification are particularly contemplated for use in this aspect of the invention.

Figure 7 is a flow diagram illustrating one embodiment of a process 200 for comparing a new nucleotide or protein sequence with a database of sequences in order to determine the homology levels between the new sequence and the sequences in the database. The database of sequences can be a private database stored within the computer system 100, or a public database such as GENBANK, PIR OR SWISSPROT that is available through the Internet.

The process 200 begins at a start state 201 and then moves to a state 202 wherein the new sequence to be compared is stored to a memory in a computer system 100. As discussed above, the memory could be any type of memory, including RAM or an internal storage device.

The process 200 then moves to a state 204 wherein a database of sequences is opened for analysis and comparison. The process 200 then moves to a state 206 wherein the first sequence stored in the database is read into a memory on the computer. A comparison is then performed at a state 210 to determine if the first sequence is the same as the second sequence. It is important to note that this step is not limited to performing an exact comparison between the new sequence and the first sequence in the

database. Well-known methods are known to those of skill in the art for comparing two nucleotide or protein sequences, even if they are not identical. For example, gaps can be introduced into one sequence in order to raise the homology level between the two tested sequences. The parameters that control whether gaps or other features are introduced into a sequence during comparison are normally entered by the user of the computer system.

Once a comparison of the two sequences has been performed at the state 210, a determination is made at a decision state 210 whether the two sequences are the same. Of course, the term "same" is not limited to sequences that are absolutely identical. Sequences that are within the homology parameters entered by the user will be marked as "same" in the process 200.

If a determination is made that the two sequences are the same, the process 200 moves to a state 214 wherein the name of the sequence from the database is displayed to the user. This state notifies the user that the sequence with the displayed name fulfills the homology constraints that were entered. Once the name of the stored sequence is displayed to the user, the process 200 moves to a decision state 218 wherein a determination is made whether more sequences exist in the database. If no more sequences exist in the database, then the process 200 terminates at an end state 220. However, if more sequences do exist in the database, then the process 200 moves to a state 224 wherein a pointer is moved to the next sequence in the database so that it can be compared to the new sequence. In this manner, the new sequence is aligned and compared with every sequence in the database.

It should be noted that if a determination had been made at the decision state 212 that the sequences were not homologous, then the process 200 would move immediately to the decision state 218 in order to determine if any other sequences were available in the database for comparison.

Accordingly, one aspect of the present invention is a computer system comprising a processor, a data storage device having stored thereon a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 or a polypeptide code of SEQ ID NOS. 812-1599, a data storage device having retrievably stored thereon reference nucleotide sequences or polypeptide sequences to be compared to the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide code of SEQ ID NOS. 812-1599 and a sequence comparer for conducting the comparison. The sequence comparer may indicate a homology level between the sequences compared or identify structural motifs in the above described nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and polypeptide codes of SEQ ID NOS. 812-1599 or it may identify structural motifs in sequences which are compared to these nucleic acid codes and polypeptide codes. In some embodiments, the data storage device may have stored thereon the sequences of at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or polypeptide codes of SEQ ID NOS. 812-1599.

Another aspect of the present invention is a method for determining the level of homology between a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a reference nucleotide sequence, comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through the use of a computer program which determines homology levels and determining homology

between the nucleic acid code and the reference nucleotide sequence with the computer program. The computer program may be any of a number of computer programs for determining homology levels, including those specifically enumerated herein, including BLAST2N with the default parameters or with any modified parameters. The method may be implemented using the computer systems described above. The method may also be performed by reading 2, 5, 10, 15, 20, 25, 30, or 50 of the above described nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 through use of the computer program and determining homology between the nucleic acid codes and reference nucleotide sequences .

Figure 8 is a flow diagram illustrating one embodiment of a process 250 in a computer for determining whether two sequences are homologous. The process 250 begins at a start state 252 and then moves to a state 254 wherein a first sequence to be compared is stored to a memory. The second sequence to be compared is then stored to a memory at a state 256. The process 250 then moves to a state 260 wherein the first character in the first sequence is read and then to a state 262 wherein the first character of the second sequence is read. It should be understood that if the sequence is a nucleotide sequence, then the character would normally be either A, T, C, G or U. If the sequence is a protein sequence, then it should be in the single letter amino acid code so that the first and sequence sequences can be easily compared.

A determination is then made at a decision state 264 whether the two characters are the same. If they are the same, then the process 250 moves to a state 268 wherein the next characters in the first and second sequences are read. A determination is then made whether the next characters are the same. If they are, then the process 250 continues this loop until two characters are not the same. If a determination is made that the next two characters are not the same, the process 250 moves to a decision state 274 to determine whether there are any more characters either sequence to read.

If there aren't any more characters to read, then the process 250 moves to a state 276 wherein the level of homology between the first and second sequences is displayed to the user. The level of homology is determined by calculating the proportion of characters between the sequences that were the same out of the total number of sequences in the first sequence. Thus, if every character in a first 100 nucleotide sequence aligned with a every character in a second sequence, the homology level would be 100%.

Alternatively, the computer program may be a computer program which compares the nucleotide sequences of the nucleic acid codes of the present invention, to reference nucleotide sequences in order to determine whether the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 differs from a reference nucleic acid sequence at one or more positions. Optionally such a program records the length and identity of inserted, deleted or substituted nucleotides with respect to the sequence of either the reference polynucleotide or the nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622. In one embodiment, the computer program may be a program which determines whether the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 contain a biallelic marker

or single nucleotide polymorphism (SNP) with respect to a reference nucleotide sequence. This single nucleotide polymorphism may comprise a single base substitution, insertion, or deletion, while this biallelic marker may comprise abour one to ten consecutive bases substituted, inserted or deleted.

Another aspect of the present invention is a method for determining the level of homology between a polypeptide code of SEQ ID NOS. 812-1599 and a reference polypeptide sequence, comprising the steps of reading the polypeptide code of SEQ ID NOS. 812-1599 and the reference polypeptide sequence through use of a computer program which determines homology levels and determining homology between the polypeptide code and the reference polypeptide sequence using the computer program.

Accordingly, another aspect of the present invention is a method for determining whether a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 differs at one or more nucleotides from a reference nucleotide sequence comprising the steps of reading the nucleic acid code and the reference nucleotide sequence through use of a computer program which identifies differences between nucleic acid sequences and identifying differences between the nucleic acid code and the reference nucleotide sequence with the computer program. In some embodiments, the computer program is a program which identifies single nucleotide polymorphisms. The method may be implemented by the computer systems described above and the method illustrated in Figure 8. The method may also be performed by reading at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 and the reference nucleotide sequences through the use of the computer program and identifying differences between the nucleic acid codes and the reference nucleotide sequences with the computer program.

In other embodiments the computer based system may further comprise an identifier for identifying features within the nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599.

An "identifier" refers to one or more programs which identifies certain features within the above-described nucleotide sequences of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the amino acid sequences of the polypeptide codes of SEQ ID NOS. 812-1599. In one embodiment, the identifier may comprise a program which identifies an open reading frame in the cDNAs codes of SEQ ID NOs. 24-811 and 1600-1622.

Figure 9 is a flow diagram illustrating one embodiment of an identifier process 300 for detecting the presence of a feature in a sequence. The process 300 begins at a start state 302 and then moves to a state 304 wherein a first sequence that is to be checked for features is stored to a memory 115 in the computer system 100. The process 300 then moves to a state 306 wherein a database of sequence features is opened. Such a database would include a list of each feature's attributes along with the name of the feature. For example, a feature name could be "Initiation Codon" and the attribute would be "ATG". Another example would be the feature name "TAATAA Box" and the feature attribute would be "TAATAA". An example of such a database is produced by the University of Wisconsin Genetics Computer Group (www.gcg.com).

Once the database of features is opened at the state 306, the process 300 moves to a state 308 wherein the first feature is read from the database. A comparison of the attribute of the first feature with the first sequence is then made at a state 310. A determination is then made at a decision state 316 whether the attribute of the feature was found in the first sequence. If the attribute was found, then the process 300 moves to a state 318 wherein the name of the found feature is displayed to the user.

The process 300 then moves to a decision state 320 wherein a determination is made whether move features exist in the database. If no more features do exist, then the process 300 terminates at an end state 324. However, if more features do exist in the database, then the process 300 reads the next sequence feature at a state 326 and loops back to the state 310 wherein the attribute of the next feature is compared against the first sequence.

It should be noted, that if the feature attribute is not found in the first sequence at the decision state 316, the process 300 moves directly to the decision state 320 in order to determine if any more features exist in the database.

In another embodiment, the identifier may comprise a molecular modeling program which determines the 3-dimensional structure of the polypeptides codes of SEQ ID NOS. 812-1599. In some embodiments, the molecular modeling program identifies target sequences that are most compatible with profiles representing the structural environments of the residues in known three-dimensional protein structures. (See, e.g., Eisenberg et al., U.S. Patent No. 5,436,850 issued July 25, 1995). In another technique, the known three-dimensional structures of proteins in a given family are superimposed to define the structurally conserved regions in that family. This protein modeling technique also uses the known three-dimensional structure of a homologous protein to approximate the structure of the polypeptide codes of SEQ ID NOS. 812-1599. (See e.g., Srinivasan, et al., U.S. Patent No. 5,557,535 issued September 17, 1996). Conventional homology modeling techniques have been used routinely to build models of proteases and antibodies. (Sowdhamini et al., Protein Engineering 10:207, 215 (1997)). Comparative approaches can also be used to develop three-dimensional protein models when the protein of interest has poor sequence identity to template proteins. In some cases, proteins fold into similar three-dimensional structures despite having very weak sequence identities. For example, the three-dimensional structures of a number of helical cytokines fold in similar three-dimensional topology in spite of weak sequence homology.

The recent development of threading methods now enables the identification of likely folding patterns in a number of situations where the structural relatedness between target and template(s) is not detectable at the sequence level. Hybrid methods, in which fold recognition is performed using Multiple Sequence Threading (MST), structural equivalencies are deduced from the threading output using a distance geometry program DRAGON to construct a low resolution model, and a full-atom representation is constructed using a molecular modeling package such as QUANTA.

According to this 3-step approach, candidate templates are first identified by using the novel fold recognition algorithm MST, which is capable of performing simultaneous threading of multiple aligned sequences onto one or more 3-D structures. In a second step, the structural equivalencies obtained from the MST output are converted into interresidue distance restraints and fed into the distance geometry program DRAGON, together with auxiliary information obtained from secondary structure predictions. The program combines the restraints in an unbiased manner and rapidly generates a large number of low resolution model confirmations. In a third step, these low resolution model confirmations are converted into full-atom models and subjected to energy minimization using the molecular modeling package QUANTA. (See e.g., Aszódi et al., Proteins:Structure, Function, and Genetics, Supplement 1:38-42 (1997)).

The results of the molecular modeling analysis may then be used in rational drug design techniques to identify agents which modulate the activity of the polypeptide codes of SEQ ID NOS. 812-1599.

Accordingly, another aspect of the present invention is a method of identifying a feature within the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 comprising reading the nucleic acid code(s) or the polypeptide code(s) through the use of a computer program which identifies features therein and identifying features within the nucleic acid code(s) or polypeptide code(s) with the computer program. In one embodiment, computer program comprises a computer program which identifies open reading frames. In a further embodiment, the computer program identifies structural motifs in a polypeptide sequence. In another embodiment, the computer program comprises a molecular modeling program. The method may be performed by reading a single sequence or at least 2, 5, 10, 15, 20, 25, 30, or 50 of the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 through the use of the computer program and identifying features within the nucleic acid codes or polypeptide codes with the computer program.

The nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 may be stored and manipulated in a variety of data processor programs in a variety of formats. For example, the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599 may be stored as text in a word processing file, such as MicrosoftWORD or WORDPERFECT or as an ASCII file in a variety of database programs familiar to those of skill in the art, such as DB2, SYBASE, or ORACLE. In addition, many computer programs and databases may be used as sequence comparers, identifiers, or sources of reference nucleotide or polypeptide sequences to be compared to the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599. The following list is intended not to limit the invention but to provide guidance to programs and databases which are useful with the nucleic acid codes of SEQ ID NOs. 24-811 and 1600-1622 or the polypeptide codes of SEQ ID NOS. 812-1599. The programs and databases which may be used include, but are not limited to: MacPattern (EMBL),

DiscoveryBase (Molecular Applications Group), GeneMine (Molecular Applications Group), Look (Molecular Applications Group), MacLook (Molecular Applications Group), BLAST and BLAST2 (NCBI), BLASTN and BLASTX (Altschul et al, *J. Mol. Biol.* 215: 403 (1990)), FASTA (Pearson and Lipman, *Proc. Natl. Acad. Sci. USA*, 85: 2444 (1988)), FASTDB (Brutlag et al. Comp. App. Biosci. 6:237-245, 1990), Catalyst (Molecular Simulations Inc.), Catalyst/SHAPE (Molecular Simulations Inc.), Cerius$^2$.DBAccess (Molecular Simulations Inc.), HypoGen (Molecular Simulations Inc.), Insight II, (Molecular Simulations Inc.), Discover (Molecular Simulations Inc.), CHARMm (Molecular Simulations Inc.), Felix (Molecular Simulations Inc.), DelPhi, (Molecular Simulations Inc.), QuanteMM, (Molecular Simulations Inc.), Homology (Molecular Simulations Inc.), Modeler (Molecular Simulations Inc.), ISIS (Molecular Simulations Inc.), Quanta/Protein Design (Molecular Simulations Inc.), WebLab (Molecular Simulations Inc.), WebLab Diversity Explorer (Molecular Simulations Inc.), Gene Explorer (Molecular Simulations Inc.), SeqFold (Molecular Simulations Inc.), the EMBL/Swissprotein database, the MDL Available Chemicals Directory database, the MDL Drug Data Report data base, the Comprehensive Medicinal Chemistry database, Derwents's World Drug Index database, the BioByteMasterFile database, the Genbank database, and the Genseqn database. Many other programs and data bases would be apparent to one of skill in the art given the present disclosure.

Motifs which may be detected using the above programs include sequences encoding leucine zippers, helix-turn-helix motifs, glycosylation sites, ubiquitination sites, alpha helices, and beta sheets, signal sequences encoding signal peptides which direct the secretion of the encoded proteins, sequences implicated in transcription regulation such as homeoboxes, acidic stretches, enzymatic active sites, substrate binding sites, and enzymatic cleavage sites.

## EXAMPLE 62

### Methods of Making Nucleic Acids

The present invention also comprises methods of making the EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids. The methods comprise sequentially linking together nucleotides to produce the nucleic acids having the preceding sequences. A variety of methods of synthesizing nucleic acids are known to those skilled in the art.

In many of these methods, synthesis is conducted on a solid support. These included the 3' phosphoramidite methods in which the 3' terminal base of the desired oligonucleotide is immobilized on an insoluble carrier. The nucleotide base to be added is blocked at the 5' hydroxyl and activated at the 3' hydroxyl so as to cause coupling with the immobilized nucleotide base. Deblocking of the new immobilized nucleotide compound and repetition of the cycle will produce the desired polynucleotide. Alternatively, polynucleotides may be prepared as described in U.S. Patent No. 5,049,656. In some embodiments, several polynucleotides prepared as described above are ligated together to generate longer polynucleotides having a desired sequence.

## EXAMPLE 63

Methods of Making Polypeptides

The present invention also comprises methods of making the polynucleotides encoded by EST-related nucleic acids, fragments of EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids and methods of making the EST-related polypeptides, fragments of EST-related polypeptides, positional segments of EST-related polypeptides, or fragments of EST-related polypeptides. The methods comprise sequentially linking together amino acids to produce the nucleic polypeptides having the preceding sequences. In some embodiments, the polypeptides made by these methods are 150 amino acid or less in length. In other embodiments, the polypeptides made by these methods are 120 amino acids or less in length.

A variety of methods of making polypeptides are known to those skilled in the art, including methods in which the carboxyl terminal amino acid is bound to polyvinyl benzene or another suitable resin. The amino acid to be added possesses blocking groups on its amino moiety and any side chain reactive groups so that only its carboxyl moiety can react. The carboxyl group is activated with carbodiimide or another activating agent and allowed to couple to the immobilized amino acid. After removal of the blocking group, the cycle is repeated to generate a polypeptide having the desired sequence. Alternatively, the methods described in U.S. Patent No. 5,049,656 may be used.

As discussed above, the EST-related nucleic acids, fragments of the EST-related nucleic acids, positional segments of the EST-related nucleic acids, or fragments of positional segments of the EST-related nucleic acids can be used for various purposes. The polynucleotides can be used to express recombinant protein for analysis, characterization or therapeutic use; production of secreted polypeptides or chimeric polypeptides, antibody production, as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination for expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein or polypeptide which binds or potentially binds to another protein or polypeptide (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris *et al.*, *Cell* 75:791-803 (1993)) to identify polynucleotides encoding the other protein or polypeptide with which binding occurs or to identify inhibitors of the binding interaction.

The proteins or polypeptides provided by the present invention can similarly be used in assays to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein or polypeptide binds or potentially binds to another protein or polypeptide (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins or polypeptides involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning; A Laboratory Manual," 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology; Guide to Molecular Cloning Techniques," Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Polynucleotides and proteins or polypeptides of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be limited only by reference to the appended claims.

Sequence Listing Free Text

The following free text appears in the accompanying Sequence Listing:

Von Heijne matrix

score

sequence

name

martinspector prediction

## CLAIMS

1. A purified nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

2. A purified nucleic acid comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622.

3. A purified or isolated polypeptide comprising a sequence selected from the group consisting of the sequences of SEQ ID NOs. 812-1599.

4. A method of making a cDNA comprising the steps of:

a) contacting a collection of mRNA molecules from human cells with a primer comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622;

b) hybridizing said primer to an mRNA in said collection that encodes said protein;

c) reverse transcribing said hybridized primer to make a first cDNA strand from said mRNA;

d) making a second cDNA strand complementary to said first cDNA strand; and

e) isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

5. A method of making a cDNA comprising the steps of:

a) obtaining a cDNA comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622;

b) contacting said cDNA with a detectable probe comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 under conditions which permit said probe to hybridize to said cDNA;

c) identifying a cDNA which hybridizes to said detectable probe; and

d) isolating said cDNA which hybridizes to said probe.

6. A method of making a cDNA comprising the steps of:

a) contacting a collection of mRNA molecules from human cells with a first primer capable of hybridizing to the polyA tail of said mRNA;

b) hybridizing said first primer to said polyA tail;

c) reverse transcribing said mRNA to make a first cDNA strand;

d) making a second cDNA strand complementary to said first cDNA strand using at least one primer comprising at least 15 consecutive nucleotides of a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622; and

e) isolating the resulting cDNA comprising said first cDNA strand and said second cDNA strand.

7. A method of making a polypeptide comprising the steps of:

a) obtaining a cDNA which encodes a polypeptide encoded by a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOs. 24-811 or a cDNA which encodes a polypeptide comprising at least 10 consecutive amino acids of a polypeptide encoded by a sequence selected from the group consisting of SEQ ID NOs. 24-811;

b) inserting said cDNA in an expression vector such that said cDNA is operably linked to a promoter;

c) introducing said expression vector into a host cell whereby said host cell produces the protein encoded by said cDNA; and

d) isolating said protein.

8. In an array of discrete ESTs or fragments thereof of at least 15 nucleotides in length, the improvement comprising inclusion in said array of at least one sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequence.

9. The array of Claim 8 including therein at least five sequences selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to the sequences of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequences.

10. An enriched population of recombinant nucleic acids, said recombinant nucleic acids comprising an insert nucleic acid and a backbone nucleic acid, wherein at least 5% of said insert nucleic acids in said population comprise a sequence selected from the group consisting of SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622, the sequences complementary to SEQ ID NOs. 24-811 and SEQ ID NOs. 1600-1622 and fragments comprising at least 15 consecutive nucleotides of said sequences.

11. An antibody composition capable of selectively binding to an epitope-containing fragment of a polypeptide comprising a contiguous span of at least 8 amino acids of any of SEQ ID NOs. 812-1599, wherein said antibody is polyclonal or monoclonal.

12. A computer readable medium having stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQ ID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

13. A computer system comprising a processor and a data storage device wherein said data storage device has stored thereon a sequence selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599.

14. The computer system of Claim 13 further comprising a sequence comparer and a data storage device having reference sequences stored thereon.

15. The computer system of Claim 14 wherein said sequence comparer comprises a computer program which indicates polymorphisms.

16. The computer system of Claim 13 further comprising an identifier which identifies features in said sequence.

17. A method for comparing a first sequence to a reference sequence wherein said first sequence is selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of:

a) reading said first sequence and said reference sequence through use of a computer program which compares sequences; and

b) determining differences between said first sequence and said reference sequence with said computer program.

18. The method of Claim 17, wherein said step of determining differences between the first sequence and the reference sequence comprises identifying polymorphisms.

19. A method for identifying a feature in a sequence selected from the group consisting of a nucleic acid code of SEQID NOs. 24-811 and 1600-1622 and a polypeptide code of SEQ ID NOs. 812-1599 comprising the steps of:

a) reading said sequence through the use of a computer program which identifies features in sequences; and

b) identifying features in said sequence with said computer program.

20. A vector comprising a nucleic acid according to either Claims 1 or 2.

21. A host cell containing a nucleic acid of Claim 20.

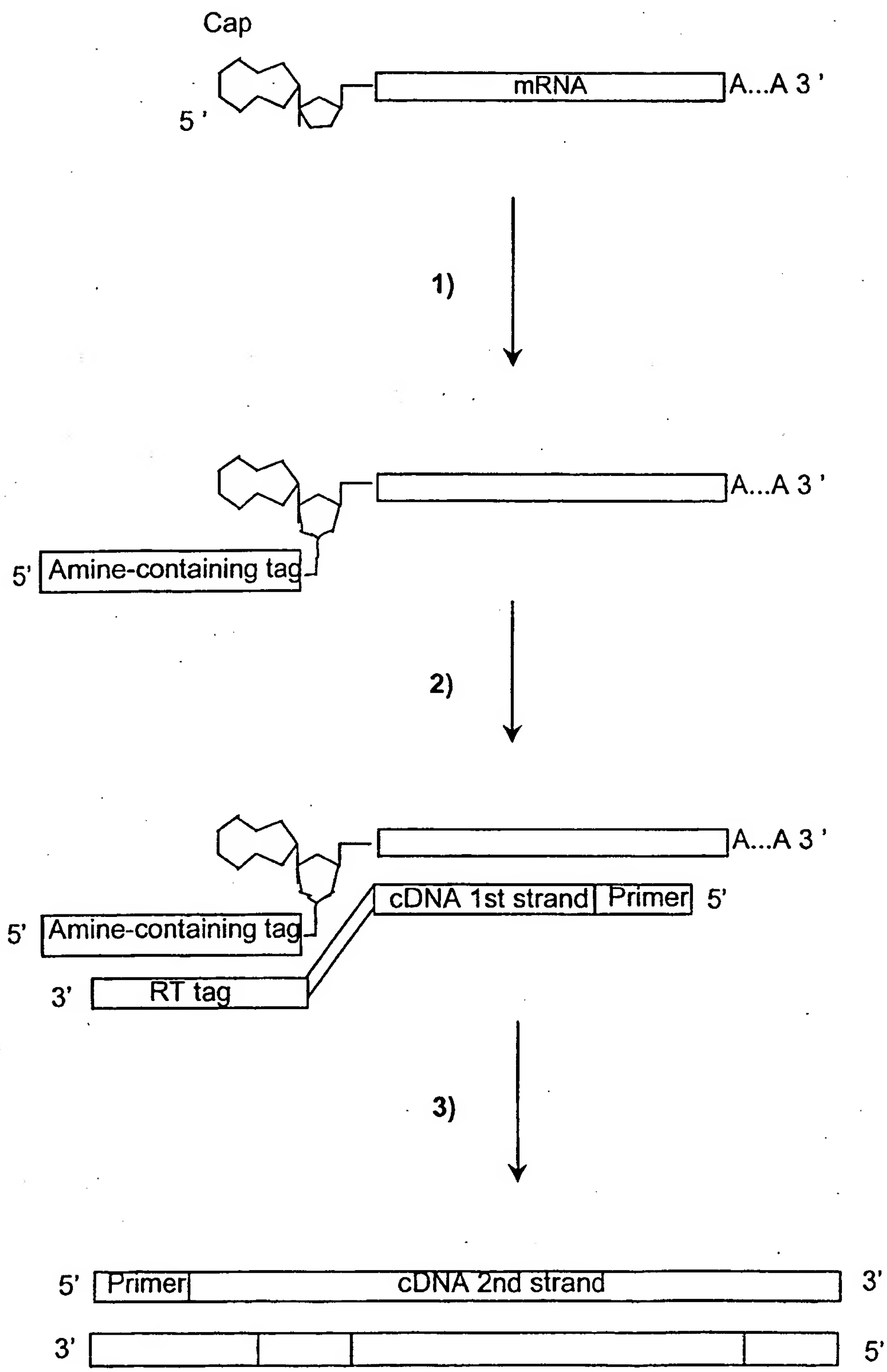
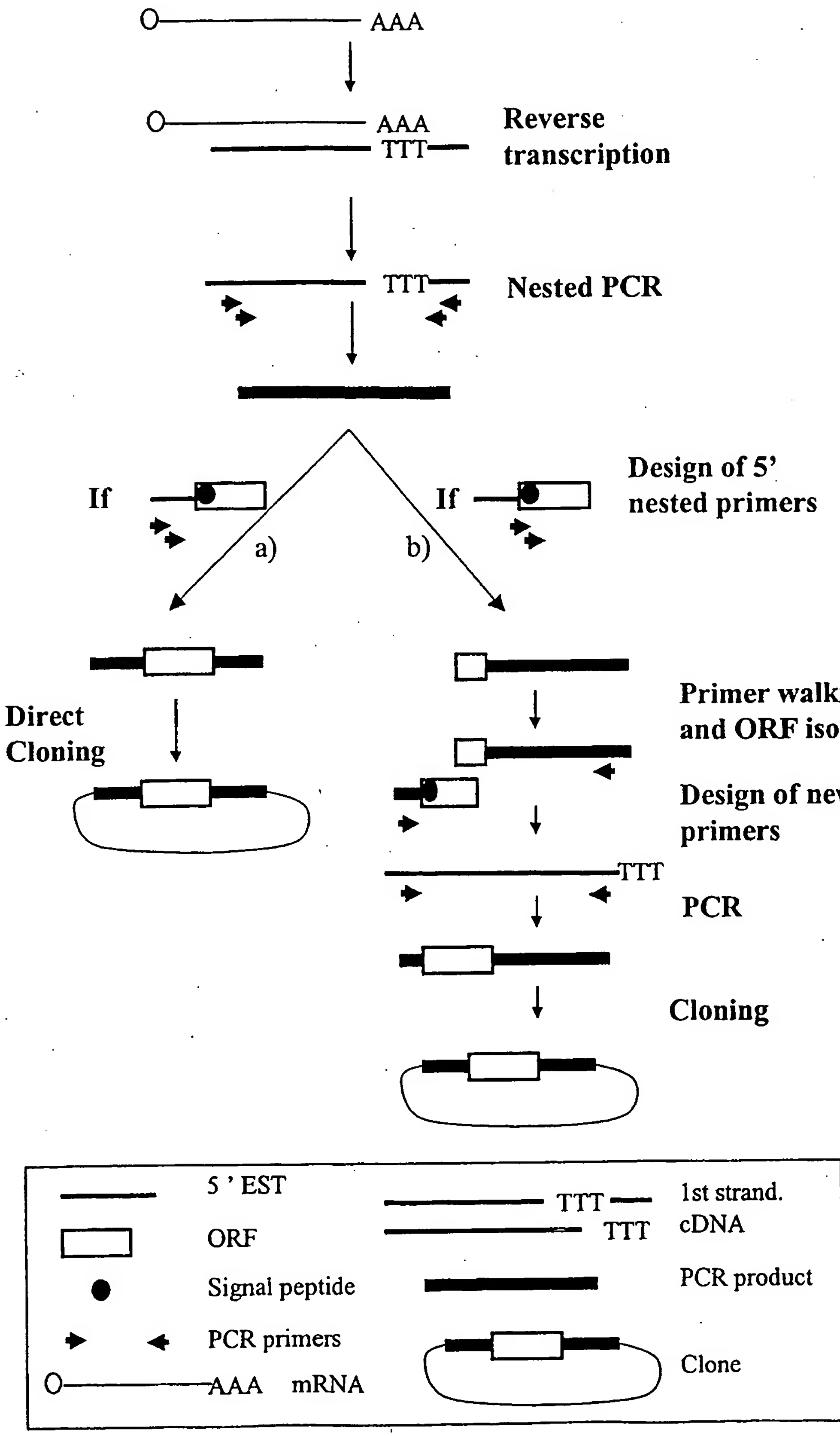

Cap
5'
mRNA
A...A 3'
1)
A...A 3'
5'
Amine-containing tag
2)
A...A 3'
cDNA 1st strand
Primer
5'
5'
Amine-containing tag
3'
RT tag
3)
5'
Primer
cDNA 2nd strand
3'
3'
5'

**Figure 1**

| Minimum signal peptide score | false positive rate | false negative rate | proba(0.1) | proba(0.2) |
|---|---|---|---|---|
| 3,5 | 0,121 | 0,036 | 0,467 | 0,664 |
| 4 | 0,096 | 0,06 | 0,519 | 0,708 |
| 4,5 | 0,078 | 0,079 | 0,565 | 0,745 |
| 5 | 0,062 | 0,098 | 0,615 | 0,782 |
| 5,5 | 0,05 | 0,127 | 0,659 | 0,813 |
| 6 | 0,04 | 0,163 | 0,694 | 0,836 |
| 6,5 | 0,033 | 0,202 | 0,725 | 0,855 |
| 7 | 0,025 | 0,248 | 0,763 | 0,878 |
| 7,5 | 0,021 | 0,304 | 0,78 | 0,889 |
| 8 | 0,015 | 0,368 | 0,816 | 0,909 |
| 8,5 | 0,012 | 0,418 | 0,836 | 0,92 |
| 9 | 0,009 | 0,512 | 0,856 | 0,93 |
| 9,5 | 0,007 | 0,581 | 0,863 | 0,934 |
| 10 | 0,006 | 0,679 | 0,835 | 0,919 |

**Figure 2**



AAA
AAA
TTT
Reverse transcription
TTT
Nested PCR
If
If
a)
b)
Design of 5' nested primers
Direct Cloning
Primer walking and ORF isolation
Design of new primers
TTT
PCR
Cloning
5 ' EST
ORF
Signal peptide
PCR primers
AAA mRNA
TTT
TTT
1st strand. cDNA
PCR product
Clone


Figure 3

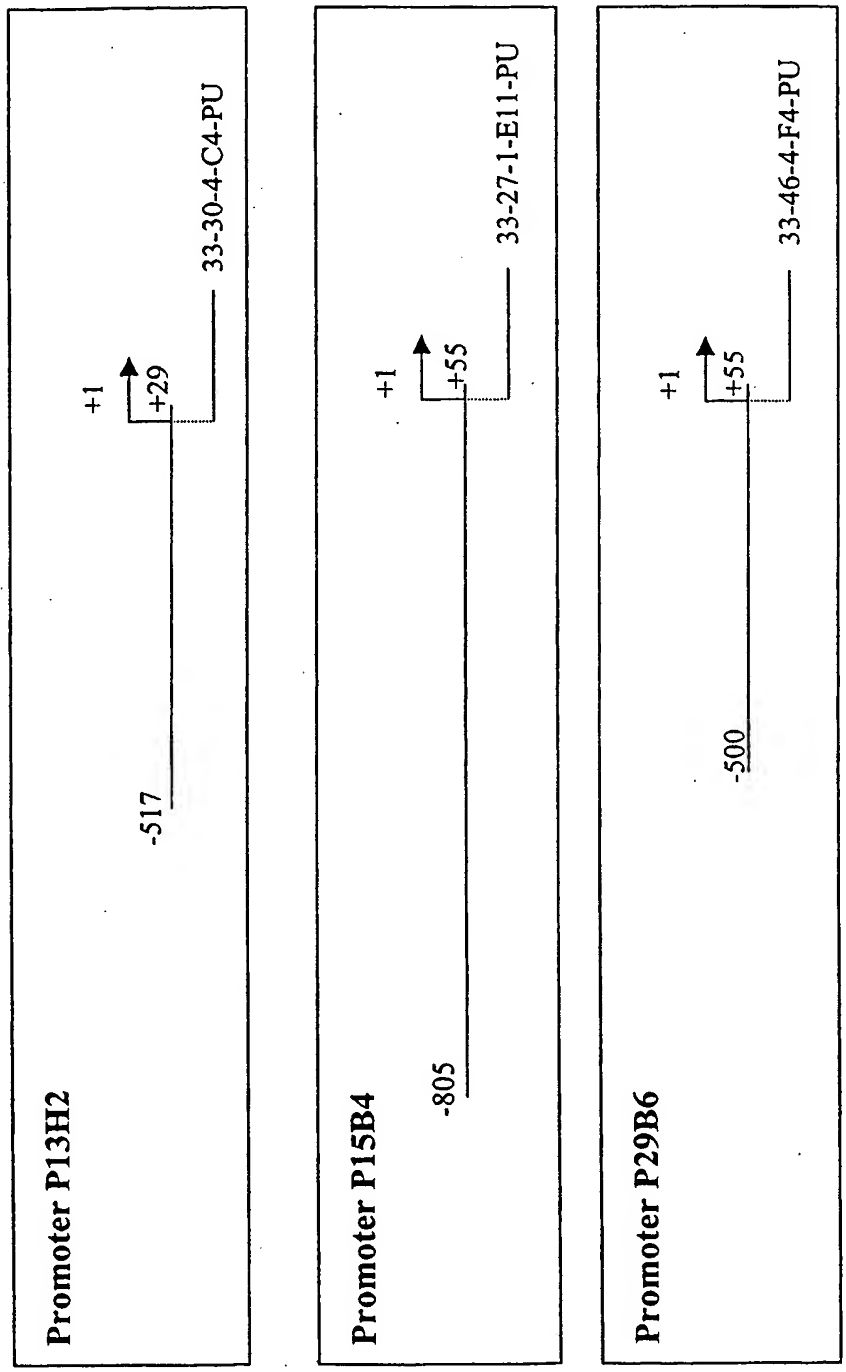

Promoter P13H2
+1
+29
-517
33-30-4-C4-PU
Promoter P15B4
+1
+55
-805
33-27-1-E11-PU
Promoter P29B6
+1
+55
-500
33-46-4-F4-PU

Figure 4

Promoter sequence P13H2 (546 bp):

| Matrix | Position | Orientation | Score | Length | Sequence |
|---|---|---|---|---|---|
| CMYB_01 | -502 | + | 0.983 | 9 | TGTCAGTTG |
| MYOD_Q6 | -501 | - | 0.961 | 10 | CCCAACTGAC |
| S8_01 | -444 | - | 0.960 | 11 | AATAGAATTAG |
| S8_01 | -425 | + | 0.966 | 11 | AACTAAATTAG |
| DELTAEF1_01 | -390 | - | 0.960 | 11 | GCACACCTCAG |
| GATA_C | -364 | - | 0.964 | 11 | AGATAAATCCA |
| CMYB_01 | -349 | + | 0.958 | 9 | CTTCAGTTG |
| GATA1_02 | -343 | + | 0.959 | 14 | TTGTAGATAGGACA |
| GATA_C | -339 | + | 0.953 | 11 | AGATAGGACAT |
| TAL1ALPHAE47_01 | -235 | + | 0.973 | 16 | CATAACAGATGGTAAG |
| TAL1BETAE47_01 | -235 | + | 0.983 | 16 | CATAACAGATGGTAAG |
| TAL1BETAITF2_01 | -235 | + | 0.978 | 16 | CATAACAGATGGTAAG |
| MYOD_Q6 | -232 | - | 0.954 | 10 | ACCATCTGTT |
| GATA1_04 | -217 | - | 0.953 | 13 | TCAAGATAAAGTA |
| IK1_01 | -126 | + | 0.963 | 13 | AGTTGGGAATTCC |
| IK2_01 | -126 | + | 0.985 | 12 | AGTTGGGAATTC |
| CREL_01 | -123 | + | 0.962 | 10 | TGGGAATTCC |
| GATA1_02 | -96 | + | 0.950 | 14 | TCAGTGATATGGCA |
| SRY_02 | -41 | - | 0.951 | 12 | TAAAACAAAACA |
| E2F_02 | -33 | + | 0.957 | 8 | TTTAGCGC |
| MZF1_01 | -5 | - | 0.975 | 8 | TGAGGGGA |

Promoter sequence P15B4 (861bp) :

| Matrix | Position | Orientation | Score | Length | Sequence |
|---|---|---|---|---|---|
| NFY_Q6 | -748 | - | 0.956 | 11 | GGACCAATCAT |
| MZF1_01 | -738 | + | 0.962 | 8 | CCTGGGGA |
| CMYB_01 | -684 | + | 0.994 | 9 | TGACCGTTG |
| VMYB_02 | -682 | - | 0.985 | 9 | TCCAACGGT |
| STAT_01 | -673 | + | 0.968 | 9 | TTCCTGGAA |
| STAT_01 | -673 | - | 0.951 | 9 | TTCCAGGAA |
| MZF1_01 | -556 | - | 0.956 | 8 | TTGGGGGA |
| IK2_01 | -451 | + | 0.965 | 12 | GAATGGGATTTC |
| MZF1_01 | -424 | + | 0.986 | 8 | AGAGGGGA |
| SRY_02 | -398 | - | 0.955 | 12 | GAAAACAAAACA |
| MZF1_01 | -216 | + | 0.960 | 8 | GAAGGGGA |
| MYOD_Q6 | -190 | + | 0.981 | 10 | AGCATCTGCC |
| DELTAEF1_01 | -176 | + | 0.958 | 11 | TCCCACCTTCC |
| S8_01 | 5 | - | 0.992 | 11 | GAGGCAATTAT |
| MZF1_01 | 16 | - | 0.986 | 8 | AGAGGGGA |

Promoter sequence P29B6 (555 bp) :

| Matrix | Position | Orientation | Score | Length | Sequence |
|---|---|---|---|---|---|
| ARNT_01 | -311 | + | 0.964 | 16 | GGACTCACGTGCTGCT |
| NMYC_01 | -309 | + | 0.965 | 12 | ACTCACGTGCTG |
| USF_01 | -309 | + | 0.985 | 12 | ACTCACGTGCTG |
| USF_01 | -309 | - | 0.985 | 12 | CAGCACGTGAGT |
| NMYC_01 | -309 | - | 0.956 | 12 | CAGCACGTGAGT |
| MYCMAX_02 | -309 | - | 0.972 | 12 | CAGCACGTGAGT |
| USF_C | -307 | + | 0.997 | 8 | TCACGTGC |
| USF_C | -307 | - | 0.991 | 8 | GCACGTGA |
| MZF1_01 | -292 | - | 0.968 | 8 | CATGGGGA |
| ELK1_02 | -105 | + | 0.963 | 14 | CTCTCCGGAAGCCT |
| CETS1P54_01 | -102 | + | 0.974 | 10 | TCCGGAAGCC |
| AP1_Q4 | -42 | - | 0.963 | 11 | AGTGACTGAAC |
| AP1FJ_Q2 | -42 | - | 0.961 | 11 | AGTGACTGAAC |
| PADS_C | 45 | + | 1.000 | 9 | TGTGGTCTC |

Figure 5

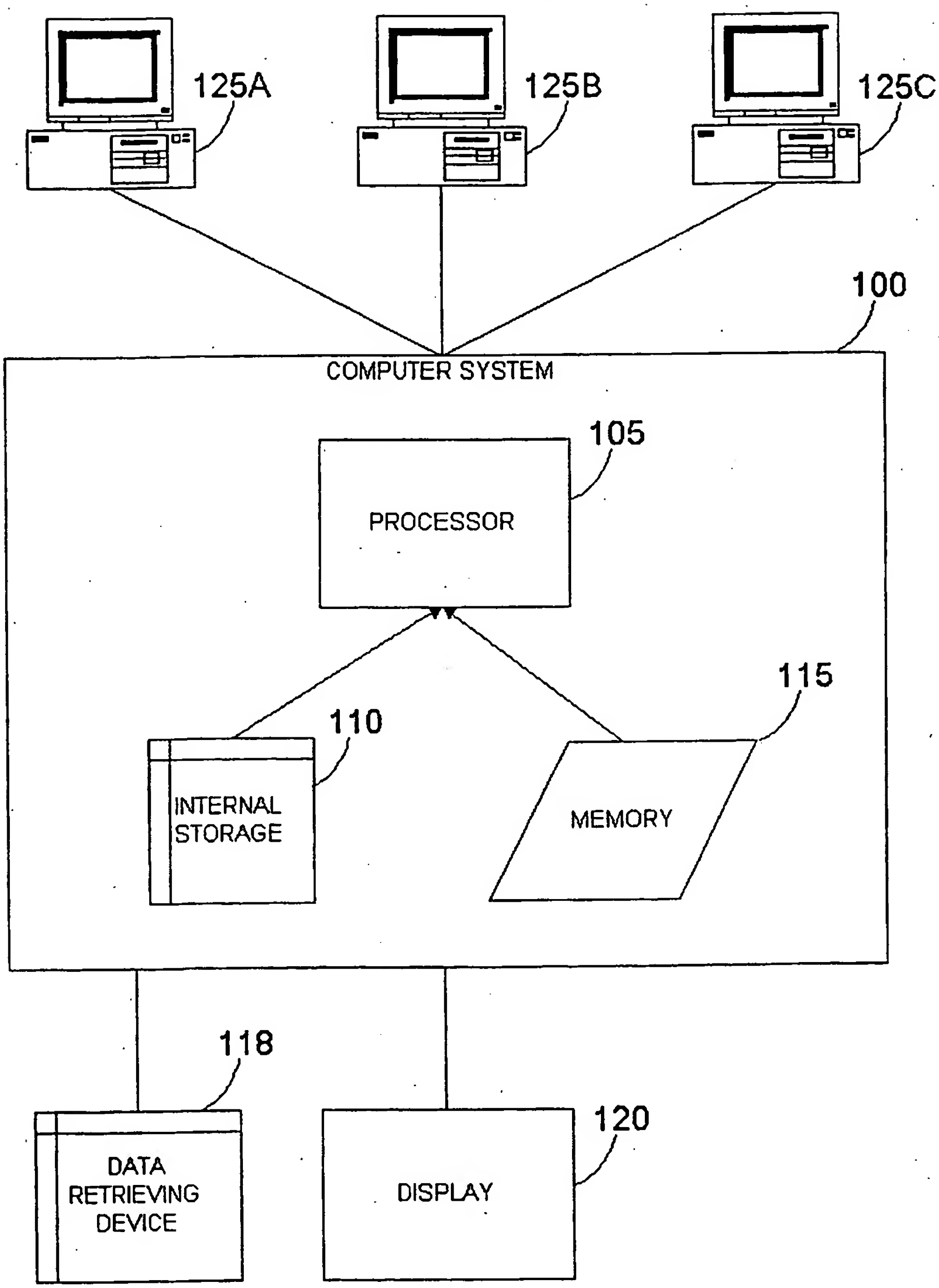
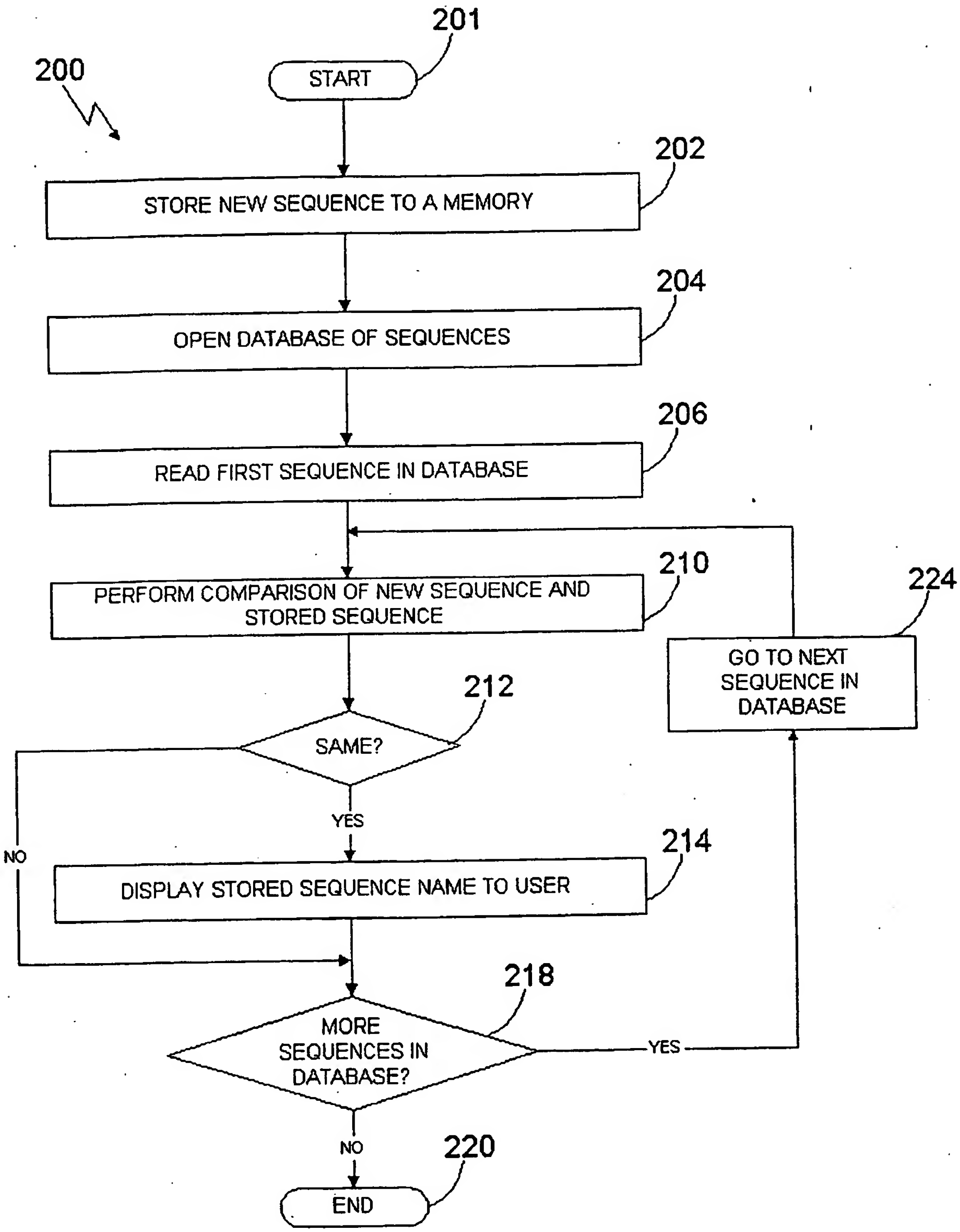

125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
110
INTERNAL STORAGE
115
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIGURE 6



200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
224
GO TO NEXT SEQUENCE IN DATABASE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END


FIGURE 7

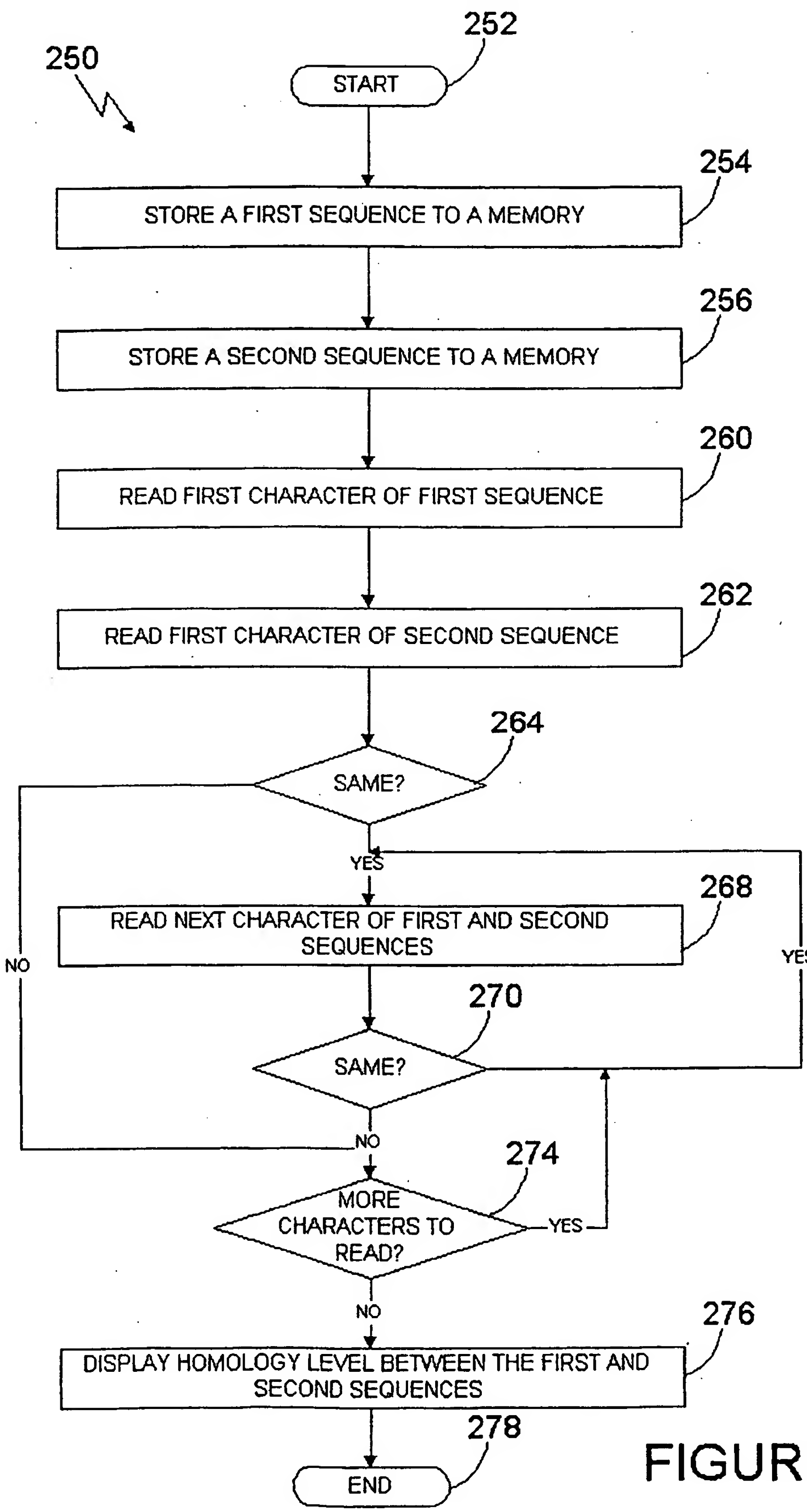

250
252
START
254
STORE A FIRST SEQUENCE TO A MEMORY
256
STORE A SECOND SEQUENCE TO A MEMORY
260
READ FIRST CHARACTER OF FIRST SEQUENCE
262
READ FIRST CHARACTER OF SECOND SEQUENCE
264
SAME?
YES
NO
268
READ NEXT CHARACTER OF FIRST AND SECOND SEQUENCES
YES
270
SAME?
NO
274
MORE CHARACTERS TO READ?
YES
NO
276
DISPLAY HOMOLOGY LEVEL BETWEEN THE FIRST AND SECOND SEQUENCES
278
END

FIGURE 8

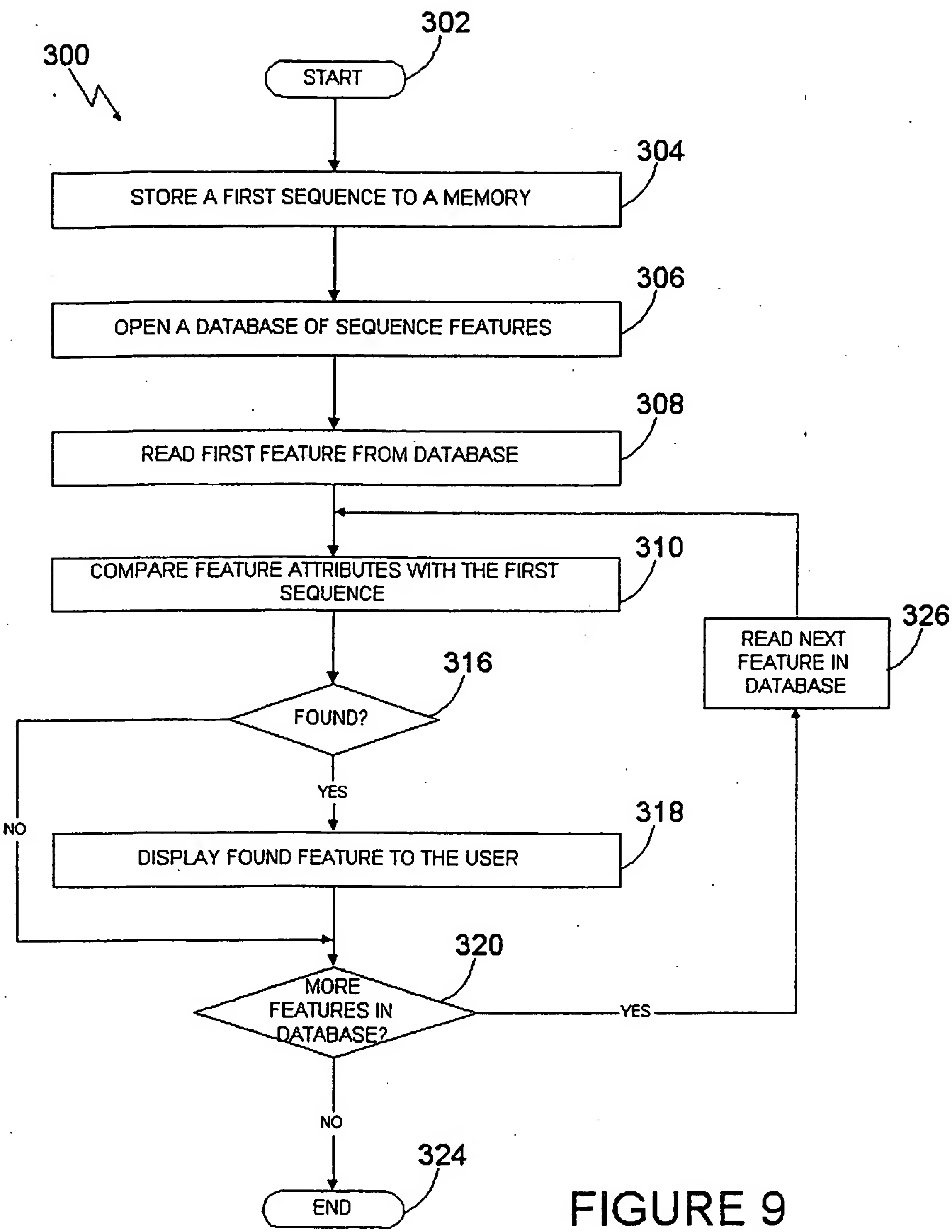

300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
326
READ NEXT FEATURE IN DATABASE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END

FIGURE 9

| | Search characteristic | | Selection Characteristics | | | |
|---|---|---|---|---|---|---|
| Step | Program | Strand | Parameters | Identity (%) | Length (bp) | Comments |
| miscellanaeous | FASTA | both | - | 90 | 15 | |
| tRNA | FASTA | both | - | 80 | 60 | |
| rRNA | BLASTN | both | S=108 | 80 | 40 | |
| mtRNA | BLASTN | both | S=108 | 80 | 40 | |
| Procaryotic | BLASTN | both | S=144 | 90 | 40 | |
| Fungal | BLASTN | both | S=144 | 90 | 40 | |
| Alu | BLASTN | both | S=72, B=5 | 70 | 40 | max 5 matches, masking |
| L1 | BLASTN | both | S=72, B=5 | 70 | 40 | max 5 matches, masking |
| Repeats | BLASTN | both | S=72 | 70 | 40 | masking |
| PolyA | BLAST2N | top | W=6, S=10, E=1000, N=12 | 90 | 10 | in the last 100 nucleotides |
| Polyadenylation signal | - | top | AATAAA allowing 1 mismatch | | | in the 50 nucleotides before the 5' end of the polA |
| Vertebrate | BLASTN then FASTA | both | - | 90 then 70 | 30 | first BLASTN, then FASTA on maching sequences |
| ESTs | BLAST2N | both | - | 90 | 30 | |
| Geneseq | BLASTN | both | W=8, B=10 | 90 | 30 | |
| ORF | BLASTP | top | W=8, B=10 | - | - | on ORF proteins, max 10 matches |
| Proteins | BLASTX | top | E = 0.001 | 70 | 30 | |

Figure 10

SEQUENCE LISTING

```
<110> Dumas Milne Edwards, J.B.
      Duclert A.
      Giordano, J.Y.
      Genset SA

<120> ESTs and Encoded Human Proteins.

<130> D18118-339 881

<150> 09/057,719
<151> 1998-04-09

<150> 09/069,047
<151> 1998-04-28

<160> 1622

<170> Patent.pm

<210> 1
<211> 822
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 346..552

<221> sig_peptide
<222> 346..408
<223> Von Heijne matrix

<221> misc_feature
<222> 115
<223> n=a, g, c or t

<400> 1
actcctttta gcataggggc ttcggcgcca gcggccagcg ctagtcggtc tggtaagtgc      60
ctgatgccga gttccgtctc tcgcgtcttt tcctggtccc aggcaaagcg gasgnagatc     120
ctcaaacggc ctagtgcttc gcgcttccgg agaaaatcag cggtctaatt aattcctctg     180
gtttgttgaa gcagttacca agaatcttca accctttccc acaaaagcta attgagtaca     240
cgttcctgtt gagtacacgt tcctgttgat ttacaaaagg tgcaggtatg agcaggtctg     300
aagactaaca ttttgtgaag ttgtaaaaca gaaaacctgt tagaa atg tgg tgg ttt     357
                                                  Met Trp Trp Phe
                                                      -20
cag caa ggc ctc agt ttc ctt cct tca gcc ctt gta att tgg aca tct       405
Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val Ile Trp Thr Ser
        -15                 -10                 -5
gct gct ttc ata ttt tca tac att act gca gta aca ctc cac cat ata       453
Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala Val Thr Leu His His Ile
    1               5                   10                  15
gac ccg gct tta cct tat atc agt gac act ggt aca gta gct cca raa       501
Asp Pro Ala Leu Pro Tyr Ile Ser Asp Thr Gly Thr Val Ala Pro Xaa
                20                  25                  30
aaa tgc tta ttt ggg gca atg cta aat att gcg gca gtt tta tgt caa       549
Lys Cys Leu Phe Gly Ala Met Leu Asn Ile Ala Ala Val Leu Cys Gln
            35                  40                  45
aaa tagaaatcag gaarataatt caacttaaag aakttcattt catgaccaaa            602
Lys
ctcttcaraa acatgtcttt acaagcatat ctcttgtatt gctttctaca ctgttgaatt     662
gtctggcaat atttctgcag tggaaaattt gatttarmta gttcttgact gataaatatg     722
```

gtaaggtggg cttttccccc tgtgtaattg gctactatgt cttactgagc caagttgtaw 782
tttgaaataa aatgatatga gagtgacaca aaaaaaaaaa 822

<210> 2
<211> 21
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> 1..21
<223> Von Heijne matrix
score 5.5
seq SFLPSALVIWTSA/AF

<400> 2
Met Trp Trp Phe Gln Gln Gly Leu Ser Phe Leu Pro Ser Ala Leu Val
1 5 10 15
Ile Trp Thr Ser Ala
20

<210> 3
<211> 526
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 90..344

<221> sig_peptide
<222> 90..140
<223> Von Heijne matrix

<221> misc_feature
<222> 290
<223> n=a, g, c or t

<400> 3
aatatrarac agctacaata ttccagggcc artcacttgc catttctcat aacagcgtca 60
gagagaaaga actgactgar acgtttgag atg aag aaa gtt ctc ctc ctg atc 113
Met Lys Lys Val Leu Leu Leu Ile
-15 -10
aca gcc atc ttg gca gtg gct gtw ggt ttc cca gtc tct caa gac cag 161
Thr Ala Ile Leu Ala Val Ala Val Gly Phe Pro Val Ser Gln Asp Gln
-5 1 5
gaa cga gaa aaa aga agt atc agt gac agc gat gaa tta gct tca ggr 209
Glu Arg Glu Lys Arg Ser Ile Ser Asp Ser Asp Glu Leu Ala Ser Gly
10 15 20
wtt ttt gtg ttc cct tac cca tat cca ttt cgc cca ctt cca cca att 257
Xaa Phe Val Phe Pro Tyr Pro Tyr Pro Phe Arg Pro Leu Pro Pro Ile
25 30 35
cca ttt cca aga ttt cca tgg ttt aga cgt aan ttt cct att cca ata 305
Pro Phe Pro Arg Phe Pro Trp Phe Arg Arg Xaa Phe Pro Ile Pro Ile
40 45 50 55
cct gaa tct gcc cct aca act ccc ctt cct agc gaa aag taaacaaraa 354
Pro Glu Ser Ala Pro Thr Thr Pro Leu Pro Ser Glu Lys
60 65
ggaaaagtca crataaacct ggtcacctga aattgaaatt gagccacttc cttgaaraat 414
caaaattcct gttaataaaa raaaaacaaa tgtaattgaa atagcacaca gcattctcta 474
gtcaatatct ttagtgatct tctttaataa acatgaaagc aaaaaaaaaa aa 526

<210> 4

<211> 17
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> 1..17
<223> Von Heijne matrix
score 8.2
seq LLLITAILAVAVG/FP

<400> 4
Met Lys Lys Val Leu Leu Leu Ile Thr Ala Ile Leu Ala Val Ala Val
1 5 10 15
Gly

<210> 5
<211> 848
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> 32..697

<221> sig_peptide
<222> 32..73
<223> Von Heijne matrix

<400> 5
aactttgcct tgtgttttcc accctgaaag a atg ttg tgg ctg ctc ttt ttt 52
Met Leu Trp Leu Leu Phe Phe
-10
ctg gtg act gcc att cat gct gaa ctc tgt caa cca ggt gca gaa aat 100
Leu Val Thr Ala Ile His Ala Glu Leu Cys Gln Pro Gly Ala Glu Asn
-5 1 5
gct ttt aaa gtg aga ctt agt atc aga aca gct ctg gga gat aaa gca 148
Ala Phe Lys Val Arg Leu Ser Ile Arg Thr Ala Leu Gly Asp Lys Ala
10 15 20 25
tat gcc tgg gat acc aat gaa gaa tac ctc ttc aaa gcg atg gta gct 196
Tyr Ala Trp Asp Thr Asn Glu Glu Tyr Leu Phe Lys Ala Met Val Ala
30 35 40
ttc tcc atg aga aaa gtt ccc aac aga gaa gca aca gaa att tcc cat 244
Phe Ser Met Arg Lys Val Pro Asn Arg Glu Ala Thr Glu Ile Ser His
45 50 55
gtc cta ctt tgc aat gta acc cag agg gta tca ttc tgg ttt gtg gtt 292
Val Leu Leu Cys Asn Val Thr Gln Arg Val Ser Phe Trp Phe Val Val
60 65 70
aca gac cct tca aaa aat cac acc ctt cct gct gtt gag gtg caa tca 340
Thr Asp Pro Ser Lys Asn His Thr Leu Pro Ala Val Glu Val Gln Ser
75 80 85
gcc ata aga atg aac aag aac cgg atc aac aat gcc ttc ttt cta aat 388
Ala Ile Arg Met Asn Lys Asn Arg Ile Asn Asn Ala Phe Phe Leu Asn
90 95 100 105
gac caa act ctg gaa ttt tta aaa atc cct tcc aca ctt gca cca ccc 436
Asp Gln Thr Leu Glu Phe Leu Lys Ile Pro Ser Thr Leu Ala Pro Pro
110 115 120
atg gac cca tct gtg ccc atc tgg att att ata ttt ggt gtg ata ttt 484
Met Asp Pro Ser Val Pro Ile Trp Ile Ile Ile Phe Gly Val Ile Phe
125 130 135
tgc atc atc ata gtt gca att gca cta ctg att tta tca ggg atc tgg 532
Cys Ile Ile Ile Val Ala Ile Ala Leu Leu Ile Leu Ser Gly Ile Trp
140 145 150

caa cgt ada ara aag aac aaa gaa cca tct gaa gtg gat gac gct gaa 580
Gln Arg Xaa Xaa Lys Asn Lys Glu Pro Ser Glu Val Asp Asp Ala Glu
155 160 165
rat aak tgt gaa aac atg atc aca att gaa aat ggc atc ccc tct gat 628
Xaa Xaa Cys Glu Asn Met Ile Thr Ile Glu Asn Gly Ile Pro Ser Asp
170 175 180 185
ccc ctg gac atg aag gga ggg cat att aat gat gcc ttc atg aca gag 676
Pro Leu Asp Met Lys Gly Gly His Ile Asn Asp Ala Phe Met Thr Glu
190 195 200
gat gag agg ctc acc cct ctc tgaagggctg ttgttctgct tcctcaaraa 727
Asp Glu Arg Leu Thr Pro Leu
205
attaaacatt tgtttctgtg tgactgctga gcatcctgaa ataccaagag cagatcatat 787
wttttgtttc accattcttc ttttgtaata aattttgaat gtgcttgaaa aaaaaaaaaa 847
c 848

<210> 6
<211> 14
<212> PRT
<213> Homo Sapiens

<220>
<221> SIGNAL
<222> 1..14
<223> Von Heijne matrix
score 10.7
seq LWLLFFLVTAIHA/EL

<400> 6
Met Leu Trp Leu Leu Phe Phe Leu Val Thr Ala Ile His Ala
1 5 10

<210> 7
<211> 826
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..695

<221> sig_peptide
<222> 15..80
<223> score 8.5
seq AALLLGLMMVVTG/DE

<400> 7
aaccagaggt gccc atg ggt tgg aca atg agg ctg gtc aca gca gca ctg 50
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu
-20 -15
tta ctg ggt ctc atg atg gtg gtc act gga gac gag gat gag aac agc 98
Leu Leu Gly Leu Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser
-10 -5 1 5
ccg tgt gcc cat gag gcc ctc ctg gac gag gac acc ctc ttt tgc cag 146
Pro Cys Ala His Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln
10 15 20
ggc ctt gaa gtt ttc tac cca gag ttg ggg aac att ggc tgc aag gtt 194
Gly Leu Glu Val Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val
25 30 35
gtt cct gat tgt aac aac tac aga cag aag atc acc tcc tgg atg gag 242
Val Pro Asp Cys Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu
40 45 50
ccg ata gtc aag ttc ccg ggg gcc gtg gac ggc gca acc tat atc ctg 290

```
Pro Ile Val Lys Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu
55                  60                  65                  70
gtg atg gtg gat cca gat gcc cct agc aga gca gaa ccc aga cag aga      338
Val Met Val Asp Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg
                75                  80                  85
ttc tgg aga cat tgg ctg gta aca gat atc aag ggc gcc gac ctg aag      386
Phe Trp Arg His Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys
            90                  95                  100
aaa ggg aag att cag ggc cag gag tta tca gcc tac cag gct ccc tcc      434
Lys Gly Lys Ile Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser
        105                 110                 115
cca ccg gca cac agt ggc ttc cat cgc tac cag ttc ttt gtc tat ctt      482
Pro Pro Ala His Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu
    120                 125                 130
cag gaa gga aag gtc atc tct ctc ctt ccc aag gaa aac aaa act cga      530
Gln Glu Gly Lys Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg
135                 140                 145                 150
ggc tct tgg aaa atg gac aga ttt ctg aac cgt ttc cac ctg ggc gaa      578
Gly Ser Trp Lys Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu
                155                 160                 165
cct gaa gca agc acc cag ttc atg acc cag aac tac cag gac tca cca      626
Pro Glu Ala Ser Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro
            170                 175                 180
acc ctc cag gct ccc aga gaa agg gcc agc gag ccc aag cac aaa aac      674
Thr Leu Gln Ala Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn
        185                 190                 195
cag gcg gag ata gct gcc tgc tagatagccg gctttgccat ccgggcatgt         725
Gln Ala Glu Ile Ala Ala Cys
    200                 205
ggccacactg cccaccaccg acgatgtggg tatggaaccc cctctggata cagaacccct    785
tcttttccaa ataaaaaaaa aatcatccaa aaaaaaaaaa a                        826

<210> 8
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1
<223> score 8.5
      seq AALLLGLMMVVTG/DE

<400> 8
Met Gly Trp Thr Met Arg Leu Val Thr Ala Ala Leu Leu Leu Gly Leu
        -20                 -15                 -10
Met Met Val Val Thr Gly Asp Glu Asp Glu Asn Ser Pro Cys Ala His
    -5                  1                   5                   10
Glu Ala Leu Leu Asp Glu Asp Thr Leu Phe Cys Gln Gly Leu Glu Val
                15                  20                  25
Phe Tyr Pro Glu Leu Gly Asn Ile Gly Cys Lys Val Val Pro Asp Cys
            30                  35                  40
Asn Asn Tyr Arg Gln Lys Ile Thr Ser Trp Met Glu Pro Ile Val Lys
        45                  50                  55
Phe Pro Gly Ala Val Asp Gly Ala Thr Tyr Ile Leu Val Met Val Asp
    60                  65                  70
Pro Asp Ala Pro Ser Arg Ala Glu Pro Arg Gln Arg Phe Trp Arg His
75                  80                  85                  90
Trp Leu Val Thr Asp Ile Lys Gly Ala Asp Leu Lys Lys Gly Lys Ile
                95                  100                 105
Gln Gly Gln Glu Leu Ser Ala Tyr Gln Ala Pro Ser Pro Pro Ala His
            110                 115                 120
Ser Gly Phe His Arg Tyr Gln Phe Phe Val Tyr Leu Gln Glu Gly Lys
```

```
        125                 130                 135
Val Ile Ser Leu Leu Pro Lys Glu Asn Lys Thr Arg Gly Ser Trp Lys
    140                 145                 150
Met Asp Arg Phe Leu Asn Arg Phe His Leu Gly Glu Pro Glu Ala Ser
155                 160                 165                 170
Thr Gln Phe Met Thr Gln Asn Tyr Gln Asp Ser Pro Thr Leu Gln Ala
                175                 180                 185
Pro Arg Glu Arg Ala Ser Glu Pro Lys His Lys Asn Gln Ala Glu Ile
            190                 195                 200
Ala Ala Cys
        205

<210> 9
<211> 852
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 229..735

<221> sig_peptide
<222> 229..492
<223> score 6.7
      seq VFALSSFLNKASA/VY

<400> 9
aatgactggc agtggcatca gcgatggcgg ctgcgtcggg gtcggttctg cagcgctgta      60
tcgtgtcgcc ggcagggagg catagcgcct ctctgatctt cctgcatggc tcaggtgatt     120
ctggacaagg attaagaatg tggatcaagc aggtttttaa atcaagattt aacattccaa     180
cacataaaaa ttatttatcc aacagctcct cccagatcat atactcct atg aaa gga      237
                                                     Met Lys Gly
gga atc tcc aat gta tgg ttt gac aga ttt aaa ata acc aat gac tgc      285
Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr Asn Asp Cys
-85                 -80                 -75                 -70
cca gaa cac ctt gaa tca att gat gtc atg tgt caa gtg ctt act gat      333
Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val Leu Thr Asp
                -65                 -60                 -55
ttg att gat gaa gaa gta aaa agt ggc atc aag aag aac agg ata tta      381
Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn Arg Ile Leu
            -50                 -45                 -40
ata gga gga ttc tct atg gga gga tgc atg gca atg cat tta gca tat      429
Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His Leu Ala Tyr
        -35                 -30                 -25
aga aat cat caa gat gtg gca gga gta ttt gct ctt tct agt ttt ctg      477
Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser Ser Phe Leu
    -20                 -15                 -10
aat aaa gca tct gct gtt tac cag gct ctt cag aag agt aat ggt gta      525
Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser Asn Gly Val
-5                  1               5                   10
ctt cct gaa tta ttt cag tgt cat ggt act gca gat gag tta gtt ctt      573
Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu Leu Val Leu
            15                  20                  25
cat tct tgg gca gaa gag aca aac tca atg tta aaa tct cta gga gtg      621
His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser Leu Gly Val
        30                  35                  40
acc acg aag ttt cat agt ttt cca aat gtt tac cat gag cta agc aaa      669
Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu Leu Ser Lys
    45                  50                  55
act gag tta gac ata ttg aag tta tgg att ctt aca aag ctg cca gga      717
Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys Leu Pro Gly
60                  65                  70                  75
gaa atg gaa aaa caa aaa tgaatgaatc aagagtgatt tgttaatgta             765
```

```
Glu Met Glu Lys Gln Lys
                80
agtgtaatgt ctttgtgaaa agtgattttt actgccaaat tataatgata attaaaatat    825
taagaaatag caaaaaaaaa aaaaaaa                                        852

<210> 10
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -88..-1
<223> score 6.7
      seq VFALSSFLNKASA/VY

<400> 10
Met Lys Gly Gly Ile Ser Asn Val Trp Phe Asp Arg Phe Lys Ile Thr
            -85                 -80                 -75
Asn Asp Cys Pro Glu His Leu Glu Ser Ile Asp Val Met Cys Gln Val
        -70                 -65                 -60
Leu Thr Asp Leu Ile Asp Glu Glu Val Lys Ser Gly Ile Lys Lys Asn
    -55                 -50                 -45
Arg Ile Leu Ile Gly Gly Phe Ser Met Gly Gly Cys Met Ala Met His
-40                 -35                 -30                 -25
Leu Ala Tyr Arg Asn His Gln Asp Val Ala Gly Val Phe Ala Leu Ser
                -20                 -15                 -10
Ser Phe Leu Asn Lys Ala Ser Ala Val Tyr Gln Ala Leu Gln Lys Ser
            -5                  1               5
Asn Gly Val Leu Pro Glu Leu Phe Gln Cys His Gly Thr Ala Asp Glu
    10                  15                  20
Leu Val Leu His Ser Trp Ala Glu Glu Thr Asn Ser Met Leu Lys Ser
25                  30                  35                  40
Leu Gly Val Thr Thr Lys Phe His Ser Phe Pro Asn Val Tyr His Glu
            45                  50                  55
Leu Ser Lys Thr Glu Leu Asp Ile Leu Lys Leu Trp Ile Leu Thr Lys
            60                  65                  70
Leu Pro Gly Glu Met Glu Lys Gln Lys
        75                  80

<210> 11
<211> 1602
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..1004

<221> sig_peptide
<222> 24..170
<223> score 5.6
      seq ACLSLGFFSLLWL/QL

<400> 11
atgcgccgcc gcctctccgc acg atg ttc ccc tcg cgg agg aaa gcg gcg cag     53
                          Met Phe Pro Ser Arg Arg Lys Ala Ala Gln
                                          -45                 -40
ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc tcc ggc ggc ctc cct      101
Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro
                -35                 -30                 -25
cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc tgc ctc tcg ctg ggc      149
Arg Lys Cys Ser Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly
```

```
                -20                     -15                     -10
ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc tct ggg gac gtg gcc      197
Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala
            -5                  1                   5
cgg gca gtc agg gga caa ggg cag gag acc tcg ggc cct ccc cgt gcc      245
Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala
10                  15                      20                  25
tgc ccc cca gag ccg ccc cct gag cac tgg gaa gaa gac gca tcc tgg      293
Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
                    30                  35                  40
ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc cgc gaa cgc ttc gag      341
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe Glu
                45                  50                  55
gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc ttc ctg agc agg aag      389
Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser Arg Lys
            60                  65                  70
aag atc cgg cac cac atc tac gtg ctc aac cag gtg gac cac ttc agg      437
Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp His Phe Arg
    75                  80                  85
ttc aac cgg gca gcg ctc atc aac gtg ggc ttc ctg gag agc agc aac      485
Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu Glu Ser Ser Asn
90                  95                  100                 105
agc acg gac tac att gcc atg cac gac gtt gac ctg ctc cct ctc aac      533
Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp Leu Leu Pro Leu Asn
                    110                 115                 120
gag gag ctg gac tat ggc ttt cct gag gct ggg ccc ttc cac gtg gcc      581
Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly Pro Phe His Val Ala
                125                 130                 135
tcc ccg gag ctc cac cct ctc tac cac tac aag acc tat gtc ggc ggc      629
Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly
            140                 145                 150
atc ctg ctg ctc tcc aag cag cac tac cgg ctg tgc aat ggg atg tcc      677
Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu Cys Asn Gly Met Ser
    155                 160                 165
aac cgc ttc tgg ggc tgg ggc cgc gag gac gac gag ttc tac cgg cgc      725
Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg
170                 175                 180                 185
att aag gga gct ggg ctc cag ctt ttc cgc ccc tcg gga atc aca act      773
Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr
                    190                 195                 200
ggg tac aag aca ttt cgc cac ctg cat gac cca gcc tgg cgg aag agg      821
Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro Ala Trp Arg Lys Arg
                205                 210                 215
gac cag aag cgc atc gca gct caa aaa cag gag cag ttc aag gtg gac      869
Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp
            220                 225                 230
agg gag gga ggc ctg aac act gtg aag tac cat gtg gct tcc cgc act      917
Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr
    235                 240                 245
gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc ctc aac atc atg ttg      965
Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu
250                 255                 260                 265
gac tgt gac aag acc gcc aca ccc tgg tgc aca ttc agc tgagctggat      1014
Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser
                    270                 275

ggacagtgag gaagcctgta cctacaggcc atattgctca ggctcaggac aaggcctcag   1074
gtcgtgggcc cagctctgac aggatgtgga gtggccagga ccaagacagc aagctacgca   1134
attgcagcca cccggccgcc aaggcaggct tgggctgggc caggacacgt ggggtgcctg   1194
ggacgctgct tgccatgcac agtgatcaga gagaggctgg ggtgtgtcct gtccgggacc   1254
ccccctgcct tcctgctcac cctactctga cctccttcac gtgcccaggc ctgtgggtag   1314
tggggagggc tgaacaggac aacctctcat cacccccact tttgttcctt cctgctgggc   1374
tgcctcgtgc agagacacag tgtaggggcc atgcagctgg cgtaggtggc agttgggcct   1434
ggtgagggtt aggacttcag aaaccagagc acaagcccca cagaggggga acagccagca   1494
```

ccgctctagc tggttgttgc catgccggaa tgtgggccta gtgttgccag atcttctgat 1554
ttttcgaaag aaactagaat gctggattct caaaaaaaaa aaaaaaaa 1602

<210> 12
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1
<223> score 5.6
seq ACLSLGFFSLLWL/QL

<400> 12
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
-45 -40 -35
Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe
-30 -25 -20
His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
-15 -10 -5
Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
1 5 10 15
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
20 25 30
Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
35 40 45
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
50 55 60
Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
65 70 75
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
80 85 90 95
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
100 105 110
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
115 120 125
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
130 135 140
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
145 150 155
Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
160 165 170 175
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
180 185 190
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
195 200 205
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
210 215 220
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
225 230 235
Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
240 245 250 255
Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
260 265 270
Thr Pro Trp Cys Thr Phe Ser
275

<210> 13
<211> 1568
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 75..1259

<221> sig_peptide
<222> 75..1004
<223> score 4.4
      seq VLILLFSLALIIL/PS

<400> 13
agaaaaggtg tagtgtttgg ggcggtcaac gggctatgct ggcttgacag ggctgggctc      60
ttcagaacag aagc atg gat ctc gga atc cct gac ctg ctg gac gcg tgg      110
                Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp
                -310                -305                -300
ctg gag ccc cca gag gat atc ttc tcg aca gga tcc gtc ctg gag ctg      158
Leu Glu Pro Pro Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu
            -295                -290                -285
gga ctc cac tgc ccc cct cca gag gtt ccg gta act agg cta cag gaa      206
Gly Leu His Cys Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu
        -280                -275                -270
cag gga ctg caa ggc tgg aag tcc ggt ggg gac cgt ggc tgt ggc ctt      254
Gln Gly Leu Gln Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu
    -265                -260                -255
caa gag agt gag cct gaa gat ttc ttg aag ctt ttc att gat ccc aat      302
Gln Glu Ser Glu Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn
-250                -245                -240                -235
gag gtg tac tgc tca gaa gca tct cct ggc agt gac agt ggc atc tct      350
Glu Val Tyr Cys Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser
                -230                -225                -220
gag gac tcc tgc cat cca gac agt ccc cct gcc ccc agg gca acc agt      398
Glu Asp Ser Cys His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser
            -215                -210                -205
tct cct atg ctc tat gag gtt gtc tat gag gca ggg gcc ctg gag agg      446
Ser Pro Met Leu Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg
        -200                -195                -190
atg cag ggg gaa act ggg cca aat gta ggc ctt atc tcc atc cag cta      494
Met Gln Gly Glu Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu
    -185                -180                -175
gat cag tgg agc cca gca ttt atg gtg cct gat tcc tgc atg gtc agt      542
Asp Gln Trp Ser Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser
-170                -165                -160                -155
gag ctg ccc ttt gat gct cat gcc cac atc ctg ccc aga gca ggc acc      590
Glu Leu Pro Phe Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr
                -150                -145                -140
gta gcc cca gtg ccc tgt aca acc ctg ctg ccc tgt caa acc ctg ttc      638
Val Ala Pro Val Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe
            -135                -130                -125
ctg acc gat gag gag aag cgt ctg ctg ggg cag gaa ggg gtt tcc ctg      686
Leu Thr Asp Glu Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu
        -120                -115                -110
ccc tct cac ctg ccc ctc acc aag gca gag gag agg gtc ctc aag aag      734
Pro Ser His Leu Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys
    -105                -100                -95
gtc agg agg aaa atc cgt aac aag cag tca gct cag gac agt cgg cgg      782
Val Arg Arg Lys Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg
-90                 -85                 -80                 -75
cgg aag aag gag tac att gat ggg ctg gag agc agg gtg gca gcc tgt      830
Arg Lys Lys Glu Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys
                -70                 -65                 -60
tct gca cag aac caa gaa tta cag aaa aaa gtc cag gag ctg gag agg      878
Ser Ala Gln Asn Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg
            -55                 -50                 -45
cac aac atc tcc ttg gta gct cag ctc cgc cag ctg cag acg cta att      926
```

His Asn Ile Ser Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile
-40 -35 -30
gct caa act tcc aac aaa gct gcc cag acc agc act tgt gtt ttg att 974
Ala Gln Thr Ser Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile
-25 -20 -15
ctt ctt ttt tcc ctg gct ctc atc atc ctg ccc agc ttc agt cca ttc 1022
Leu Leu Phe Ser Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe
-10 -5 1 5
cag agt cga cca gaa gct ggg tct gag gat tac cag cct cac gga gtg 1070
Gln Ser Arg Pro Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val
10 15 20
act tcc aga aat atc ctg acc cac aag gac gta aca gaa aat ctg gag 1118
Thr Ser Arg Asn Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu
25 30 35
acc caa gtg gta gag tcc aga ctg agg gag cca cct gga gcc aag gat 1166
Thr Gln Val Val Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp
40 45 50
gca aat ggc tca aca agg aca ctg ctt gag aag atg gga ggg aag cca 1214
Ala Asn Gly Ser Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro
55 60 65 70
aga ccc agt ggg cgc atc cgg tcc gtg ctg cat gca gat gag atg 1259
Arg Pro Ser Gly Arg Ile Arg Ser Val Leu His Ala Asp Glu Met
75 80 85
tgagctggaa cagaccttcc tggcccactt cctgatcaca aggaatcctg ggcttcctta 1319
tggctttctt cccactggga ttcctactta ggtgtctgcc ctcaggggtc caaatcactt 1379
caggacaccc caagagatgt cctttagtct ctgcctgagg cctagtctgc atttgtttgc 1439
atatatgaga gggtacctca aatacttctg ttatgtatct gtgattttat ttcttctttg 1499
ggtatagggt tgaggggaaa taagttttga gtgagaaata aacgttttag ctgaaaaaaa 1559
aaaaaaaaa 1568

<210> 14
<211> 395
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -310..-1
<223> score 4.4
seq VLILLFSLALIIL/PS

<400> 14
Met Asp Leu Gly Ile Pro Asp Leu Leu Asp Ala Trp Leu Glu Pro Pro
-310 -305 -300 -295
Glu Asp Ile Phe Ser Thr Gly Ser Val Leu Glu Leu Gly Leu His Cys
-290 -285 -280
Pro Pro Pro Glu Val Pro Val Thr Arg Leu Gln Glu Gln Gly Leu Gln
-275 -270 -265
Gly Trp Lys Ser Gly Gly Asp Arg Gly Cys Gly Leu Gln Glu Ser Glu
-260 -255 -250
Pro Glu Asp Phe Leu Lys Leu Phe Ile Asp Pro Asn Glu Val Tyr Cys
-245 -240 -235
Ser Glu Ala Ser Pro Gly Ser Asp Ser Gly Ile Ser Glu Asp Ser Cys
-230 -225 -220 -215
His Pro Asp Ser Pro Pro Ala Pro Arg Ala Thr Ser Ser Pro Met Leu
-210 -205 -200
Tyr Glu Val Val Tyr Glu Ala Gly Ala Leu Glu Arg Met Gln Gly Glu
-195 -190 -185
Thr Gly Pro Asn Val Gly Leu Ile Ser Ile Gln Leu Asp Gln Trp Ser
-180 -175 -170
Pro Ala Phe Met Val Pro Asp Ser Cys Met Val Ser Glu Leu Pro Phe
-165 -160 -155
Asp Ala His Ala His Ile Leu Pro Arg Ala Gly Thr Val Ala Pro Val

```
-150                -145                -140                -135
Pro Cys Thr Thr Leu Leu Pro Cys Gln Thr Leu Phe Leu Thr Asp Glu
                -130                -125                -120
Glu Lys Arg Leu Leu Gly Gln Glu Gly Val Ser Leu Pro Ser His Leu
            -115                -110                -105
Pro Leu Thr Lys Ala Glu Glu Arg Val Leu Lys Lys Val Arg Arg Lys
        -100                -95                 -90
Ile Arg Asn Lys Gln Ser Ala Gln Asp Ser Arg Arg Arg Lys Lys Glu
    -85                 -80                 -75
Tyr Ile Asp Gly Leu Glu Ser Arg Val Ala Ala Cys Ser Ala Gln Asn
-70                 -65                 -60                 -55
Gln Glu Leu Gln Lys Lys Val Gln Glu Leu Glu Arg His Asn Ile Ser
                -50                 -45                 -40
Leu Val Ala Gln Leu Arg Gln Leu Gln Thr Leu Ile Ala Gln Thr Ser
            -35                 -30                 -25
Asn Lys Ala Ala Gln Thr Ser Thr Cys Val Leu Ile Leu Leu Phe Ser
        -20                 -15                 -10
Leu Ala Leu Ile Ile Leu Pro Ser Phe Ser Pro Phe Gln Ser Arg Pro
    -5                  1                   5                   10
Glu Ala Gly Ser Glu Asp Tyr Gln Pro His Gly Val Thr Ser Arg Asn
                15                  20                  25
Ile Leu Thr His Lys Asp Val Thr Glu Asn Leu Glu Thr Gln Val Val
            30                  35                  40
Glu Ser Arg Leu Arg Glu Pro Pro Gly Ala Lys Asp Ala Asn Gly Ser
        45                  50                  55
Thr Arg Thr Leu Leu Glu Lys Met Gly Gly Lys Pro Arg Pro Ser Gly
    60                  65                  70
Arg Ile Arg Ser Val Leu His Ala Asp Glu Met
75                  80                  85

&lt;210&gt; 15
&lt;211&gt; 25
&lt;212&gt; DNA
&lt;213&gt; Artificial Sequence
&lt;400&gt; 15
gggaagatgg agatagtatt gcctg                                          25

&lt;210&gt; 16
&lt;211&gt; 26
&lt;212&gt; DNA
&lt;213&gt; Artificial Sequence
&lt;400&gt; 16
ctgccatgta catgatagag agattc                                         26

&lt;210&gt; 17
&lt;211&gt; 546
&lt;212&gt; DNA
&lt;213&gt; Homo Sapiens

&lt;220&gt;
&lt;221&gt; promoter
&lt;222&gt; 1..517

&lt;221&gt; transcription start site
&lt;222&gt; 518

&lt;221&gt; protein_bind
&lt;222&gt; 17..25
&lt;223&gt; matinspector prediction
      name CMYB_01
      score 0.983
      sequence tgtcagttg
```

<221> protein_bind
<222> complement(18..27)
<223> matinspector prediction
name MYOD_Q6
score 0.961
sequence cccaactgac

<221> protein_bind
<222> complement(75..85)
<223> matinspector prediction
name S8_01
score 0.960
sequence aatagaattag

<221> protein_bind
<222> 94..104
<223> matinspector prediction
name S8_01
score 0.966
sequence aactaaattag

<221> protein_bind
<222> complement(129..139)
<223> matinspector prediction
name DELTAEF1_01
score 0.960
sequence gcacacctcag

<221> protein_bind
<222> complement(155..165)
<223> matinspector prediction
name GATA_C
score 0.964
sequence agataaatcca

<221> protein_bind
<222> 170..178
<223> matinspector prediction
name CMYB_01
score 0.958
sequence cttcagttg

<221> protein_bind
<222> 176..189
<223> matinspector prediction
name GATA1_02
score 0.959
sequence ttgtagataggaca

<221> protein_bind
<222> 180..190
<223> matinspector prediction
name GATA_C
score 0.953
sequence agataggacat

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1ALPHAE47_01
score 0.973
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1BETAE47_01
score 0.983
sequence cataacagatggtaag

<221> protein_bind
<222> 284..299
<223> matinspector prediction
name TAL1BETAITF2_01
score 0.978
sequence cataacagatggtaag

<221> protein_bind
<222> complement(287..296)
<223> matinspector prediction
name MYOD_Q6
score 0.954
sequence accatctgtt

<221> protein_bind
<222> complement(302..314)
<223> matinspector prediction
name GATA1_04
score 0.953
sequence tcaagataaagta

<221> protein_bind
<222> 393..405
<223> matinspector prediction
name IK1_01
score 0.963
sequence agttgggaattcc

<221> protein_bind
<222> 393..404
<223> matinspector prediction
name IK2_01
score 0.985
sequence agttgggaattc

<221> protein_bind
<222> 396..405
<223> matinspector prediction
name CREL_01
score 0.962
sequence tgggaattcc

<221> protein_bind
<222> 423..436
<223> matinspector prediction
name GATA1_02
score 0.950
sequence tcagtgatatggca

<221> protein_bind
<222> complement(478..489)
<223> matinspector prediction
name SRY_02
score 0.951
sequence taaaacaaaaca

<221> protein_bind
<222> 486..493
<223> matinspector prediction
name E2F_02
score 0.957
sequence tttagcgc

<221> protein_bind
<222> complement(514..521)
<223> matinspector prediction
name MZF1_01
score 0.975
sequence tgagggga

<400> 17
```
tgagtgcagt gttacatgtc agttgggtta agtttgttaa tgtcattcaa atcttctatg     60
tcttgatttg cctgctaatt ctattatttc tggaactaaa ttagtttgat ggttctatta    120
gttattgact gaggtgtgct aatctcccat tatgtggatt tatctatttc ttcagttgta    180
gataggacat tgatagatac ataagtacca ggacaaaagc agggagatct tttttccaaa    240
atcaggagaa aaaaatgaca tctggaaaac ctatagggaa aggcataaca gatggtaagg    300
atactttatc ttgagtagga gagccttcct gtggcaacgt ggagaaggga agaggtcgta    360
gaattgagga gtcagctcag ttagaagcag ggagttggga attccgttca tgtgatttag    420
catcagtgat atggcaaatg tgggactaag ggtagtgatc agagggttaa aattgtgtgt    480
tttgttttag cgctgctggg gcatcgcctt gggtcccctc aaacagattc ccatgaatct    540
cttcat                                                               546
```

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence
<400> 18
```
gtaccaggga ctgtgaccat tgc                                             23
```

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence
<400> 19
```
ctgtgaccat tgctcccaag agag                                            24
```

<210> 20
<211> 861
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..806

<221> transcription start site
<222> 807

<221> protein_bind
<222> complement(60..70)
<223> matinspector prediction
name NFY_Q6
score 0.956
sequence ggaccaatcat

<221> protein_bind
<222> 70..77
<223> matinspector prediction
name MZF1_01

score 0.962
sequence cctgggga

<221> protein_bind
<222> 124..132
<223> matinspector prediction
name CMYB_01
score 0.994
sequence tgaccgttg

<221> protein_bind
<222> complement(126..134)
<223> matinspector prediction
name VMYB_02
score 0.985
sequence tccaacggt

<221> protein_bind
<222> 135..143
<223> matinspector prediction
name STAT_01
score 0.968
sequence ttcctggaa

<221> protein_bind
<222> complement(135..143)
<223> matinspector prediction
name STAT_01
score 0.951
sequence ttccaggaa

<221> protein_bind
<222> complement(252..259)
<223> matinspector prediction
name MZF1_01
score 0.956
sequence ttggggga

<221> protein_bind
<222> 357..368
<223> matinspector prediction
name IK2_01
score 0.965
sequence gaatgggatttc

<221> protein_bind
<222> 384..391
<223> matinspector prediction
name MZF1_01
score 0.986
sequence agagggga

<221> protein_bind
<222> complement(410..421)
<223> matinspector prediction
name SRY_02
score 0.955
sequence gaaaacaaaaca

<221> protein_bind
<222> 592..599
<223> matinspector prediction
name MZF1_01

```
      score 0.960
      sequence gaagggga

<221> protein_bind
<222> 618..627
<223> matinspector prediction
      name MYOD_Q6
      score 0.981
      sequence agcatctgcc

<221> protein_bind
<222> 632..642
<223> matinspector prediction
      name DELTAEF1_01
      score 0.958
      sequence tcccaccttcc

<221> protein_bind
<222> complement(813..823)
<223> matinspector prediction
      name S8_01
      score 0.992
      sequence gaggcaattat

<221> protein_bind
<222> complement(824..831)
<223> matinspector prediction
      name MZF1_01
      score 0.986
      sequence agagggga

<221> misc_feature
<222> 335,376
<223> n=a, g, c or t

<400> 20
tactataggg cacgcgtggt cgacggccgg gctgttctgg agcagagggc atgtcagtaa    60
tgattggtcc ctggggaagg tctggctggc tccagcacag tgaggcattt aggtatctct   120
cggtgaccgt tggattcctg gaagcagtag ctgttctgtt tggatctggt agggacaggg   180
ctcagagggc taggcacgag ggaaggtcag aggagaaggs aggsarggcc cagtgagarg   240
ggagcatgcc ttccccccaac cctggcttsc ycttggymam agggcgktty tgggmacttr  300
aaytcagggc ccaascagaa scacaggccc aktcntggct smaagcacaa tagcctgaat   360
gggatttcag gttagncagg gtgagagggg aggctctctg gcttagtttt gttttgtttt   420
ccaaatcaag gtaacttgct cccttctgct acgggccttg gtcttggctt gtcctcaccc   480
agtcggaact ccctaccact ttcaggagag tggttttagg cccgtggggc tgttctgttc   540
caagcagtgt gagaacatgg ctggtagagg ctctagctgt gtgcggggcc tgaaggggag   600
tgggttctcg cccaaagagc atctgcccat ttcccacctt cccttctccc accagaagct   660
tgcctgagct gtttggacaa aaatccaaac cccacttggc tactctggcc tggcttcagc   720
ttggaaccca atacctaggc ttacaggcca tcctgagcca ggggcctctg gaaattctct   780
tcctgatggt cctttaggtt tgggcacaaa atataattgc ctctcccctc tcccatttc    840
tctcttggga gcaatggtca c                                             861

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence
<400> 21
ctgggatgga aggcacggta                                                20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence
```

<400> 22
gagaccacac agctagacaa 20

<210> 23
<211> 555
<212> DNA
<213> Homo Sapiens

<220>
<221> promoter
<222> 1..500

<221> transcription start site
<222> 501

<221> protein_bind
<222> 191..206
<223> matinspector prediction
name ARNT_01
score 0.964
sequence ggactcacgtgctgct

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name NMYC_01
score 0.965
sequence actcacgtgctg

<221> protein_bind
<222> 193..204
<223> matinspector prediction
name USF_01
score 0.985
sequence actcacgtgctg

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name USF_01
score 0.985
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name NMYC_01
score 0.956
sequence cagcacgtgagt

<221> protein_bind
<222> complement(193..204)
<223> matinspector prediction
name MYCMAX_02
score 0.972
sequence cagcacgtgagt

<221> protein_bind
<222> 195..202
<223> matinspector prediction
name USF_C
score 0.997
sequence tcacgtgc

```
<221> protein_bind
<222> complement(195..202)
<223> matinspector prediction
      name USF_C
      score 0.991
      sequence gcacgtga

<221> protein_bind
<222> complement(210..217)
<223> matinspector prediction
      name MZF1_01
      score 0.968
      sequence catgggga

<221> protein_bind
<222> 397..410
<223> matinspector prediction
      name ELK1_02
      score 0.963
      sequence ctctccggaagcct

<221> protein_bind
<222> 400..409
<223> matinspector prediction
      name CETS1P54_01
      score 0.974
      sequence tccggaagcc

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
      name AP1_Q4
      score 0.963
      sequence agtgactgaac

<221> protein_bind
<222> complement(460..470)
<223> matinspector prediction
      name AP1FJ_Q2
      score 0.961
      sequence agtgactgaac

<221> protein_bind
<222> 547..555
<223> matinspector prediction
      name PADS_C
      score 1.000
      sequence tgtggtctc

<400> 23
ctatagggca cgcktggtcg acggcccggg ctggtctggt ctgtkgtgga gtcgggttga     60
aggacagcat ttgtkacatc tggtctactg caccttccct ctgccgtgca cttggccttt    120
kawaagctca gcaccggtgc ccatcacagg gccggcagca cacacatccc attactcaga    180
aggaactgac ggactcacgt gctgctccgt ccccatgagc tcagtggacc tgtctatgta    240
gagcagtcag acagtgcctg ggatagagtg agagttcagc cagtaaatcc aagtgattgt    300
cattcctgtc tgcattagta actcccaacc tagatgtgaa aacttagttc tttctcatag    360
gttgctctgc ccatggtccc actgcagacc caggcactct ccggaagcct ggaaatcacc    420
cgtgtcttct gcctgctccc gctcacatcc cacacttgtg ttcagtcact gagttacaga    480
ttttgcctcc tcaatttctc ttgtcttagt cccatcctct gttcccctgg ccagtttgtc    540
tagctgtgtg gtctc                                                     555

<210> 24
```

<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 13..249

<221> sig_peptide
<222> 13..81
<223> Von Heijne matrix
score 11.8000001907349
seq CLFVCLFLSQSFA/FV

<400> 24
aaaagtattg gg atg cct agt tac aar gtg tgt ggg gtt ttt tgt ttg ttt 51
Met Pro Ser Tyr Lys Val Cys Gly Val Phe Cys Leu Phe
-20 -15
gtt tgt ttg ttt ttg agc cag agt ttt gct ttt gtc ctc cag gct gga 99
Val Cys Leu Phe Leu Ser Gln Ser Phe Ala Phe Val Leu Gln Ala Gly
-10 -5 1 5
gtg cag tgg cgc gat ctc tgc tca ctg caa cct cag ctt ccc agg ttc 147
Val Gln Trp Arg Asp Leu Cys Ser Leu Gln Pro Gln Leu Pro Arg Phe
10 15 20
ggg cca tcc tcc tgc ctc agc ctc cca agt ggc tgg gac tgc agg cgc 195
Gly Pro Ser Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg
25 30 35
cca cca cca cgc ctg gct aat tct tgt gtt ttc ggt gga gac ggg gtt 243
Pro Pro Pro Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val
40 45 50
tca ccg gg 251
Ser Pro
55

<210> 25
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..274

<221> sig_peptide
<222> 35..82
<223> Von Heijne matrix
score 14.8000001907349
seq SLPLLLLLLGAWA/IP

<400> 25
acagactaca cttgctgaac tggctcctgg ggcc atg agg ctg tca ctg cca ctg 55
Met Arg Leu Ser Leu Pro Leu
-15 -10
ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc ggg gac 103
Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu Gly Asp
-5 1 5
agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag gag atg 151
Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu Glu Met
10 15 20
tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc aga gct 199
Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys Arg Ala
25 30 35
gtg gct tac cag gtg agt cct tca cca ctg tca cct gcc ctg ctc aca 247

```
Val Ala Tyr Gln Val Ser Pro Ser Pro Leu Ser Pro Ala Leu Leu Thr
40                  45                  50                  55
ccc ctt ctc aag cca gcc ccc acc ggg                                274
Pro Leu Leu Lys Pro Ala Pro Thr Gly
                60

<210> 26
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..229

<221> sig_peptide
<222> 29..94
<223> Von Heijne matrix
      score 13.8000001907349
      seq LGLLLLWLRGARC/GV

<400> 26
aaggagtcag tctcagtcag gacacagc atg gac atg agg gtc ccc gct cag      52
                               Met Asp Met Arg Val Pro Ala Gln
                                       -20                 -15
ctc ctg ggg ctc ctg cta ctc tgg ctc cga ggt gcc aga tgt ggc gtc     100
Leu Leu Gly Leu Leu Leu Leu Trp Leu Arg Gly Ala Arg Cys Gly Val
                -10                 -5                  1
cag atg acc cag ttt cca ctg tcc ctg tct gca tcg gta gga gac aga     148
Gln Met Thr Gln Phe Pro Leu Ser Leu Ser Ala Ser Val Gly Asp Arg
        5                   10                  15
gtc acc atc act tgc cgg aca agc cat ata att aac atc ttt tta aat     196
Val Thr Ile Thr Cys Arg Thr Ser His Ile Ile Asn Ile Phe Leu Asn
    20                  25                  30
tgg tat cag cag aaa cca ggc aaa gcc cct tgg g                       230
Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Trp
35                  40                  45

<210> 27
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..193

<221> sig_peptide
<222> 44..112
<223> Von Heijne matrix
      score 13.8000001907349
      seq VLLLLLLSGDVQS/SE

<400> 27
agagggcttc cggggctgcc ggtctgagtg cagagctgct gtc atg gcg gcc gct      55
                                                Met Ala Ala Ala
                                                            -20
ctg tgg ggc ttc ttt ccc gtc ctg ctg ctg ctg ctg cta tcg ggg gat     103
Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu Leu Leu Ser Gly Asp
                -15                 -10                 -5
gtc cag agc tcg gag gtg ccc ggg gct gct gct gag gga tcg gga ggg     151
Val Gln Ser Ser Glu Val Pro Gly Ala Ala Ala Glu Gly Ser Gly Gly
            1                   5                   10
```

```
agt ggg gtc ggc ata gga gak cgc ttc aag att gag gga ctg gg        195
Ser Gly Val Gly Ile Gly Xaa Arg Phe Lys Ile Glu Gly Leu
    15                  20                  25
```

<210> 28
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..276

<221> sig_peptide
<222> 25..90
<223> Von Heijne matrix
score 13.5
seq LGLLLLWLXGARC/DI

<400> 28

```
agtcagtctc agacaggaca cagc atg gac atg agg gtc ccc gct cag ctc     51
                           Met Asp Met Arg Val Pro Ala Gln Leu
                                       -20                 -15
ctg ggg ctc ctg cta ctc tgg ctc yka ggt gcc aga tgt gac atc cag    99
Leu Gly Leu Leu Leu Leu Trp Leu Xaa Gly Ala Arg Cys Asp Ile Gln
            -10                 -5                  1
atg aca cag tct cca gtc ctg cct gca tct gta gga gac aga gtc acc   147
Met Thr Gln Ser Pro Val Leu Pro Ala Ser Val Gly Asp Arg Val Thr
    5                   10                  15
atc act tgc cgg gca agt cag agc att ggc agc tat tta aac tgg tat   195
Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Ser Tyr Leu Asn Trp Tyr
20                  25                  30                  35
cag cat aaa cca ggg cat gcc cct cgc ctc ctg atc tat gct gca act   243
Gln His Lys Pro Gly His Ala Pro Arg Leu Leu Ile Tyr Ala Ala Thr
                40                  45                  50
act ttg tcg agg ggc ggs ccg gcc aga ttc agt                       276
Thr Leu Ser Arg Gly Gly Pro Ala Arg Phe Ser
            55                  60
```

<210> 29
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..240

<221> sig_peptide
<222> 25..120
<223> Von Heijne matrix
score 13.5
seq LLLLLLLPPPGSC/AG

<400> 29

```
agggcgctgc gcggcgcagc gaaa atg gcg gct tcc agg tgg gcg cgc aag     51
                           Met Ala Ala Ser Arg Trp Ala Arg Lys
                                       -30                 -25
gcc gtg gtc ctg ctt tgt gcc tct gac ctg ctg ctg ctg ctg cta ctg    99
Ala Val Val Leu Leu Cys Ala Ser Asp Leu Leu Leu Leu Leu Leu Leu
            -20                 -15                 -10
cta cca ccg cct ggg tcc tgc gcc ggc cga agg tcg ccy dgg acg ccc   147
Leu Pro Pro Pro Gly Ser Cys Ala Gly Arg Arg Ser Pro Xaa Thr Pro
```

```
        -5                  1                 5
gac gag tct acc cca cct ccc cgg aag aag aag aag gat att cgc gat       195
Asp Glu Ser Thr Pro Pro Pro Arg Lys Lys Lys Lys Asp Ile Arg Asp
10                  15                  20                  25
tac aat gat gca gac atg gcg cgt ctt ctg gag caa ggg gag ggg           240
Tyr Asn Asp Ala Asp Met Ala Arg Leu Leu Glu Gln Gly Glu Gly
                30                  35                  40
```

<210> 30
<211> 461
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..460

<221> sig_peptide
<222> 80..136
<223> Von Heijne matrix
score 13.5
seq WVLLLALLEGVQC/DV

<221> misc_feature
<222> 280..281,311..313
<223> n=a, g, c or t

<400> 30

```
agctctcaga gaggtgcctt agccctggat tccaaggcat ttccacttgg tgatcagcac      60
tgaacacaga ggactcacc atg gag ttg ggg ctg tgc tgg gtt ctc ctt tta     112
                     Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu
                                     -15                 -10
gct ctt tta gaa ggt gtc caa tgt gac gtg gaa tta gtg gag tct ggg      160
Ala Leu Leu Glu Gly Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly
            -5                  1               5
ggc ggc ttg gtg cag cct gga ggg tct ctg aga ctt tcc tgt gca gcc      208
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
    10                  15                  20
tct gga ttc aat ttt agc act tat gag atg cat tgg atc cgc cag gct      256
Ser Gly Phe Asn Phe Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala
25                  30                  35                  40
cca ggg aag ggg ccg gag tgg gtn nca tat gtc agt ggt gga ggt gga      304
Pro Gly Lys Gly Pro Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly
                45                  50                  55
acc agh nnn aac gcv sac tct gtg aag ggc cga ttc acc atc tcc aga      352
Thr Xaa Xaa Asn Ala Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
            60                  65                  70
gac aat gcc aac agt ttt gtg tat cta caa atg gac agt ctg cga gtc      400
Asp Asn Ala Asn Ser Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val
        75                  80                  85
gag gac acc gct ctc tat tac tgt gcg aga rgg gat tac gac ttc tgg      448
Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp
    90                  95                  100
agt ggt tat tat a                                                    461
Ser Gly Tyr Tyr
105
```

<210> 31
<211> 112
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> 28..111

<221> sig_peptide
<222> 28..84
<223> Von Heijne matrix
      score 13.3999996185303
      seq LLLLLSHCTGSLS/QP

<400> 31
aactgtgcat gtcaggctgt gtccacc atg gcc tgg act cct ctt ctt ctc ttg      54
                              Met Ala Trp Thr Pro Leu Leu Leu Leu
                                              -15
ctc ctc tct cac tgc aca ggt tcc ctc tcc cag cct gtg ctg act cag       102
Leu Leu Ser His Cys Thr Gly Ser Leu Ser Gln Pro Val Leu Thr Gln
-10                 -5                   1               5
cca cgc ggg g                                                         112
Pro Arg Gly

<210> 32
<211> 445
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..445

<221> sig_peptide
<222> 80..136
<223> Von Heijne matrix
      score 12.8000001907349
      seq WVFLVALLRGVQC/QV

<221> misc_feature
<222> 2,7
<223> n=a, g, c or t

<400> 32
anctctngga gaggagccca gcactagaag tcggcggtgt ttccattcgg tgatcagcac      60
tgaacacaga ggactcacc atg gag ttt ggg ctg aat tgg gtt ttc ctc gtt      112
                     Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val
                                     -15                 -10
gct ctt tta aga ggt gtc cag tgt cag gtt cag ttg gtg gag tct ggg       160
Ala Leu Leu Arg Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly
            -5                   1               5
gga ggc gtg gtc cag cct ggg acg tcc ctg aca ctt tcc tgt gca ggc       208
Gly Gly Val Val Gln Pro Gly Thr Ser Leu Thr Leu Ser Cys Ala Gly
    10                  15                  20
tcg gga ttc agt ttc agt gat tat ggc atc cac tgg gtc cgc cag gct       256
Ser Gly Phe Ser Phe Ser Asp Tyr Gly Ile His Trp Val Arg Gln Ala
25                  30                  35                  40
cca ggc aag ggg ctg gaa tgg gtg gcg gtt att tca cac gat gga aat       304
Pro Gly Lys Gly Leu Glu Trp Val Ala Val Ile Ser His Asp Gly Asn
                45                  50                  55
aac aaa tat tat gga ggc tcc atg aag ggc cga gtc acc atc tcc aga       352
Asn Lys Tyr Tyr Gly Gly Ser Met Lys Gly Arg Val Thr Ile Ser Arg
            60                  65                  70
gac aac tcc agg cat acc gtg tct ttg caa atg agc agc ttg gga cct       400
Asp Asn Ser Arg His Thr Val Ser Leu Gln Met Ser Ser Leu Gly Pro
        75                  80                  85
gag gac acg gca gtg tat tac tgt gcg aaa gat cga acc ggg ggg           445
Glu Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Arg Thr Gly Gly
```

```
90                  95                  100

<210> 33
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..319

<221> sig_peptide
<222> 41..97
<223> Von Heijne matrix
      score 12.6000003814697
      seq FLLLLAAPRWVLS/QV

<400> 33
aaatacttts kgcagagtcc tggacctcct gtgcaagaac atg aaa ctt ctg tgg        55
                                            Met Lys Leu Leu Trp
                                                            -15
ttc ttc ctt ctc ctg ctg gca gct ccc aga tgg gtc ctg tcc cag gtg       103
Phe Phe Leu Leu Leu Leu Ala Ala Pro Arg Trp Val Leu Ser Gln Val
                -10                 -5                  1
cag ctg gtg smg tcg ggc cca gga ctg gtg aag cct tcg ggg acc ctg       151
Gln Leu Val Xaa Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu
        5                   10                  15
tcc cta acg tgc act gts ksb ggk grs ksc ata act aat tac tac tgg       199
Ser Leu Thr Cys Thr Val Xaa Gly Xaa Xaa Ile Thr Asn Tyr Tyr Trp
    20                  25                  30
agt bgg atc cgg cag tcc cca ggg aag gga ctg gag tgg att ggg act       247
Ser Xaa Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly Thr
35                  40                  45                  50
atc tac tac agt ggg agc gcc gac cac aac ccc tcc ctc agg agt mga       295
Ile Tyr Tyr Ser Gly Ser Ala Asp His Asn Pro Ser Leu Arg Ser Arg
                55                  60                  65
gcc act att tca tta gac acg cgc gg                                    321
Ala Thr Ile Ser Leu Asp Thr Arg
            70

<210> 34
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..192

<221> sig_peptide
<222> 49..108
<223> Von Heijne matrix
      score 12.5
      seq LLXLLTALPPLWS/SS

<400> 34
agagctcagg gtgckgagcg tgtgaccagc agtgagcaga ggccggcc atg gcc agc        57
                                                     Met Ala Ser
                                                     -20
ctg ggg ctg ctg ctc ctg ckc tta ctg aca gca ctg cca ccg ctg tgg       105
Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro Pro Leu Trp
        -15                 -10                 -5
tcc tcc tca ctg cct ggg ctg gac ack gct gaa agt aaa gcc acc akt       153
```

```
Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys Ala Thr Xaa
    1               5                   10                  15
gca gac ctg atc ctg tct gcg ctg gag aga gcc acc ggg g                193
Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly
                20                  25

<210> 35
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 151..438

<221> sig_peptide
<222> 151..234
<223> Von Heijne matrix
      score 12.5
      seq LLLLLLLPLRGQA/NT

<400> 35
acgagaaggg gagggggccc agccctgctt tgggcaatcc ttgctctgac cactcagaca     60
ccgtgtcctc ttgcctggga gaggggaagc agatctgagg acatctctgt gccaggccag    120
aaaccgccca cctgcagttc cttctccggg atg gac gtg ggg ccc agc tcc ctg    174
                                 Met Asp Val Gly Pro Ser Ser Leu
                                             -25
ccc cac ctt ggg ctg aag ctg ctg ctg ctc ctg ctg ctg ctg ccc ctc      222
Pro His Leu Gly Leu Lys Leu Leu Leu Leu Leu Leu Leu Leu Pro Leu
-20                 -15                 -10                 -5
agg ggc caa gcc aac aca ggc tgc tac ggg atc cca ggg atg ccc ggc      270
Arg Gly Gln Ala Asn Thr Gly Cys Tyr Gly Ile Pro Gly Met Pro Gly
                1               5                   10
ctg ccc ggg gca cca ggg aag gat ggg tac gac gga ctg ccg ggg ccc      318
Leu Pro Gly Ala Pro Gly Lys Asp Gly Tyr Asp Gly Leu Pro Gly Pro
        15                  20                  25
aag ggg gag cca gga atc cca gcc att ccc ggg atc cga gga ccc aaa      366
Lys Gly Glu Pro Gly Ile Pro Ala Ile Pro Gly Ile Arg Gly Pro Lys
    30                  35                  40
ggg cag aag gga gaa ccc ggc tta ccc ggc cat cct ggg aaa aat ggc      414
Gly Gln Lys Gly Glu Pro Gly Leu Pro Gly His Pro Gly Lys Asn Gly
45                  50                  55                  60
ccc atg gga ccc cct ggg atg cca                                      438
Pro Met Gly Pro Pro Gly Met Pro
                65

<210> 36
<211> 488
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..487

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
      score 12.3999996185303
      seq ILLLVAAATGTHA/QV

<221> misc_feature
<222> 26..28
```

<223> n=a, g, c or t

<400> 36
atcacacaac agmcacatcs swmvsnnnmc agaagccccc agagtgcagc acctcacc 58
atg gac tgc acc tgg agg atc ctc ctc ttg gtg gca gca gct aca ggc 106
Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly
-15 -10 -5
acc cac gcc cag gtc cag ttg gta cag tct ggg cct gag gtg aaa aag 154
Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
1 5 10
cct ggg gcc tca gtg aag gtc tcc tgc cag gtt tcc gga tac aac gtc 202
Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val
15 20 25
gtg gaa tta tcc atc cac tgg gtg cgt cag tcg cct gga aaa ggg ctt 250
Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
30 35 40 45
gag tgg atg gga ggt ttt gac ctt gaa agt ggt gaa aca atc tac gca 298
Glu Trp Met Gly Gly Phe Asp Leu Glu Ser Gly Glu Thr Ile Tyr Ala
50 55 60
cag agg ttc cag ggc aga atc acc atg acc gag gac tca tct tca gac 346
Gln Arg Phe Gln Gly Arg Ile Thr Met Thr Glu Asp Ser Ser Ser Asp
65 70 75
aca gcc ttc atg gag ctg atc agc ctg aga cct gaa gat gcg gcc gtc 394
Thr Ala Phe Met Glu Leu Ile Ser Leu Arg Pro Glu Asp Ala Ala Val
80 85 90
tac tac tgt gca acg atc cgg ctg cca gta gtg ctt ttt ttc gcg gct 442
Tyr Tyr Cys Ala Thr Ile Arg Leu Pro Val Val Leu Phe Phe Ala Ala
95 100 105
tct ggg gcc agg gaa ccc tgg tcg ccg tct cct cag cmt cca cgg g 488
Ser Gly Ala Arg Glu Pro Trp Ser Pro Ser Pro Gln Xaa Pro Arg
110 115 120

<210> 37
<211> 138
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..136

<221> sig_peptide
<222> 26..79
<223> Von Heijne matrix
score 12.1000003814697
seq VLLLAVLLLAVLC/KV

<400> 37
ttttacccga cccgacgccg gcgtg atg tgg ctt ccg ctg gtg ctg ctc ctg 52
Met Trp Leu Pro Leu Val Leu Leu Leu
-15 -10
gct gtg ctg ctg ctg gcc gtc ctc tgc aaa gtt tac ttg gga cta ttc 100
Ala Val Leu Leu Leu Ala Val Leu Cys Lys Val Tyr Leu Gly Leu Phe
-5 1 5
tct ggc agc tcc ccg aat cct ttc tcc gaa gaa agg gg 138
Ser Gly Ser Ser Pro Asn Pro Phe Ser Glu Glu Arg
10 15

<210> 38
<211> 163
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 9..161

<221> sig_peptide
<222> 9..83
<223> Von Heijne matrix
      score 11.8999996185303
      seq WLLLLPLLLGLNA/GA

<400> 38
aacttgtc atg gag ctg gca ctg cgg cgc tct ccc gtc ccg cgg tgg ttg       50
         Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu
         -25                 -20                 -15
ctg ctg ctg ccg ctg ctg ctg ggc ctg aac gca gga gct gtc att gac        98
Leu Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
    -10                 -5                  1               5
tgg ccc aca gag gag ggc aag gaa gta tgg gat tat gtg acg gtc cgc       146
Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg
                10                  15                  20
aag gat gcc tac atg gg                                                163
Lys Asp Ala Tyr Met
            25

<210> 39
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..427

<221> sig_peptide
<222> 35..91
<223> Von Heijne matrix
      score 11.8999996185303
      seq FLFLLTCCPGSNS/QA

<221> misc_feature
<222> 138..139
<223> n=a, g, c or t

<400> 39
tctggcacca ggggtccctt ccaatatcag cacc atg gcc tgg act cct ctc ttt       55
                                      Met Ala Trp Thr Pro Leu Phe
                                                          -15
ctg ttc ctc ctc act tgc tgc cca ggg tcc aat tcc cag gct gtg gkg       103
Leu Phe Leu Leu Thr Cys Cys Pro Gly Ser Asn Ser Gln Ala Val Xaa
        -10                 -5                  1
act cag gag ccc ctc act gac tgt gtc ccc cgg ann aca gtc act ctc       151
Thr Gln Glu Pro Leu Thr Asp Cys Val Pro Arg Xaa Thr Val Thr Leu
5                   10                  15                  20
acc tgt ggc tcc agt att gga gct gtc acc aat ggt cat ttt ccc tac       199
Thr Cys Gly Ser Ser Ile Gly Ala Val Thr Asn Gly His Phe Pro Tyr
                25                  30                  35
tgg ttc caa cag aag cct ggc caa gcc ccc agg aca ctg att tct gat       247
Trp Phe Gln Gln Lys Pro Gly Gln Ala Pro Arg Thr Leu Ile Ser Asp
            40                  45                  50
acg ttc aac aga cag tcc tcg aca cct gcc cgc ttc tct ggc tcc ctc       295
Thr Phe Asn Arg Gln Ser Ser Thr Pro Ala Arg Phe Ser Gly Ser Leu
        55                  60                  65
ctg ggg ggc aaa gct gtc ctg act ctt tcg gat gcg caa cct gac gat       343
```

```
Leu Gly Gly Lys Ala Val Leu Thr Leu Ser Asp Ala Gln Pro Asp Asp
    70                  75                  80
gag gct gaa tat tat tgt gtc ctc tcc tat agt ggt ggt cgg ccg gtg      391
Glu Ala Glu Tyr Tyr Cys Val Leu Ser Tyr Ser Gly Gly Arg Pro Val
85                  90                  95                  100
ttc ggc gga ggg acc aag ctg acc gtc cta agt cag                      427
Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser Gln
                105                 110

<210> 40
<211> 97
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..96

<221> sig_peptide
<222> 22..84
<223> Von Heijne matrix
      score 11.8999996185303
      seq LALCLLLGPLAGA/KP

<400> 40
agatcaggaa gcaccgggaa g atg cag gcc tgc atg gtg ccg ggg ctg gcc       51
                        Met Gln Ala Cys Met Val Pro Gly Leu Ala
                            -20                 -15
ctc tgc ctc cta ctg ggg cct ctt gca ggg gcc aag cct gtg cag g        97
Leu Cys Leu Leu Leu Gly Pro Leu Ala Gly Ala Lys Pro Val Gln
    -10                 -5                  1

<210> 41
<211> 536
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 266..535

<221> sig_peptide
<222> 266..307
<223> Von Heijne matrix
      score 15
      seq LLPLLLLLPMCWA/VE

<400> 41
acttttgggg tcacgtgctc attccgtttc cctacctccc ccaaccttat cccgcccctg     60
ggggttcgcg ggcatttttc aggaactttc tttccggctt gagaagccgc cactcccaag    120
atgsagcagg aaccgcggct gctggacaag aggggtgcgg tggatactga cctttgctcc    180
ggcctcgtcg tgaagacaca gcgcatctcc ccgctgtagg cttcctccca cagaacccgt    240
ttcgggcctc agagcgtctg gtgag atg ctg ttg ccg ctg ctg ctg ctg cta      292
                            Met Leu Leu Pro Leu Leu Leu Leu Leu
                                                -10
ccc atg tgc tgg gcc gtg gag gtc aag agg ccc cgg ggc gtc tcc ctc      340
Pro Met Cys Trp Ala Val Glu Val Lys Arg Pro Arg Gly Val Ser Leu
-5                  1                   5                   10
acc aat cat cac ttc tac gat gag tcc aag cct ttc acc tgc ctg gac      388
Thr Asn His His Phe Tyr Asp Glu Ser Lys Pro Phe Thr Cys Leu Asp
            15                  20                  25
ggt tcg gcc acc atc cca ttt gat cag gtc aac gat gac tat tgc gac      436
Gly Ser Ala Thr Ile Pro Phe Asp Gln Val Asn Asp Asp Tyr Cys Asp
```

```
        30                  35                  40
tgc aaa gat ggc tct gac gag cca ggc acg gct gcc tgt cct aat ggc      484
Cys Lys Asp Gly Ser Asp Glu Pro Gly Thr Ala Ala Cys Pro Asn Gly
    45                  50                  55
agc ttc cac tgc acc aac act ggc tat aag ccc ctg tat atc ccc tcc      532
Ser Phe His Cys Thr Asn Thr Gly Tyr Lys Pro Leu Tyr Ile Pro Ser
60                  65                  70                  75
aac c                                                                536
Asn
```

<210> 42
<211> 319
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 143..319

<221> sig_peptide
<222> 143..205
<223> Von Heijne matrix
      score 11.6000003814697
      seq LLLCLALSGAAET/KP

<221> misc_feature
<222> 139
<223> n=a, g, c or t

<400> 42

```
agcagaggga acagggaaga aacctaaagg ctgcaggctg ccaggtgtgc ttggagagcc     60
cccttcttcc gccgggcctc gcaagcagcg taggactgtg gagaagggcg gtgggcaagg    120
agggaactcg agagcarcny cc atg ggc aca cag gag ggc tgg wgc ctg ctg     172
                         Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu
                             -20                 -15
ctc tgc ctg gct cta tct gga gca gca gaa acc aag ccc cac cca gca      220
Leu Cys Leu Ala Leu Ser Gly Ala Ala Glu Thr Lys Pro His Pro Ala
    -10                 -5                  1                   5
gag ggg cag tgg cgg gca gtg gdc gtg gtc cta gac ygt ttc ctg gtg      268
Glu Gly Gln Trp Arg Ala Val Xaa Val Val Leu Asp Xaa Phe Leu Val
                10                  15                  20
aag gac svt gcg cac cgt gga gct ctc gcc agc agt gag gac agg gca      316
Lys Asp Xaa Ala His Arg Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala
            25                  30                  35
agg                                                                  319
Arg
```

<210> 43
<211> 412
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..412

<221> sig_peptide
<222> 35..82
<223> Von Heijne matrix
      score 11.1999998092651
      seq LVVFLLLWGVTWG/PV

<221> misc_feature

```
<222> 148
<223> n=a, g, c or t

<400> 43
agacactcac tgcaccggag tgagcgcgac catc atg tcc atg ctc gtg gtc ttt      55
                                     Met Ser Met Leu Val Val Phe
                                             -15                 -10
ctc ttg ctg tgg ggt gtc acc tgg ggc cca gtg aca gaa gca gcc ata      103
Leu Leu Leu Trp Gly Val Thr Trp Gly Pro Val Thr Glu Ala Ala Ile
                -5                  1                   5
ttt tat gag acg cag scc agc ctg tgg gca gag tcc gaa cac tgn ctg      151
Phe Tyr Glu Thr Gln Xaa Ser Leu Trp Ala Glu Ser Glu His Xaa Leu
        10                  15                  20
aaa acc ctt ggc caa tgt gac gct gac gtg cca ggc ccg cct gga gac      199
Lys Thr Leu Gly Gln Cys Asp Ala Asp Val Pro Gly Pro Pro Gly Asp
    25                  30                  35
tcc aga ctt cca gct gtt caa gaa tgg ggg gcc cag gag cct gtg cac      247
Ser Arg Leu Pro Ala Val Gln Glu Trp Gly Ala Gln Glu Pro Val His
40                  45                  50                  55
ctt gac tca cct gcc atc aag cac cag ttc ctg ctg acg ggt gac acc      295
Leu Asp Ser Pro Ala Ile Lys His Gln Phe Leu Leu Thr Gly Asp Thr
                60                  65                  70
cag ggc cgc tac cgc tgc cgc tcg ggc ttg tcc aca gga tgg mcc cag      343
Gln Gly Arg Tyr Arg Cys Arg Ser Gly Leu Ser Thr Gly Trp Xaa Gln
            75                  80                  85
ctg agc aag ctc ctg gag ctg aca ggg cca aaa gtc ctt gcc tgc tcc      391
Leu Ser Lys Leu Leu Glu Leu Thr Gly Pro Lys Val Leu Ala Cys Ser
        90                  95                  100
ctg gct ctc gat ggc gcc agt                                          412
Leu Ala Leu Asp Gly Ala Ser
    105                 110

<210> 44
<211> 331
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..331

<221> sig_peptide
<222> 32..88
<223> Von Heijne matrix
      score 11.1999998092651
      seq IGFLLLWVPASRG/EI

<400> 44
atgagcaaaa ctgacaagtc aaggcaggaa g atg ttg cca tca caa ctc att      52
                                   Met Leu Pro Ser Gln Leu Ile
                                                       -15
ggg ttt ctg ctg ctc tgg gtt cca gcc tcc agg ggt gaa att gtg ctg      100
Gly Phe Leu Leu Leu Trp Val Pro Ala Ser Arg Gly Glu Ile Val Leu
        -10                 -5                  1
act cag tct cca gac ttt ctg tct gtg act cca aag gag aaa gtc acc      148
Thr Gln Ser Pro Asp Phe Leu Ser Val Thr Pro Lys Glu Lys Val Thr
5                   10                  15                  20
atc acc tgc cgg gcc agt sag agc att ggt agt agt tta tac tgg tac      196
Ile Thr Cys Arg Ala Ser Xaa Ser Ile Gly Ser Ser Leu Tyr Trp Tyr
                25                  30                  35
cag cag aaa cca cat cag tct cca aag ctc gtc atc aag tat gct tcc      244
Gln Gln Lys Pro His Gln Ser Pro Lys Leu Val Ile Lys Tyr Ala Ser
            40                  45                  50
```

```
cag tcc ttc tca ggg gtc tcc tcg agg ttc agt ggc agt gga tct ggg      292
Gln Ser Phe Ser Gly Val Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
        55                  60                  65
aca gat ttc acc ctc aca atc aat agc ctg gaa cct ggg                  331
Thr Asp Phe Thr Leu Thr Ile Asn Ser Leu Glu Pro Gly
    70                  75                  80
```

<210> 45
<211> 520
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 176..520

<221> sig_peptide
<222> 176..235
<223> Von Heijne matrix
score 11.1999998092651
seq AFLLLVALSYTLA/RD

<400> 45

```
gaagataatc acttggggaa aggaaggttc gtttctgagt tagcaacaag taaatgcagc     60
actagtgggt gggattgagg tatgccctgg tgcataaata gagactcagc tgtgctggca    120
cactcagaag cttggaccgc atcctagccg ccgactcaca caaggcagag ttgcc atg     178
                                                             Met
                                                             -20
gag aaa att cca gtg tca gca ttc ttg ctc ctt gtg gcc ctc tcc tac      226
Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser Tyr
            -15                 -10                 -5
act ctg gcc aga gat acc aca gtc aaa cct gga gcc aaa aag gac aca      274
Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp Thr
            1                   5                   10
aag gac tct cga ccc aaa ctg ccc cag acc ctc tcc aga ggt tgg ggt      322
Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp Gly
    15                  20                  25
gac caa ctc atc tgg act cag aca tat gaa gaa gct cta tat aaa tcc      370
Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys Ser
30                  35                  40                  45
aag aca agc aac aaa ccc ttg atg att att cat cac ttg gat gag tgc      418
Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu Cys
                50                  55                  60
cca cac agt caa gct tta aag aaa gtg ttt gct gaa aat aaa gaa atc      466
Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu Ile
            65                  70                  75
cag aaa ttg gca gag cag ttt gtc ctc ctc aat ctg gtt tat gaa aca      514
Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu Thr
        80                  85                  90
act gac                                                              520
Thr Asp
    95
```

<210> 46
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..381

<221> sig_peptide

```
<222> 25..84
<223> Von Heijne matrix
      score 11.1000003814697
      seq LLALLFFLGQAAG/DL

<400> 46
agcggctcca gctaagagga caag atg agg ccc ggc ctc tca ttt ctc cta        51
                           Met Arg Pro Gly Leu Ser Phe Leu Leu
                           -20                 -15
gcc ctt ctg ttc ttc ctt ggc caa gct gca ggg gat ttg ggg gat gtg        99
Ala Leu Leu Phe Phe Leu Gly Gln Ala Ala Gly Asp Leu Gly Asp Val
    -10                 -5                  1               5
gga cct cca att ccc agc ccc ggc ttc agc tct ttc cca ggt gtt gac       147
Gly Pro Pro Ile Pro Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp
                10                  15                  20
tcc agc tcc agc ttc agc tcc agc tcc agg tcg ggc tcc agc tcc agc       195
Ser Ser Ser Ser Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser
            25                  30                  35
cgc agc tta ggc agc gga ggt tct gtg tcc cag ttg ttt tcc aat ttc       243
Arg Ser Leu Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe
        40                  45                  50
acc ggc tcc gtg gat gac cgt ggg acc tgc cag tgc tct gtt tcc ctg       291
Thr Gly Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu
    55                  60                  65
cca gac acc acc ttt ccc gtg gac aga gtg gaa cgc ttg gaa ttc aca       339
Pro Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
70                  75                  80                  85
gct cat gtt ctt tct cag aag ttt gag aaa gaa ctt tct aaa gc            383
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys
                90                  95


<210> 47
<211> 459
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..457

<221> sig_peptide
<222> 17..94
<223> Von Heijne matrix
      score 11.1000003814697
      seq FLLLVAAPRWVRS/QV

<221> misc_feature
<222> 399
<223> n=a, g, c or t

<400> 47
atactttctg agactc atg gac ctc ctg cac aag aac atg aaa cac ctg tgg     52
                  Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp
                      -25                 -20                 -15
ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc cgg tct car gtg      100
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Arg Ser Gln Val
                -10                 -5                  1
cag ctg cak gag tcg ggc cca gga ctg gtg aag cct tcg ggg acc ctg      148
Gln Leu Xaa Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu
        5                   10                  15
tcc ctc atc tgc ggt gtc tct ggt gat tcc gtc acc att agt ggt tgg      196
Ser Leu Ile Cys Gly Val Ser Gly Asp Ser Val Thr Ile Ser Gly Trp
    20                  25                  30
```

```
tgg agt tgg gtc cgc cag ccc cca ggg aag gga ctg gag tgg att tcg     244
Trp Ser Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Ser
35                  40                  45                  50
gaa atc gat cat ggt gga aac acc aat tac aac ccg tcc ctc aag agt     292
Glu Ile Asp His Gly Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser
                55                  60                  65
cga gtc kcc att tct tta gac aag tcc aag aat aag ttc tcc ctg agg     340
Arg Val Xaa Ile Ser Leu Asp Lys Ser Lys Asn Lys Phe Ser Leu Arg
            70                  75                  80
ctg acc tct gtg acc gcc gcg gac acc gcc atg tat kac tgt gcg aga     388
Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Met Tyr Xaa Cys Ala Arg
        85                  90                  95
ggc ggt gcg bnc agc tcg tcc gct ttt gat gtc tgg ggc cta rgg aca     436
Gly Gly Ala Xaa Ser Ser Ser Ala Phe Asp Val Trp Gly Leu Xaa Thr
    100                 105                 110
atg gtc atc atc tct tca gcc tc                                      459
Met Val Ile Ile Ser Ser Ala
115                 120
```

<210> 48
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..436

<221> sig_peptide
<222> 20..76
<223> Von Heijne matrix
score 11
seq TLLLLTVPSWVLS/QV

<400> 48

```
gtgaatcctg ctctccacc atg gac ata ctt tgt tcc acg ctc ctg ctm ctg      52
                     Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu
                                         -15                 -10
ack gtc ccg tcc tgg gtc tta tcc car gtc acc ttg arg gaa tct ggt     100
Thr Val Pro Ser Trp Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly
            -5                  1                   5
cct gcg ctg gtg aaa gcc aca cag acc ctc aga ctg acc tgc acc ttc     148
Pro Ala Leu Val Lys Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe
    10                  15                  20
tct ggg ttc tca ctc agc act aat aga atg cgt gtg agt tgg atc cgt     196
Ser Gly Phe Ser Leu Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg
25                  30                  35                  40
cag ccc cca ggg aag gcc ctg gag tgg ctt gca cgg att gat tgg gat     244
Gln Pro Pro Gly Lys Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp
                45                  50                  55
gat tat aag agg tac agc aca tct ctg aag acc agg gtc acc atc tcc     292
Asp Tyr Lys Arg Tyr Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser
            60                  65                  70
aag gac acg tcc aaa aac cag gtg atc ctg aca atg acc aac gtg gac     340
Lys Asp Thr Ser Lys Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp
        75                  80                  85
cct gcg gac aca gcc acc tat tac tgt gca cgc ctt tca acg gca gct     388
Pro Ala Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Leu Ser Thr Ala Ala
    90                  95                  100
acc cca cag ttt ttt gac ttc tgg ggc cag gga gtc ctg gtc tcc gtc t   437
Thr Pro Gln Phe Phe Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
105                 110                 115                 120
```

```
<210> 49
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..456

<221> sig_peptide
<222> 40..96
<223> Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

<400> 49
aaatactttc tgagagtcct ggacctcctg tgcaagaac atg adw cat ctg tgg        54
                                           Met Xaa His Leu Trp
                                                           -15
ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg      102
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
            -10                 -5                  1
cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg kwg acc ctg      150
Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Xaa Thr Leu
        5                   10                  15
tcc ctc acc tgc act gtc tct ggt gac tcc atc agt agt tac tac tgg      198
Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile Ser Ser Tyr Tyr Trp
    20                  25                  30
agc tgg atc cgg cag ccc cca ggg aag gga ctg gag tgg att ggc tat      246
Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr
35                  40                  45                  50
atc tat tac agt ggg agc acc aac tac aac ccc tcc ctc aag agt cga      294
Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
                55                  60                  65
gtc acc ata tca gtg gac acg tcc aag aac caa ttc tcc ctg aag ctg      342
Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Lys Leu
            70                  75                  80
agc tct gtg acc gca gcg gac acg gcc gtg tat tac tgt gcg aga sgg      390
Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg Xaa
        85                  90                  95
ctg cma tac tat gat agg agt ggt tat ttc aga tat ttt gac tac tgg      438
Leu Xaa Tyr Tyr Asp Arg Ser Gly Tyr Phe Arg Tyr Phe Asp Tyr Trp
    100                 105                 110
ggc cag gga acc tgg tca                                              456
Gly Gln Gly Thr Trp Ser
115                 120

<210> 50
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..445

<221> sig_peptide
<222> 38..94
<223> Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

<221> misc_feature
```

<222> 16
<223> n=a, g, c or t

<400> 50

```
atactttctg agagtnctgg acctcctgtg caagaac atg aaa cat ctg tgg ttc    55
                                         Met Lys His Leu Trp Phe
                                                         -15
ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag    103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
            -10                 -5                  1
ctg cag gag tcg ggc cca gga ctg gtg aag cct tca cag acc ctg tcc    151
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr Leu Ser
    5                   10                  15
ctc acc tgc aca gtc tct ggt ggc tcc atc gac agt ggt aat tac tac    199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Asp Ser Gly Asn Tyr Tyr
20                  25                  30                  35
tgg agc tgg atc cgg cag ccc gcc ggg aag gga ctg gag tgg att ggg    247
Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys Gly Leu Glu Trp Ile Gly
                40                  45                  50
cgc atc tat agt act ggg agc acc aat tac aac ccc tcc ctc agc agt    295
Arg Ile Tyr Ser Thr Gly Ser Thr Asn Tyr Asn Pro Ser Leu Ser Ser
            55                  60                  65
cga gtc cag ata tcg tta gac acg tcc aag aac ctg ctc tcc ttg aac    343
Arg Val Gln Ile Ser Leu Asp Thr Ser Lys Asn Leu Leu Ser Leu Asn
        70                  75                  80
ctg acc tct gtg acc gcc gca gac acg gcc gtc tat ttt tgt gcg cga    391
Leu Thr Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg
    85                  90                  95
acc ttc ccc ttc tac tgg tac ctc gat ctc tgg ggc cgt ggc atc ctg    439
Thr Phe Pro Phe Tyr Trp Tyr Leu Asp Leu Trp Gly Arg Gly Ile Leu
100                 105                 110                 115
gtc act gt                                                          447
Val Thr
```

<210> 51
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..466

<221> sig_peptide
<222> 38..94
<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAPRWVLS/QV

<221> misc_feature
<222> 423
<223> n=a, g, c or t

<400> 51

```
atactttctg agagtcctgg acctcctgtg caagaac atg aaa cac ctg tgg ttc    55
                                         Met Lys His Leu Trp Phe
                                                         -15
ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag    103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
            -10                 -5                  1
ctg cag gag tcg ggc cca aga ctg gtg aag cct tca cag acc ctg tcc    151
```

```
Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gln Thr Leu Ser
    5                   10                  15
ctc acc tgc act gtc tct ggt ggc tcc atc agc agt ggt ggt tac ttc      199
Leu Thr Cys Thr Val Ser Gly Gly Ser Ile Ser Ser Gly Gly Tyr Phe
20                  25                  30                  35
tgg agt tgg atc cgc cag cac cca ggg cgg ggc ctg gag tgg att ggc      247
Trp Ser Trp Ile Arg Gln His Pro Gly Arg Gly Leu Glu Trp Ile Gly
                40                  45                  50
tac atc tat tac aat tgg agc acc tac tac aat ccg tcc ctc agg agt      295
Tyr Ile Tyr Tyr Asn Trp Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser
            55                  60                  65
cga gtt acc atg tca atg gac acg tct aag aac cag ttc tcc ctg aac      343
Arg Val Thr Met Ser Met Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
        70                  75                  80
ctg aac tct gta act gcc gcg gac acg gsc atg tat tac tgt gcs aga      391
Leu Asn Ser Val Thr Ala Ala Asp Thr Xaa Met Tyr Tyr Cys Ala Arg
    85                  90                  95
ggt cgc gga cgc ctt ggc tgg ttc ash mct tng ggg mca ggg rac cca      439
Gly Arg Gly Arg Leu Gly Trp Phe Xaa Xaa Xaa Gly Xaa Gly Xaa Pro
100                 105                 110                 115
ggt cac cgt ctc atc agc cgt cca ggg                                  466
Gly His Arg Leu Ile Ser Arg Pro Gly
                120

&lt;210&gt; 52
&lt;211&gt; 392
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 59..391

&lt;221&gt; sig_peptide
&lt;222&gt; 59..115
&lt;223&gt; Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

&lt;221&gt; misc_feature
&lt;222&gt; 342
&lt;223&gt; n=a, g, c or t


&lt;400&gt; 52
agggtcctgc tcacatggga aatactttct gagagtcctg gacctcctgt gcaagaac       58
atg aaa cac ctg tgg ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg      106
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
gtc ctg tcc cag gtg cag ctg cag gag tcg ggc cca gga ctg gtg aag      154
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            1                   5                   10
cct tca gag acc ctg tcc ctc acc tgc act gtc tct ggt ggc tcc atc      202
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
    15                  20                  25
agg act ggt tct tac tac tgg act tgg gtt cgc cag ccc ccc ggg aag      250
Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys
30                  35                  40                  45
ggc ctg gag tgg att ggc tac att tat tat act ggg gac acc tac tac      298
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr
                50                  55                  60
aac ccg tcc ctc aag agt cga att acc atg tcr cta gac acg tny wag      346
Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa
```

```
              65                  70                    75
aac cag ttc kcc ctg agc ctg acc tct gtg act gtc gca gac acg g          392
Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr
        80                  85                  90
```

<210> 53
<211> 172
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..172

<221> sig_peptide
<222> 14..58
<223> Von Heijne matrix
score 10.8999996185303
seq LSVCLLLVTLALC/CY

<400> 53

```
aaaacaagcc acc atg aag ctg tcg gtg tgt ctc ctg ctg gtc acg ctg          49
               Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu
               -15                 -10                 -5
gcc ctc tgc tgc tac cag gcc aat gcc gag ttc tgc cca gct ctt gtt        97
Ala Leu Cys Cys Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val
            1               5                   10
tct gag ctg tta gac ttc ttc ttc att agt gaa cct ctg ttc aag tta        145
Ser Glu Leu Leu Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu
    15                  20                  25
agt ctt gcc aaa ttt gat gcc cct cga                                    172
Ser Leu Ala Lys Phe Asp Ala Pro Arg
30                  35
```

<210> 54
<211> 259
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 190..258

<221> sig_peptide
<222> 190..237
<223> Von Heijne matrix
score 10.8999996185303
seq VLLVLSLSQCLLS/DP

<400> 54

```
tacctggaaa gaacagaaat ttgttaattt acaggtctga aggtgagaaa tctgaaatta       60
gtcttacaaa actaaaatga agttgttgga agccttggct ccttctggag gttccagggg      120
aaaaaagtat gtttccttga ctttccagcc kstacaggcc cacagcattc ctgcttgcag      180
ccctatgtc atg tca cct gtc ctc ttg gtg ctg tca ttg tca caa tgc ctt      231
          Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu
              -15                 -10                 -5
ctt tct gac cct gtc att cct ggc ctc c                                  259
Leu Ser Asp Pro Val Ile Pro Gly Leu
        1               5
```

<210> 55
<211> 320
<212> DNA

```
<213> Homo sapiens

<220>
<221> CDS
<222> 40..318

<221> sig_peptide
<222> 40..96
<223> Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

<400> 55
aaacacsyyc tgagagtcct ggacctcctg tgcaggacc atg aaa cat ctg tgg        54
                                           Met Lys His Leu Trp
                                                           -15
ttc ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg      102
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
                -10                 -5                  1
cgg ctg cag gag tcg ggc cca cgg ctg gtg aag cct tcg gag amc ctg      150
Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Glu Xaa Leu
        5                   10                  15
tcc ctc acc tgt agt gtc tct ggt gtc tcc gtc act aat ttc ttc tgg      198
Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val Thr Asn Phe Phe Trp
    20                  25                  30
aac tgg atc cgg aag ccc cca ggc aag ggc ctg gag tgg ctt ggc tac      246
Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Tyr
35                  40                  45                  50
atg tct tat ggc gtg agc aca aac tat cac ccc gcc tac cag agt cgg      294
Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro Ala Tyr Gln Ser Arg
                55                  60                  65
gtc agt ata tcg att gac acg tgg gg                                   320
Val Ser Ile Ser Ile Asp Thr Trp
            70

<210> 56
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..455

<221> sig_peptide
<222> 39..95
<223> Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

<400> 56
aatactttct gagagtcctg gacctcctgt gcaagaac atg aaa cat ctg tgg ttc     56
                                          Met Lys His Leu Trp Phe
                                                          -15
ttc ctt ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag      104
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
            -10                 -5                  1
ctg cag gag gcg ggc cca cga ctg gtg aag cct tcg gag gcc ctg tcc      152
Leu Gln Glu Ala Gly Pro Arg Leu Val Lys Pro Ser Glu Ala Leu Ser
    5                   10                  15
ctc acc tgc act gtc tct ggt gtc tcc agc agc aat tac gac tgg agt      200
Leu Thr Cys Thr Val Ser Gly Val Ser Ser Ser Asn Tyr Asp Trp Ser
20                  25                  30                  35
```

```
tgg att cgg cag gcc cca ggg aag gga ctg gaa tgg att ggg tat ata      248
Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Tyr Ile
                40                  45                  50
gac gat agt aag aat aga ggg agt acg acc tac aac ccc tcc ctc aag      296
Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr Tyr Asn Pro Ser Leu Lys
            55                  60                  65
agt cga gtc acc ata tcg stg gac acg tcc aag ast cag ttg tcc ctg      344
Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser Lys Xaa Gln Leu Ser Leu
        70                  75                  80
agg ctg acc tct gtg acc kcs gca gac acg gcc gtc tat tat tgt gcg      392
Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr Ala Val Tyr Tyr Cys Ala
    85                  90                  95
aga aag tca tct atg cat agt agt ggc tgg cat aac cgg agt ctc tac      440
Arg Lys Ser Ser Met His Ser Ser Gly Trp His Asn Arg Ser Leu Tyr
100                 105                 110                 115
tgg tac ttc gat cct gg                                               457
Trp Tyr Phe Asp Pro
                120

<210> 57
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..418

<221> sig_peptide
<222> 17..94
<223> Von Heijne matrix
      score 10.8999996185303
      seq FLLLVAAPRWVLS/QV

<400> 57
atactttctg agactc atg gac ctc ctg cac aag aac atg aaa gac ctg tgg     52
                  Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp
                      -25                 -20                 -15
ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tct cag gtg      100
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val
                -10                  -5                   1
ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg acc ctg tcc      148
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser
        5                   10                  15
ctc acc tgc gct gtc tct ggt ggc tcc atc ata agt agt aat tgg tgg      196
Leu Thr Cys Ala Val Ser Gly Gly Ser Ile Ile Ser Ser Asn Trp Trp
    20                  25                  30
agt tgg gtc cgc cag acc cca ggg aag ggg ctg gag tgg att ggg gaa      244
Ser Trp Val Arg Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu
35                  40                  45                  50
atc tat gaa gat ggg atc acc aac tac aac ccg tcc ctc aag agt cga      292
Ile Tyr Glu Asp Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
                55                  60                  65
gtc atc att tca gtg gac aag gcc aag aac cag ttc tcc ctg aag atg      340
Val Ile Ile Ser Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met
            70                  75                  80
agg tct gtg acc gcc tcg gac acg gcc gtc tat tac tgt gcg aga ggt      388
Arg Ser Val Thr Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly
        85                  90                  95
agc agc tcg gtt cgg aca gac tac tgg ggc ca                           420
Ser Ser Ser Val Arg Thr Asp Tyr Trp Gly
    100                 105
```

<210> 58
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..469

<221> sig_peptide
<222> 38..94
<223> Von Heijne matrix
score 10.8999996185303
seq FLLLVAAPRWVLS/QV

<400> 58
atactttctg agagtcctgg acctcctgtg caagaac atg aaa cac ctg tgg ttc 55
Met Lys His Leu Trp Phe
-15
ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag gtg cag 103
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Gln
-10 -5 1
ctg cag gag tcc ggt tca gga ccg gtg gat sct tsa cag acc ctg tsc 151
Leu Gln Glu Ser Gly Ser Gly Pro Val Asp Xaa Xaa Gln Thr Leu Xaa
5 10 15
ctc acc tgc act gks tct ggt gtc tcc atc agc agt agt gat aat tgt 199
Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile Ser Ser Ser Asp Asn Cys
20 25 30 35
tgg agc tgg atc cgg cag cca cca ggg aag ggc ctg gag tgg att gga 247
Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
40 45 50
tac atc tat cay agt ggg ggg acc tac tac aac ccg acc ctc aag agc 295
Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr Asn Pro Thr Leu Lys Ser
55 60 65
cga gtc acc atc tcg gba gac agg atc agg aac caa ttc tcc ctg aag 343
Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg Asn Gln Phe Ser Leu Lys
70 75 80
ctg agc tct gtg acg gcc gyg gac acg gcc gtg tat kac tgt ggc aga 391
Leu Ser Ser Val Thr Ala Xaa Asp Thr Ala Val Tyr Xaa Cys Gly Arg
85 90 95
gca cag ggt aga atg ggg atc ggg acg acg att ttt gat ctc tgg ggc 439
Ala Gln Gly Arg Met Gly Ile Gly Thr Thr Ile Phe Asp Leu Trp Gly
100 105 110 115
ggg gga caa tgg tca ccg tct ctg cag cct 469
Gly Gly Gln Trp Ser Pro Ser Leu Gln Pro
120 125

<210> 59
<211> 471
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..471

<221> sig_peptide
<222> 52..108
<223> Von Heijne matrix
score 10.8000001907349
seq ILFLVAAATGAHS/QV

<221> misc_feature

<222> 210
<223> n=a, g, c or t

<400> 59
```
acccaacaac cacatccctc ctcagmagcc cccagagcac aackcctyac c atg gac      57
                                                         Met Asp
tgg acc tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gcc cac      105
Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala His
        -15                 -10                 -5
tcc cag gtc cag ctt gtg cag tct ggg gct gag gtg aag aag cct ggg      153
Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
    1               5                   10                  15
gcc tca gtg aag gtt tcc tgc aag gct tct gga tac ayc ttc act ary      201
Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe Thr Xaa
                20                  25                  30
tmt gct atn cat tgg gtg cgc cag gcc ccc gga car agr ctt gag tgg      249
Xaa Ala Xaa His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu Glu Trp
            35                  40                  45
atg ggr tgg atc aac gct gcc amt ggt wam aca awa tat tca cag aas      297
Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser Gln Xaa
        50                  55                  60
ttc cag grc aga gtc acc wtt acc agg gac aca tcc gcg agc aca gtc      345
Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser Thr Val
    65                  70                  75
tcc atg gag ctg agc agc ctg aga tct gaa gac acg gct gtg tat ttc      393
Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
80                  85                  90                  95
tgt gcg aga gat tgg gaa att gca gta gta cca act gct ata aac tct      441
Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile Asn Ser
                100                 105                 110
tac ggg ttc gac cct ggg gcc agg gaa cct                              471
Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro
            115                 120
```

<210> 60
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 193..348

<221> sig_peptide
<222> 193..270
<223> Von Heijne matrix
score 10.8000001907349
seq VLFLCVFLGMSWA/GA

<400> 60
```
agagcaaaga ggcaatctga agagaaaagc ataggaaagg aaacagtggt aataggaatt      60
ggggtaaaat gaggatcctt ccccacaaac attgctatta ttcagctcat ttcaaaggat     120
tccgstgcwg ccatttgtga gagccgctgg aggctgagtg aaagtcattt tgaaagactg     180
atccaaagaa ga atg gag gcc aga gtg gag cgt gct gtg cag aaa agg caa     231
              Met Glu Ala Arg Val Glu Arg Ala Val Gln Lys Arg Gln
                  -25                 -20                 -15
gtc tta ttt ctt tgt gta ttt ctg gga atg tct tgg gct ggc gcc gaa      279
Val Leu Phe Leu Cys Val Phe Leu Gly Met Ser Trp Ala Gly Ala Glu
            -10                 -5                  1
ccg ctt cgg tat ttt gtg gcg gag gaa acc gag aga ggc acc tdk ctt      327
Pro Leu Arg Tyr Phe Val Ala Glu Glu Thr Glu Arg Gly Thr Xaa Leu
    5                   10                  15
```

```
acc aac ttg gca aaa gac cta                                          348
Thr Asn Leu Ala Lys Asp Leu
20                  25

<210> 61
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 55..456

<221> sig_peptide
<222> 55..111
<223> Von Heijne matrix
      score 10.8000001907349
      seq ILFLVAAATGAHS/QV

<400> 61
acccaaaaac cacacccctc cttgggagaa tcccctagat cacagctcct cacc atg       57
                                                            Met
gac tgg acc tgg agc atc ctt ttc ttg gtg gca gca gcg aca ggt gcc      105
Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Ala
            -15                 -10                 -5
cac tcc cag gtt cag ctg gtg cag tct gga ggt gag gtg aag aag cct      153
His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys Pro
        1               5                   10
ggg gcc tcc gtc aag gtc tcc tgc aag gct tct ggt tac acc ttt acc      201
Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
15                  20                  25                  30
aga tat gat atc aac tgg gtg cga cag gcc cct gga caa ggg ctt gag      249
Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu
                35                  40                  45
tgg atg gga tgg atc agc gct dcc aat ggt aac aca aat tat gca cag      297
Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala Gln
            50                  55                  60
daa gtc cag ggc aga gtc acc atg acc aca gac aca tcc acg aga aca      345
Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg Thr
        65                  70                  75
gcc tac atg gaa ctg agg agc ctg cga tct gac gac acg gcc att tat      393
Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile Tyr
    80                  85                  90
tac tgt gcg cga gag atm bta gtg gba sta tgt gat gga cag ttg ggg      441
Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu Gly
95                  100                 105                 110
cca ggg aac ctg gtc a                                                457
Pro Gly Asn Leu Val
                115

<210> 62
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..437

<221> sig_peptide
<222> 18..95
<223> Von Heijne matrix
      score 10.8000001907349
```

seq FLLLVAAPRWVLS/QE

<400> 62

```
agtgcttyct gasagtc atg gac gtc ctg cac aaa cac atg aaa cac ctg        50
                   Met Asp Val Leu His Lys His Met Lys His Leu
                       -25                 -20
tgg ttc ttc ctc ctc ctg gtg gca gct ccc aga tgg gtc ctg tcc cag       98
Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln
-15                 -10                 -5                  1
gag cag tta cgg cag tgg ggc gca sga ctg ttg aag cct tcg gag acc      146
Glu Gln Leu Arg Gln Trp Gly Ala Xaa Leu Leu Lys Pro Ser Glu Thr
            5                   10                  15
ctg tcc ctc acc tgt agt gtc tat ggt ggg tcc ttc aat ggt tac tac      194
Leu Ser Leu Thr Cys Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr
        20                  25                  30
tgg agc tgg atc cgc cag tcc cca ggg aag ggg ctg gag tgg att ggg      242
Trp Ser Trp Ile Arg Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly
    35                  40                  45
gga atc aat cac agc gga agc acc ctc tcc aac ccg tcc ctc aag agt      290
Gly Ile Asn His Ser Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser
50                  55                  60                  65
cgc gtc gac ctc tca gtt gat gcg tcc aag gac cag gtg tcc ctg agg      338
Arg Val Asp Leu Ser Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg
                70                  75                  80
ctg aaa ctt gtg acc gcc gcg gac acg gct gtg tac ttc tgc gcg aga      386
Leu Lys Leu Val Thr Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg
            85                  90                  95
ccc cat tac gat atg tcg act gat tct tcg ttt gac ggt ttt gat ctc      434
Pro His Tyr Asp Met Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu
        100                 105                 110
tgg gg                                                               439
Trp
```

<210> 63
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 82..213

<221> sig_peptide
<222> 82..126
<223> Von Heijne matrix
score 10.6999998092651
seq LLALFFLLRIALA/SQ

<400> 63

```
accattggtg tgtctgtttt tatgccagta ctgtgatgtt ttggttatat agctttgtaa     60
tatattttga agccagatag t atg atg ctt cta gct ttg ttc ttt ttg ctt      111
                        Met Met Leu Leu Ala Leu Phe Phe Leu Leu
                            -15                 -10
agg att gct ttg gct agt caa ggt ctt ttg tgg ttc cat aca aat ttt      159
Arg Ile Ala Leu Ala Ser Gln Gly Leu Leu Trp Phe His Thr Asn Phe
-5                  1               5                   10
aag gtt ttt gtt gtt tcy att tgt gtg aag act atc att ggg att tcg      207
Lys Val Phe Val Val Ser Ile Cys Val Lys Thr Ile Ile Gly Ile Ser
            15                  20                  25
ggg ggc a                                                            214
Gly Gly
```

<210> 64

```
<211> 297
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..296

<221> sig_peptide
<222> 63..119
<223> Von Heijne matrix
      score 10.6999998092651
      seq ILFLVAAATGALS/QV

<400> 64
gtgcatcacc cagcaaccac atctgtcctc tagagaatcc cctgagadht ccgttcctca      60
cc atg gac tgg acc tgg agg atc ctc ttc ttg gtg gca gcr gcc aca        107
   Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr
               -15                 -10                 -5
gga gcc ctc tcc cag gtg cag ctg gtr cag tct gga ggt gar gtg aag       155
Gly Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys
                1               5                   10
aag cct ggg gcc tca gtg agg gtc tcc tgc aag gcc tct gga tac agc       203
Lys Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser
        15                  20                  25
ttc atc ggc tat tat gta cac tgg ata cga cag act cct ggg cga sgc       251
Phe Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa
    30                  35                  40
ctt gag tgg atg ggg tgg gtc aac cct crs act ggc gac aac ggg g         297
Leu Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly
45                  50                  55

<210> 65
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 237..368

<221> sig_peptide
<222> 237..347
<223> Von Heijne matrix
      score 10.6000003814697
      seq YLLLVLSLSLSLC/CS

<400> 65
aaaggtacac aattgaaaaa aattgtatcc ttcacaacag atgtgggcag tcaactttta      60
gaccttgtgt ctttagtttg acctgtcctt cagtgagtgt atataaaatt ctaagctaaa     120
acatattttc tgaaattgtg aaggtattgc atgtctatct tcttgcctac tctaaatata     180
tcaatcgttt tcttgggaag ttagtctttc tttcacactt gtctgtagat ctttac atg     239
                                                              Met
ttc ttt cag ttt tgg aag tcc tct gca tat tta ata ttt gtt agt att       287
Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser Ile
    -35                 -30                 -25
tgt aaa ggt ttt ctt cct gtc tac ctc ctt ctt gtt ctc tct ctc tct       335
Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Leu Val Leu Ser Leu Ser
-20                 -15                 -10                 -5
ctc tct ctc tgt tgc tct ctc ttg ctc tct ctc ca                        370
Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu
                1               5
```

<210> 66
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..428

<221> sig_peptide
<222> 45..101
<223> Von Heijne matrix
score 10.6000003814697
seq ILFLVAAATGVHS/QV

<221> misc_feature
<222> 342..343
<223> n=a, g, c or t

<400> 66
```
aaccacmycc ctcctcagaa gcccccagag cacaacgcct cacc atg gac tgg acc        56
                                                 Met Asp Trp Thr
tgg agg atc ctc ttt ttg gtg gca gca gcc aca ggt gtc cac tcc cag        104
Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly Val His Ser Gln
-15                 -10                 -5                  1
gtc cac ctt gtt cag tct ggg gct gar gtg aag aag cct ggg act ccg        152
Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Thr Pro
            5                   10                  15
gtg aac att tcc tgt aag gct ttt ggc tac acc ttc cct gcc ttt gct        200
Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe Pro Ala Phe Ala
        20                  25                  30
ata cat tgg gtt cgc cag gcc ccc gga caa agt ctt gag tgg atg gga        248
Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu Glu Trp Met Gly
    35                  40                  45
tgg gtc aac att ggc cat ggc aac aca aag tat tca cag aag ttt cag        296
Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser Gln Lys Phe Gln
50                  55                  60                  65
ggc aga ctc gcc atc tcc aga gac acg tcc gcg aac ata gtc tac nng        344
Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn Ile Val Tyr Xaa
                70                  75                  80
gaa ctg agc ggc ctg aga tct gaa gac acg gct gtc tat tac tgt gcg        392
Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            85                  90                  95
agg gat aat ctt ttc ttt ggc agt atg ggc ttt gac                        428
Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp
        100                 105
```

<210> 67
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..493

<221> sig_peptide
<222> 38..85
<223> Von Heijne matrix
score 10.6000003814697
seq TVLLLGLLSHCTG/SV

```
<400> 67
ctgggcctaa ggaagcagca ctggtggtgc ctcagcc atg gcc tgg acc gtt ctc      55
                                         Met Ala Trp Thr Val Leu
                                                 -15
ctc ctc ggc ctc ctc tct cac tgc aca ggc tct gtg acc tcc tat gtg      103
Leu Leu Gly Leu Leu Ser His Cys Thr Gly Ser Val Thr Ser Tyr Val
-10                 -5                  1               5
ctg act cag cct ccc tcg gtg tca gtg gcc cca gga aag acg gcc agc      151
Leu Thr Gln Pro Pro Ser Val Ser Val Ala Pro Gly Lys Thr Ala Ser
        10                  15                  20
att acc tgt ggg gga gac aac att gaa agt caa gtt gta cac tgg cac      199
Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser Gln Val Val His Trp His
        25                  30                  35
cag cag aag cca ggg cag gcc cct ata ttg gtc atc tat gat gat acc      247
Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Ile Tyr Asp Asp Thr
    40                  45                  50
gac cgg ccc tca ggg atc cct gac cga ttc tct ggc tcc aac tct ggg      295
Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser Asn Ser Gly
55                  60                  65                  70
cac acg gcc acc ctg acc atc agc agg gtc gaa gcc ggg gat gag gcc      343
His Thr Ala Thr Leu Thr Ile Ser Arg Val Glu Ala Gly Asp Glu Ala
                75                  80                  85
gac tat tat tgt cag gtg tgg gat aga agt agt ggt cag gga ata ttc      391
Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser Ser Gly Gln Gly Ile Phe
            90                  95                  100
ggc gga ggg acc aag ctg acc gtc cta cgt cag ccc aag gct gcc ccc      439
Gly Gly Gly Thr Lys Leu Thr Val Leu Arg Gln Pro Lys Ala Ala Pro
        105                 110                 115
tcg gtc act ctg ttc ccg ccc tcc tct gag gag ctt caa gcc aac aag      487
Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn Lys
    120                 125                 130
gcc aca                                                              493
Ala Thr
135

<210> 68
<211> 180
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..179

<221> sig_peptide
<222> 36..80
<223> Von Heijne matrix
      score 10.6000003814697
      seq LLFLLLFVCFSRQ/GL

<400> 68
tggcagttac tccagctccc aaatatagat attcc atg agg ttg ttg ttt ttg        53
                                       Met Arg Leu Leu Phe Leu
                                       -15                 -10
ttg ttg ttt gtt tgt ttt tcg aga cag ggt ctc gct ttg tct ctc agg      101
Leu Leu Phe Val Cys Phe Ser Arg Gln Gly Leu Ala Leu Ser Leu Arg
                -5                  1               5
ctg gaa tgc agt ggt atg atc atg gct tac tgc agc atc agc ctc cca      149
Leu Glu Cys Ser Gly Met Ile Met Ala Tyr Cys Ser Ile Ser Leu Pro
        10                  15                  20
ggc tca agc agt cct ctc acc tca gcc tcc a                            180
Gly Ser Ser Ser Pro Leu Thr Ser Ala Ser
    25                  30
```

```
<210> 69
<211> 259
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..259

<221> sig_peptide
<222> 38..94
<223> Von Heijne matrix
      score 10.6000003814697
      seq FLLLVSAPRWVLS/QV

<400> 69
atacttyctg agagtcctgg acctcctgca caagaac atg aaa cac ctg tgg ttc      55
                                         Met Lys His Leu Trp Phe
                                                             -15
ttc ctc ctc ctg gtg tca gct ccc aga tgg gtc ctg tct cag gtg cag      103
Phe Leu Leu Leu Val Ser Ala Pro Arg Trp Val Leu Ser Gln Val Gln
            -10                 -5                  1
cta cag gag tcg ggc cca gga ctg gtg aag cct tcg ggg agg ctg tcc      151
Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Arg Leu Ser
    5                   10                  15
ctc gcc tgc gat gtg gtg gaa ttg agt ccg ccg gcc ccc agg ggc ggg      199
Leu Ala Cys Asp Val Val Glu Leu Ser Pro Pro Ala Pro Arg Gly Gly
20                  25                  30                  35
tct gca gtg cat ctc aga aat ctt tca tca tgg gag ccc cac cta caa      247
Ser Ala Val His Leu Arg Asn Leu Ser Ser Trp Glu Pro His Leu Gln
                40                  45                  50
ccc gtc tcg ggg                                                      259
Pro Val Ser Gly
            55

<210> 70
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..177

<221> sig_peptide
<222> 7..102
<223> Von Heijne matrix
      score 10.6000003814697
      seq VVFLLLLVSTLSS/VV

<400> 70
cgtata atg act tac ttt cct ctg ggt aga tac cca gta atg gga ttg       48
       Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu
               -30                 -25                 -20
ctg gat caa atg gta gtt gtg ttt tta ctt ctt tta gtc tcc aca ctt      96
Leu Asp Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu
            -15                 -10                 -5
tct tcc gta gtg gtt tta cta gtt tgc att ccc acc agc agt gta aaa      144
Ser Ser Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys
        1               5                   10
ttg ttc cct ttt cac cat atc cac acc aac tgg g                        178
Leu Phe Pro Phe His His Ile His Thr Asn Trp
```

```
15                    20                    25

<210> 71
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..129

<221> sig_peptide
<222> 40..96
<223> Von Heijne matrix
      score 10.5
      seq WVLLVAMLRGLQC/QV

<400> 71
agctctggga gacgagccca gctctgcagt ggactcacc atg gag ttt ggg ctg        54
                                           Met Glu Phe Gly Leu
                                                           -15
agc tgg gtt ctc ctc gtt gct atg tta aga ggt ctc cag tgt caa gtg      102
Ser Trp Val Leu Leu Val Ala Met Leu Arg Gly Leu Gln Cys Gln Val
                -10                 -5                  1
cag ctg gtg gag tct ggg gga acc gcg gg                               131
Gln Leu Val Glu Ser Gly Gly Thr Ala
        5                   10

<210> 72
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..217

<221> sig_peptide
<222> 47..91
<223> Von Heijne matrix
      score 10.5
      seq LSLLILLLENVSG/FP

<400> 72
ttgcttacaa ttttaatgtg tctcattgct actggtcctc cttcta atg tat ctg        55
                                                   Met Tyr Leu
                                                   -15
agc ttg tta att cta ctt ttg gaa aat gtc agt ggc ttt ccc ttt cct      103
Ser Leu Leu Ile Leu Leu Leu Glu Asn Val Ser Gly Phe Pro Phe Pro
        -10                 -5                  1
cta att ttc cag ctt cat gca tcc cct ggc cat aag ata ctt cca gac      151
Leu Ile Phe Gln Leu His Ala Ser Pro Gly His Lys Ile Leu Pro Asp
5                   10                  15                  20
tgt atg ata tat tct atc act gtc agc ctt atg ttc cct gtg gtt gac      199
Cys Met Ile Tyr Ser Ile Thr Val Ser Leu Met Phe Pro Val Val Asp
                25                  30                  35
tat ata agc acg caa ggg                                              217
Tyr Ile Ser Thr Gln Gly
            40

<210> 73
<211> 192
<212> DNA
```

```
<213> Homo sapiens

<220>
<221> CDS
<222> 100..192

<221> sig_peptide
<222> 100..183
<223> Von Heijne matrix
      score 10.5
      seq SLWFXCLLFLLFA/WP

<400> 73
agttaaaatc atgtactgtg atcagtcacc tggtttttga tttttatgaa ggttttttt     60
gtttagatag ttgttaaatt tggtgttcct gtggggagg atg atg aga gcc ttc      114
                                           Met Met Arg Ala Phe
                                                           -25
tat ttg gct atc ttg ttc tgc ctc tct ctc tcc tta tgg ttc tdk tgt     162
Tyr Leu Ala Ile Leu Phe Cys Leu Ser Leu Ser Leu Trp Phe Xaa Cys
            -20                 -15                 -10
tta ctt ttt ttg ctt ttt gct tgg cct ggg                             192
Leu Leu Phe Leu Leu Phe Ala Trp Pro Gly
        -5                  1

<210> 74
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..328

<221> sig_peptide
<222> 23..82
<223> Von Heijne matrix
      score 10.3999996185303
      seq FLTLLLHCTGSLA/QL

<400> 74
agagctctgg ggagtctgca cc atg gct tgg acc cca ctc ctc ttc ctc acc     52
                         Met Ala Trp Thr Pro Leu Leu Phe Leu Thr
                         -20                 -15
ctc ctc ctc cac tgc aca ggg tct ctc gcc cag ctt gtg ctg act caa     100
Leu Leu Leu His Cys Thr Gly Ser Leu Ala Gln Leu Val Leu Thr Gln
-10                 -5                  1               5
tcg ccc tct gcc tct gcc tcc ctg gga gcc tcg gtc aag ctc acc tgc     148
Ser Pro Ser Ala Ser Ala Ser Leu Gly Ala Ser Val Lys Leu Thr Cys
            10                  15                  20
act ctg agc agt ggg cac agc aac tac ggc atc gct tgg tat cag cag     196
Thr Leu Ser Ser Gly His Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln
        25                  30                  35
cag cca gag aag ggc cct cga ttc ttg atg aaa gtt aac agt gat ggc     244
Gln Pro Glu Lys Gly Pro Arg Phe Leu Met Lys Val Asn Ser Asp Gly
    40                  45                  50
agc cac atg aag gcg gac ggg atc cct gat cgc ttc tca ggc tcc agc     292
Ser His Met Lys Ala Asp Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser
55                  60                  65                  70
tct ggg gct gag cgc tac ctc tcc atc tcc agc ctc a                   329
Ser Gly Ala Glu Arg Tyr Leu Ser Ile Ser Ser Leu
                75                  80

<210> 75
```

```
<211> 314
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 259..312

<221> sig_peptide
<222> 259..300
<223> Von Heijne matrix
      score 10.3999996185303
      seq PLALFFLLSVALA/IQ

<400> 75
tagggtgaga gatggggatc tagttttatt cttctgcata tggatatcca gttttcccag      60
taacatttat tgaagagact ggcctttccc caatgagtgt tcttggcacc tttgtcaaaa     120
gtcagttggc cgtagatatg tggattaatt tctgtgttcc ctgttttgtt ccattggcct     180
atgtgtctgt ttttatgaca gtaccaggtt gttttggtta ctacagcttt gtagtttact     240
ttgaggtctg ttagtgtg atg cct cta gct ttg ttc ttt ttg ctc agt gtt       291
                    Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val
                                    -10                 -5
gct ttg gct att cag ggt cag gg                                        314
Ala Leu Ala Ile Gln Gly Gln
            1

<210> 76
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..445

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
      score 10.3999996185303
      seq XFCLLAVAPGAHS/QV

<400> 76
atcatccaac aaccacatcc cttctctaca gaagcctctg agaggaaagt tcttcacc        58
atg gac tgg acc tgg agg rwc ttc tgc ttg ctg gct gta gct cca ggt      106
Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly
                -15                 -10                 -5
gct cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag      154
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            1               5                   10
cct ggg gcc tca gtg aag gtt tcc tgc aag gca tct gga tac acc ttc      202
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25
acc agc cac tat atg cac tgg gtg cga cag gcc cct gga caa ggg ctt      250
Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45
gag tgg atg gga ata atc tac cct gat agt gat acc act aag tac cba      298
Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa
                50                  55                  60
cag aac ttc cag ggc aga gtc acc atg act agg gac acg tcc acg agc      346
Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
            65                  70                  75
aca gtc tac atg gag ctg agc agc ctg aca tct gac gac acg gcc gtg      394
Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
```

```
        80                  85                  90
tat tat tgt gct aga gag gcg tat agt ggg agc tac cgc ttt gac tac       442
Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr
    95                  100                 105
tgg gg                                                                447
Trp
110
```

<210> 77
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..387

<221> sig_peptide
<222> 16..93
<223> Von Heijne matrix
      score 10.3000001907349
      seq LLLLVAAPRWVLS/QL

<400> 77

```
agctttctga gagtc atg gat ctc atg tgc aag aaa atg aga cac ctg tgg      51
                 Met Asp Leu Met Cys Lys Lys Met Arg His Leu Trp
                     -25                 -20                 -15
ttc ctc ctc ctg ctg gtg gcg gct ccc aga tgg gtc ctg tcc cag ctg       99
Phe Leu Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu
                -10                  -5                   1
cag ctt cag gag tcg ggc cca gga ctg gtg aag gct tcg gag acc ctg      147
Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Ala Ser Glu Thr Leu
        5                   10                  15
tcc ctc gcc tgc agt gtc tct ggt gac tcc atc agc agt ggt aat tat      195
Ser Leu Ala Cys Ser Val Ser Gly Asp Ser Ile Ser Ser Gly Asn Tyr
    20                  25                  30
tac tgg ggc tgg atc cgg cag ccc cca ggg aag gga ctg cag tgg ctt      243
Tyr Trp Gly Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Leu
35                  40                  45                  50
ggg agt ctt tgg aat cgt ggc ggt ccg caa tac aay hcc tcc ctc aag      291
Gly Ser Leu Trp Asn Arg Gly Gly Pro Gln Tyr Asn Xaa Ser Leu Lys
                55                  60                  65
aat cga gtc acc gtg tcc gta gac acg tcc acg aat cat ttc ttt ctg      339
Asn Arg Val Thr Val Ser Val Asp Thr Ser Thr Asn His Phe Phe Leu
            70                  75                  80
aga ctg aat tcc gtg aay vgh gga cac ggc aat tta tta ctg tgc gcg a    388
Arg Leu Asn Ser Val Asn Xaa Gly His Gly Asn Leu Leu Leu Cys Ala
        85                  90                  95
```

<210> 78
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..120

<221> sig_peptide
<222> 25..72
<223> Von Heijne matrix
      score 10.1999998092651
      seq XLXLSVLLGXXXX/KX

<400> 78
ctgaccttcc ctcccggcag cagc atg cgg grg tkg ctg kys ttg agt gtc 51
Met Arg Xaa Xaa Leu Xaa Leu Ser Val
-15 -10
ctg ttr ggg sck rts tbt kgc aag gmg gac ttt gtg ggg cat cag gtg 99
Leu Leu Gly Xaa Xaa Xaa Xaa Lys Xaa Asp Phe Val Gly His Gln Val
-5 1 5
ctc cga atc tct gta gcc gat g 121
Leu Arg Ile Ser Val Ala Asp
10 15

<210> 79
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..149

<221> sig_peptide
<222> 36..143
<223> Von Heijne matrix
score 10.1999998092651
seq FLLFFCFVFCLRG/QG

<400> 79
tccgagcagc cagctctgtg taagcacatc cagga atg gca gaa tcc agg gag 53
Met Ala Glu Ser Arg Glu
-35
gaa ggt gaa agc tgt gtt gag agc cac tgt gtg ctc ttt ttc acc ctg 101
Glu Gly Glu Ser Cys Val Glu Ser His Cys Val Leu Phe Phe Thr Leu
-30 -25 -20 -15
ttt ttt ttg ttg ttt ttt tgt ttt gtt ttt tgt ttg agg gga cag ggg 149
Phe Phe Leu Leu Phe Phe Cys Phe Val Phe Cys Leu Arg Gly Gln Gly
-10 -5 1

<210> 80
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..409

<221> sig_peptide
<222> 80..136
<223> Von Heijne matrix
score 10.1000003814697
seq WLFLVAFLKGVQC/EV

<400> 80
agctctgaga gaggagccca gccctgggat tttcaggtgt tttcatgtgg tgatcaggac 60
tgaacagaga gaactcacc atg gag ctt ggg ctg agc tgg ctt ttt ctt gtg 112
Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val
-15 -10
gct ttt tta aaa ggt gtc cag tgt gag gtg cag ttg ttg gag tct ggg 160
Ala Phe Leu Lys Gly Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly
-5 1 5
gga ggc ttg gtc cag cct ggg ggg tcc ctg aga ctc tca tgt gca gcc 208
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala

```
    10                  15                  20
tcc gga ttc acc ttt agc tcc tat gcc atg ctc tgg gtc cgc cag gct      256
Ser Gly Phe Thr Phe Ser Ser Tyr Ala Met Leu Trp Val Arg Gln Ala
25                  30                  35                  40
cca ggt aag ggg ctg gag tgg gtc tca ggt att agt gct ggt gct gat      304
Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Ser Ala Gly Ala Asp
                45                  50                  55
gat aca tat gat gca gac tcc gtg aag ggc cgg ttc acc att tcc aga      352
Asp Thr Tyr Asp Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
            60                  65                  70
gac gat tcc aag aaa atc cta tat cta caa atg aac agc ctg aga gcc      400
Asp Asp Ser Lys Lys Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala
        75                  80                  85
gag gac agg c                                                        410
Glu Asp Arg
    90
```

<210> 81
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..217

<221> sig_peptide
<222> 38..106
<223> Von Heijne matrix
      score 10.1000003814697
      seq VLGLLVLFLTCYA/DD

<400> 81

```
gaacaattta tctgcacgaa taccccgtgc taccaga atg gct gtc tca gta ctt      55
                                         Met Ala Val Ser Val Leu
                                                         -20
cgc ctg aca gtt gtc ctg gga ctg ctt gtc tta ttc ctg acc tgc tat      103
Arg Leu Thr Val Val Leu Gly Leu Leu Val Leu Phe Leu Thr Cys Tyr
        -15                 -10                 -5
gca gac gac aaa cca gac aag cca gac gac aag cca gac gac tcg ggc      151
Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp Lys Pro Asp Asp Ser Gly
    1               5                   10                  15
aaa gac cca aag cca gac ttc ccc aaa ttc cta agc ctc ctg ggc aca      199
Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe Leu Ser Leu Leu Gly Thr
                20                  25                  30
gag atc att gag aat gcg gg                                           219
Glu Ile Ile Glu Asn Ala
            35
```

<210> 82
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..398

<221> sig_peptide
<222> 81..152
<223> Von Heijne matrix
      score 10
      seq LLLLQALPSPLSA/RA

```
<400> 82
gaagaagagg gtagaggagg agagggagga ggaggaggga ggtggcggcg ccgtggcgga      60
ggagcaggag caggaggggg atg gag agg aga agg ctc ctg ggt ggc atg gcg    113
                      Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala
                                      -20                 -15
ctc ctg ctc ctc cag gcg ctg ccc agc ccc ttg tca gcc agg gct gaa      161
Leu Leu Leu Leu Gln Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu
            -10                 -5                   1
ccc ccg cag gat aag gaa gcc tgt gtg ggt acc aac aat caa agc tac      209
Pro Pro Gln Asp Lys Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr
    5                   10                  15
atc tgt gac aca gga cac tgc tgt gga cag tct cag tgc tgy aac tac      257
Ile Cys Asp Thr Gly His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr
20                  25                  30                  35
tac tat gaa ctc tgg tgg ttc tgg ctg gtg tgg acc atc atc atc atc      305
Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile
                40                  45                  50
ctg agc tgc tgc tgt gtt tgc cac cac cgc cga gcc aag cac cgc ctt      353
Leu Ser Cys Cys Cys Val Cys His His Arg Arg Ala Lys His Arg Leu
            55                  60                  65
cag gcc cag cag cgg caa cat gaa atc aac ctg atc gct tac cga g        399
Gln Ala Gln Gln Arg Gln His Glu Ile Asn Leu Ile Ala Tyr Arg
        70                  75                  80

<210> 83
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 288..398

<221> sig_peptide
<222> 288..368
<223> Von Heijne matrix
      score 9.89999961853027
      seq LCLLLFSLSLFLC/HE

<400> 83
cactctacct ctgacagcat gtatattgca ccagtagcta acaaaaactg gtctagtcaa      60
accaaatggg cacaaaagaa ccaggatacc aaaagttaag ctcatacagc tgcaaaccat     120
atcacttctt ggtaacaatg caagacctca taaacctaaa gaagagaaag aaaagaaaac     180
ttttgttact ttvctttttt gcttgtcact tatatacagg ctatgtgaga atataatttg     240
taggtataac acattaagaa aaagttatct tcattggata gaattgga atg gtg gtc      296
                                                     Met Val Val
                                                             -25
gct gat agg aat agg gcg tcc tct agc tct tat ctc tgt ctc tta ctc      344
Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys Leu Leu Leu
                -20                 -15                 -10
ttt tct ctt tct ctt ttt ctc tgt cat gag act gtg tgt gac agg gcc      392
Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys Asp Arg Ala
            -5                   1               5
acc tgt                                                              398
Thr Cys
    10

<210> 84
<211> 488
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 62..487

<221> sig_peptide
<222> 62..118
<223> Von Heijne matrix
      score 9.89999961853027
      seq FLFVVAAATGVQS/QV

<221> misc_feature
<222> 210,293
<223> n=a, g, c or t


<400> 84
agcatcacat aacaaccaca ttcctcctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt     109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                  -15                 -10                  -5
gtc cag tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag       157
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            1               5                  10
cct ggg tcc tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc       205
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
    15                  20                  25
agc anc tat gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt       253
Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45
gag tgg atg gga ggg atc atc cct atc ttt ggt aca gca nac tac gca       301
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala
                50                  55                  60
cag aag ttc cag ggc aga gtc acs att acc gcg gac gra tcc acg asc       349
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Xaa Ser Thr Xaa
            65                  70                  75
aca rcc tac atg gag ctg agc agc ctg aga tct gag gac acg gcc stg       397
Thr Xaa Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Xaa
        80                  85                  90
tat tac tgt gcg aga ggt caa gcc ccc ggt agg gta gta gta cca ctt       445
Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu
    95                  100                 105
ttc ctc tgg ggc cag gga acc tgg tca ccg tct cct cag cct c             488
Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro
110                 115                 120

<210> 85
<211> 290
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..290

<221> sig_peptide
<222> 30..164
<223> Von Heijne matrix
      score 9.89999961853027
      seq LLSLLSFLDETSG/LS

<400> 85
cttcttttc ttcgtaactt catggcaac atg acc tac agt tac tca ttt ttc         53
                               Met Thr Tyr Ser Tyr Ser Phe Phe
```

```
                                        -45                  -40
agg cct gag ttg atc gtt aat cat ctt aat tat gtt cat tct gaa gcc      101
Arg Pro Glu Leu Ile Val Asn His Leu Asn Tyr Val His Ser Glu Ala
        -35                 -30                 -25
aac agg aga acc aag acc aaa act tta ttg tct ctg ctt tca ttt ctt      149
Asn Arg Arg Thr Lys Thr Lys Thr Leu Leu Ser Leu Leu Ser Phe Leu
    -20                 -15                 -10
gat gaa acc tct gga cta agc aca cat ctt cct tgt tta tct ctc tca      197
Asp Glu Thr Ser Gly Leu Ser Thr His Leu Pro Cys Leu Ser Leu Ser
-5                  1               5                   10
aag gag tgt gga gtg ctt cat ctg gac atc cac ggg aag aag gaa gac      245
Lys Glu Cys Gly Val Leu His Leu Asp Ile His Gly Lys Lys Glu Asp
            15                  20                  25
atg aga gat gag gtc ttg ctg gcc ttg aac tyc tgc acc cac agg          290
Met Arg Asp Glu Val Leu Leu Ala Leu Asn Xaa Cys Thr His Arg
        30                  35                  40
```

<210> 86
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..336

<221> sig_peptide
<222> 100..156
<223> Von Heijne matrix
score 9.89999961853027
seq ILFLVFLLAGLRS/KA

<400> 86

```
ccagatctgt tctgcaacat tcaccgttct ctgcatccag ctctgcttat ctgctgttac     60
cttggacacc agagcagcta taggtatctg ccagragcw atg aaa tca ttc agc       114
                                           Met Lys Ser Phe Ser
                                                           -15
cgg atc ctc ttc ctc gtc ttc ctc ctc gcc ggc ctg agg tcc aag gcc      162
Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly Leu Arg Ser Lys Ala
                -10                 -5                  1
gct ccc tca gcc cct ctg cct ttg ggc tgt ggc ttt ccg gac atg gcc      210
Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly Phe Pro Asp Met Ala
        5                   10                  15
cac ccc tct gag act tcc cct ctg aag ggt gct tct gaa aat tcc aaa      258
His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala Ser Glu Asn Ser Lys
    20                  25                  30
cga gat cgc ctt aac cca gaa ttt cct ggg act cct tac cct gag cct      306
Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr Pro Tyr Pro Glu Pro
35                  40                  45                  50
tcc aag cta cct cat acg gtt tcc ctg gaa                              336
Ser Lys Leu Pro His Thr Val Ser Leu Glu
                55                  60
```

<210> 87
<211> 262
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 108..260

<221> sig_peptide

<222> 108..230
<223> Von Heijne matrix
score 9.89999961853027
seq SLCHLGWSAVVQS/QP

<400> 87

```
taggagtgga gtgactgggt gatatgataa ctctatgttt aactttttaa ggaactgcta     60
gacttttctg aagtgactat gccattttac attaacacca ggagtgt atg agg gtg      116
                                                    Met Arg Val
                                                        -40
ccg att ttt cca cat cct cac caa ctc tcg tta tta ttc atc cat tta      164
Pro Ile Phe Pro His Pro His Gln Leu Ser Leu Leu Phe Ile His Leu
            -35                 -30                 -25
ttt att tat tta ttt aga gaa agg gtc tct ctc tgt cac cta ggc tgg      212
Phe Ile Tyr Leu Phe Arg Glu Arg Val Ser Leu Cys His Leu Gly Trp
        -20                 -15                 -10
agt gca gtg gta caa tca cag cca act aca acc ttg acc tcc cgc gct      260
Ser Ala Val Val Gln Ser Gln Pro Thr Thr Thr Leu Thr Ser Arg Ala
    -5                  1               5                   10
am                                                                   262
```

<210> 88
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..149

<221> sig_peptide
<222> 18..128
<223> Von Heijne matrix
score 9.89999961853027
seq FLFVLFCFGGSRA/LL

<400> 88

```
ttcggagctt gaccagc atg tgg aag gag agc tct cat ggc tgc aat aac        50
                   Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn
                           -35                 -30
tta ggg agt tcc tac ctg gat gac act ggg gta gga agt ttt ctg ttt       98
Leu Gly Ser Ser Tyr Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe
    -25                 -20                 -15
gtt ttg ttc tgt ttc gga ggg tcc cgt gca ctt ctc ttg cct gga tct      146
Val Leu Phe Cys Phe Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser
-10                 -5                  1               5
ggg                                                                  149
Gly
```

<210> 89
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 236..313

<221> sig_peptide
<222> 236..283
<223> Von Heijne matrix
score 9.69999980926514
seq FLCLLFYLIVSCG/AV

```
<400> 89
gtaaaagaca aataacttgt atggtttgca aaatgatctg aatatgtgct tttataacat      60
tcagaataca cccaaaagta aactttaggt ttaatgtaca gtatgtttc tatgtaattg      120
ttttgaataa gtaatamcat ybtacatggc ttaaaactga aaaacgtatt cctgttactt      180
cttgatgctt ttgagaaatg aataatgttt tctccctttt aaatggtagt acagc atg      238
                                                                 Met
cac act ttt ctg tgc ttg ctt ttt tat ctc ata gta tct tgt gga gct      286
His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly Ala
-15                 -10                 -5                  1
gtt ttc tta aca gtc cct tct ccc caa gg                               315
Val Phe Leu Thr Val Pro Ser Pro Gln
            5                   10

<210> 90
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..179

<221> sig_peptide
<222> 24..140
<223> Von Heijne matrix
      score 9.69999980926514
      seq SIILXLXFPGILG/QA

<221> misc_feature
<222> 57
<223> n=a, g, c or t


<400> 90
agmrctctgg ggcagtctgc acc atg gcc tgg cac ccc act cct cct cct ctt     53
                          Met Ala Trp His Pro Thr Pro Pro Pro Leu
                                          -35                 -30
csb ncw cct cct cca ctg mac agg gwc tcy ctc cca gcc tgt gct gac      101
Xaa Xaa Pro Pro Pro Leu Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp
                -25                 -20                 -15
tca atc atc ctc tgm ctc tgm ttc cct ggg atc ctc ggw caa gct cac      149
Ser Ile Ile Leu Xaa Leu Xaa Phe Pro Gly Ile Leu Gly Gln Ala His
            -10                 -5                  1
ctg mac tct gag cag tgg aca cag tac cta                              179
Leu Xaa Ser Glu Gln Trp Thr Gln Tyr Leu
    5                   10

<210> 91
<211> 423
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 311..421

<221> sig_peptide
<222> 311..373
<223> Von Heijne matrix
      score 9.69999980926514
      seq LHLLILLSGTCFT/WI
```

```
<400> 91
gactctatag srcaaatggt taagaacata tacttgggag tcagttgatc tgggttcaaa      60
ttctagctgt gctactttct acctatgctg tattggacaa atgatactgt gtatctgttt     120
cttcaaccgt aagttgggta tattaatatc cttacctcaa aaggtcatga tgattaagtg     180
agtbaatgca tgtaaaatgc cttctgtgcc gggcagtcag aaaccactca ataaatattg     240
attattctca ccaaagatgt gcttcctgac ctcaaaagcc tgtcagccta atataaagac     300
agtgtgacaa atg cca atc ctg cct cag gac atc ttg cac ttg ctg atc        349
           Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile
               -20                 -15                 -10
ctt ctg tct gga aca tgc ttc act tgg att ctt ttg tgg ctt cca ctc       397
Leu Leu Ser Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu
            -5                  1               5
tcc cct ctg ttg ggc ctg aaa tgc ta                                    423
Ser Pro Leu Leu Gly Leu Lys Cys
    10                  15

<210> 92
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..316

<221> sig_peptide
<222> 62..121
<223> Von Heijne matrix
      score 9.60000038146973
      seq LLALLLCGRPGRG/QT

<221> misc_feature
<222> 264,266
<223> n=a, g, c or t


<400> 92
accgcagctc cagagccctg cgggaggact cagagtcagg gacacagcag cgtccggcga      60
g atg aag gcg ctc ggg gct gtc ctg ctt gcb ctc ttg ctg tgc ggg cgg     109
  Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
  -20                 -15                 -10                 -5
cca ggg aga ggg cag aca cag cag gag gaa gag gaa gag gac gag gac       157
Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Glu Asp Glu Asp
                1               5                   10
cac ggg cca gat gac tac gac gag gaa gat gag gat gag gtt gaa gag       205
His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
        15                  20                  25
gag gag acc aac agg ctc cct ggt ggc agg agc aga gtg ctg ctg cgg       253
Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
    30                  35                  40
tgc tac acc tnk nag tcc ctg ccc agg gac gag cgc tgc aac ctg acg       301
Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr
45                  50                  55                  60
cag aac tgc tca cat                                                   316
Gln Asn Cys Ser His
                65

<210> 93
<211> 508
<212> DNA
<213> Homo sapiens

<220>
```

```
<221> CDS
<222> 245..508

<221> sig_peptide
<222> 245..289
<223> Von Heijne matrix
      score 9.60000038146973
      seq EYVLLLFLALCSA/KP

<400> 93
agtactaaca tggactaatc tgtgggagca gtttattcca gtatcaccca gggtgcagcc     60
acaccaggac tgtgttgaag ggtgtttttt ttcttttaaa tgtaatacct cctcatcttt    120
tcttcttaca cagtgtctga gaacatttac attatagata agtagtacat ggtggataac    180
ttctactttt aggaggacta ctctcttctg acagtcctag actggtcttc tacactaaga    240
cacc atg aag gag tat gtg ctc cta tta ttc ctg gct ttg tgc tct gcc     289
     Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala
     -15                 -10                 -5
aaa ccc ttc ttt agc cct tca cac atc gca ctg aag aat atg atg ctg      337
Lys Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu
1               5                   10                  15
aag gat atg gaa gac aca gat gat gat gat gat gat gat gat gat gat      385
Lys Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp
            20                  25                  30
gat gat gat gag gac aac tct ctt ttt cca aca aga gag cca aga agc      433
Asp Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser
        35                  40                  45
cat ttt ttt cca ttt gat ctg ttt cca atg tgt cca ttt gga tgt cag      481
His Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln
    50                  55                  60
tgc tat tca cga gtt gta cat tgc tca                                  508
Cys Tyr Ser Arg Val Val His Cys Ser
65                  70

<210> 94
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..320

<221> sig_peptide
<222> 36..92
<223> Von Heijne matrix
      score 9.60000038146973
      seq FLLLVAAPRWAMS/QV

<400> 94
actttctgag aggcctggac ctcctgcaca agaac atg aaa cac ctg tgg ttc        53
                                       Met Lys His Leu Trp Phe
                                                       -15
ttc ctc ctc ctg gtg gca gct ccc aga tgg gcc atg tct cag gtg caa      101
Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Met Ser Gln Val Gln
            -10                 -5                  1
ctg cag gaa tcg ggc ccg aga ctg gtg aaa cct tcg ggg acc ctg tcc      149
Leu Gln Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gly Thr Leu Ser
    5                   10                  15
ctc acc tgc agt gtc tct ggt ggc tcc atg gcc act agt gac tgg tgg      197
Leu Thr Cys Ser Val Ser Gly Gly Ser Met Ala Thr Ser Asp Trp Trp
20                  25                  30                  35
agt tgg ttt cga cag acm ccg gag aag ggt ctg gag tgg att ggg gaa      245
Ser Trp Phe Arg Gln Thr Pro Glu Lys Gly Leu Glu Trp Ile Gly Glu
```

```
                40                  45                  50
atc ttt cag act ggg ccc acc aat tac aac ccg tcc ctc aag agc cgc      293
Ile Phe Gln Thr Gly Pro Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg
            55                  60                  65
gtc tcc atg tca gtg gac atg tcc aag a                                321
Val Ser Met Ser Val Asp Met Ser Lys
        70                  75
```

<210> 95
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..401

<221> sig_peptide
<222> 15..92
<223> Von Heijne matrix
score 9.5
seq FLLLVAAPRWALS/QL

<400> 95

```
gctttctgag agtc atg gat ctc acg tgc aag aaa atg aag cac ctg tgg       50
                Met Asp Leu Thr Cys Lys Lys Met Lys His Leu Trp
                    -25                 -20                 -15
ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg gcc ctg tcc caa ctg       98
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Ala Leu Ser Gln Leu
                -10                 -5                  1
cag ctg cag gag tcg ggc cca gga ctg gtg aag cct tcg gag acc ctg      146
Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu
        5                   10                  15
tcc ctc acg tgc act gtc tct ggt gaa tcc atc acc act aat tca ttc      194
Ser Leu Thr Cys Thr Val Ser Gly Glu Ser Ile Thr Thr Asn Ser Phe
    20                  25                  30
tgc tgg gcc tgg atc cgc cag ccc ccg ggg aag ggg ctg gaa tgg ctt      242
Cys Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35                  40                  45                  50
ggg act gta tgt tat ggt ggg acc acc tac krc aac kcg tcc ctg aag      290
Gly Thr Val Cys Tyr Gly Gly Thr Thr Tyr Xaa Asn Xaa Ser Leu Lys
                55                  60                  65
agt cga gtc aag tta tcg ttg gac acg tcc acg aat cag ttc tcc ctg      338
Ser Arg Val Lys Leu Ser Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu
            70                  75                  80
aag gtc acc tct atg acc gcc gga gac gcg gct gtc cat tac tgt gcg      386
Lys Val Thr Ser Met Thr Ala Gly Asp Ala Ala Val His Tyr Cys Ala
        85                  90                  95
ggg ctg cgt gtt agt g                                                402
Gly Leu Arg Val Ser
    100
```

<210> 96
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 118..315

<221> sig_peptide
<222> 118..306

```
<223> Von Heijne matrix
      score 9.5
      seq VLLFLILLYMSWS/AS

<400> 96
agagacacac ttggacgrtt cctgcagraa tcagtgaggc agtctcctcc caggggcttg      60
gsgcctggct cgaggcgagg ctgccggccc ggacgctgac tgcccagtgc cacagac        117
atg gcc aac ggg acc aac gcc tct gcc cca tac tac agc tat gaa tac       165
Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr
            -60                 -55                 -50
tac ctg gac tat ctg gac ctc att ccc gtg gac gag aag aag ctg aaa       213
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys
        -45                 -40                 -35
gcc cac aaa cat tcc atc gtg atc gca ttc tgg gtg agc ctg gct gcc       261
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala
    -30                 -25                 -20
ttc gtg gtg ctg ctc ttc ctc atc ttg ctc tac atg tcc tgg tcc gcs       309
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala
-15                 -10                 -5                  1
tcc ccg                                                               315
Ser Pro

<210> 97
<211> 460
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..460

<221> sig_peptide
<222> 62..118
<223> Von Heijne matrix
      score 9.39999961853027
      seq FLFVVAAATGVQS/QX

<400> 97
agcatcacat aacaaccasa ttcctcctct aaagaagccc ctgggagcac agctcatcac      60
c atg gac tgg acc tgg agg ttc ctc ttt gtg gtg gca gca gct aca ggt     109
  Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                  -15                 -10                 -5
gtc cag tcm cag gks cas ctg gwg cag tct ggg gct gag gtg aag aag       157
Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
            1               5                   10
cct ggg tcc tcg gtg aaa gtc tcc tgc arg gcy tct gga ggc atc ytc       205
Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
    15                  20                  25
agc asc tat agc ttc aac tgg gtg cgm cag gcc cct gga cag ggg ttt       253
Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
30                  35                  40                  45
gag tgg ttg gga agg atc atc ccc atc ctc ggt ata aca aac tac gca       301
Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
                50                  55                  60
gag aag ttt cgg ggc aga ctc acg atc acc gtg gac aaa tcc acg cgt       349
Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg
            65                  70                  75
gtt gtt tac atg gag cag agc agt ctg aca tct gcg gac acg gcc gta       397
Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val
        80                  85                  90
tat tat tgt gcg aaa ccg act atg act tcg gaa cta cgg gtc tac tat       445
Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr
    95                  100                 105
```

```
cag wct aca cta tgg                                                    460
Gln Xaa Thr Leu Trp
110

<210> 98
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 140..229

<221> sig_peptide
<222> 140..205
<223> Von Heijne matrix
      score 9.39999961853027
      seq LLLLSAFTSQTVS/GQ

<400> 98
aacagaacaa tatcaaatag ctaacttcac ccccaaccac agtccttgct gttggcattt      60
actcaactag tctttaattc ctgttttgac aaactttata aggtgctaca agacagatga     120
tttttcacca tctaccata atg tgg aac aga tat ttt gtc ttc tat ctc ctg      172
                     Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu
                             -20                 -15
ctt ttg tca gcg ttt acg agt caa aca gta tcc gga caa aga aag aaa       220
Leu Leu Ser Ala Phe Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys
    -10                 -5                  1               5
gga ccc cgg g                                                         230
Gly Pro Arg

<210> 99
<211> 467
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..465

<221> sig_peptide
<222> 40..96
<223> Von Heijne matrix
      score 9.39999961853027
      seq FLLLVAAPRWVLS/QL

<400> 99
aaatactttc tgagagccct ggacctcctg tgcaagaac atg aaa cac ctg ggg         54
                                           Met Lys His Leu Gly
                                                           -15
ttc ttc ctc ctg ctg gtg gca gct ccc aga tgg gtc ctg tcc cag ctg       102
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu
                -10                 -5                  1
cag ctc cag gag tcc ggc tca gga ctg gag aag cct tca cag acc ctg       150
Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys Pro Ser Gln Thr Leu
        5                   10                  15
tcc ctc acc tgc tct gtc tct ggt ggc tcc atc agt agt gat gat ttg       198
Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile Ser Ser Asp Asp Leu
    20                  25                  30
tcg tgg agc tgg atc cga cag ccg cca ggg aag ggc ctg gag tgg att       246
Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile
35                  40                  45                  50
ggc tac att tat caa aat gag agg acc ctc tac aac ccg tcc ctc aag       294
```

```
Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr Asn Pro Ser Leu Lys
                55                  60                  65
agt cga gcc gcc att tca gtg gac agg tcc aag aac cag ttc tcc ctg      342
Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys Asn Gln Phe Ser Leu
            70                  75                  80
aaa ctg acc tct gtg acc gcc gcg gac atg gcc gta tat tac tgt gcc      390
Lys Leu Thr Ser Val Thr Ala Ala Asp Met Ala Val Tyr Tyr Cys Ala
        85                  90                  95
acc agt gtc atg awt tcc ttt ggg ggc gtt ctc gtc cct aat ctg ttt      438
Thr Ser Val Met Xaa Ser Phe Gly Gly Val Leu Val Pro Asn Leu Phe
    100                 105                 110
ttg act act ggg gcc agg gaa tct cgt ca                               467
Leu Thr Thr Gly Ala Arg Glu Ser Arg
115                 120
```

<210> 100
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..503

<221> sig_peptide
<222> 39..95
<223> Von Heijne matrix
score 9.30000019073486
seq FLLLVAGPRWVLS/QV

<400> 100

```
aatactttct gagagtcctg gacctcctgt gcaagaac atg aaa cac ctg tgg ttc     56
                                          Met Lys His Leu Trp Phe
                                                          -15
ttc ctc ctg ctg gtg gca ggt ccc aga tgg gtc ctg tcc cag gtg cag      104
Phe Leu Leu Leu Val Ala Gly Pro Arg Trp Val Leu Ser Gln Val Gln
            -10                 -5                  1
ctg sdk gag tcg ggc cca aga ctg gtg aag cct tca cag acc ctg tcc      152
Leu Xaa Glu Ser Gly Pro Arg Leu Val Lys Pro Ser Gln Thr Leu Ser
    5                   10                  15
ctc acc tgc act gta tct ggg gcc tcc gtc agc agt cgt ggg tac tat      200
Leu Thr Cys Thr Val Ser Gly Ala Ser Val Ser Ser Arg Gly Tyr Tyr
20                  25                  30                  35
tgg acc tgg atc cgc cag ctc cca ggg aag ggc ctg gag tgg att ggc      248
Trp Thr Trp Ile Arg Gln Leu Pro Gly Lys Gly Leu Glu Trp Ile Gly
                40                  45                  50
tac atc tgk tac act ggg agc acc ttc tac aac ccg tcc ctc aag agt      296
Tyr Ile Xaa Tyr Thr Gly Ser Thr Phe Tyr Asn Pro Ser Leu Lys Ser
            55                  60                  65
cga tta acc ata tca ata gac acg tct aag aat cag ttc tcc ctg aac      344
Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
        70                  75                  80
ctg agg tct gtg act acc gcg gac acg gcc gtc tat tac tgt gcg aga      392
Leu Arg Ser Val Thr Thr Ala Asp Thr Ala Val Tyr Tyr Cys Ala Arg
    85                  90                  95
gac cat ttc gat ctt cta ttc gac ccc tgg ggc cag gga acc ctg gtc      440
Asp His Phe Asp Leu Leu Phe Asp Pro Trp Gly Gln Gly Thr Leu Val
100                 105                 110                 115
acc gtc tcc tct gcm tcc acc aag ggc cca tcg gtc ttc ccc ctg gca      488
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
                120                 125                 130
scc tcc tcc aag agc a                                                504
Xaa Ser Ser Lys Ser
```

135

<210> 101
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..336

<221> sig_peptide
<222> 148..270
<223> Von Heijne matrix
score 9.30000019073486
seq VLXLFCFVFEAES/RS

<400> 101
```
agagctcgcg gtggactccg acccggcgca acatggccgc agcctcgcct ctgcgcgact    60
gccaggcctg gaaggatgcg aggctcccgc tctccaccac aagcaacgaa gcctgcaagc   120
tgttcgatgc cacgctgacc cagggta atg gcc tgc cga gag agg ccg cgg ccc   174
                              Met Ala Cys Arg Glu Arg Pro Arg Pro
                                  -40                 -35
ctt ctg tgg agg tct agg gga agg ttt ttt aat tgg gga aag ctg ttt     222
Leu Leu Trp Arg Ser Arg Gly Arg Phe Phe Asn Trp Gly Lys Leu Phe
        -30                 -25                 -20
ttt tgt ttt gtt ttg mtt ttg ttt tgt ttt gtt ttt gag gcg gag tct     270
Phe Cys Phe Val Leu Xaa Leu Phe Cys Phe Val Phe Glu Ala Glu Ser
    -15                 -10                 -5
cgc tct gtc gcc cag gct gga gtg cag tgg cgc tat ttc ggc tca cta     318
Arg Ser Val Ala Gln Ala Gly Val Gln Trp Arg Tyr Phe Gly Ser Leu
1               5                   10                  15
caa gct ttg cct ccc tgg                                             336
Gln Ala Leu Pro Pro Trp
            20
```

<210> 102
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 214..288

<221> sig_peptide
<222> 214..276
<223> Von Heijne matrix
score 9.19999980926514
seq FILFHWSLCLCLC/QY

<400> 102
```
cccttatgtt ttcttttagt aatttcatag tttcaagttt tatatataag tctttaatcc    60
attttgagtt gatttgtgta tatggtggag acagggtcta gtcttggtct tctgcatgtg   120
actttccaat tttcccagca ccatttattg gagaaactgt ctttttccca gtgcatgttc   180
ttggcacctt tgttgaaaaa cagttggcca tag atg cat gaa ttt att tct ggg    234
                                     Met His Glu Phe Ile Ser Gly
                                         -20                 -15
ttc ttt att ctc ttt cat tgg tct ctg tgt ttg tgt tta tgc caa tac     282
Phe Phe Ile Leu Phe His Trp Ser Leu Cys Leu Cys Leu Cys Gln Tyr
                -10                 -5                  1
cat gcc g                                                           289
His Ala
```

```
<210> 103
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 252..383

<221> sig_peptide
<222> 252..377
<223> Von Heijne matrix
      score 9.19999980926514
      seq LLVCLFAVTSILC/SS

<400> 103
atcctccagc taataagtgt ccaagctggg actcaaactt gggcctttta actgtgctgc     60
tattctacct ctcccttgct ctttccagac caggcttggg acataacact aacacccttt    120
tcctttcatt tcatctcttg tccttcagtc attcctaaac attgacaybc attgagttcc    180
ttggctctgg ccatagtcct ttctcccttt cccctctggg gcatcaaata gtgattacag    240
tatccacagg g atg gca tat gcc att tca cca ttt cac agt tcc tgg aat     290
             Met Ala Tyr Ala Ile Ser Pro Phe His Ser Ser Trp Asn
                     -40                 -35                 -30
cca ctt ttc act tct cat aaa gct tca gca agc cat tct cat ctt ggg      338
Pro Leu Phe Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly
                -25                 -20                 -15
ttg ctt gtt tgc cta ttt gct gtt aca tcc att ctc tgc tcc tca          383
Leu Leu Val Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser
            -10                 -5                  1

<210> 104
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..209

<221> sig_peptide
<222> 30..74
<223> Von Heijne matrix
      score 9.19999980926514
      seq PVLLLALLGFILP/LP

<221> misc_feature
<222> 83
<223> n=a, g, c or t


<400> 104
agaaagagat taccagccac agacgggtc atg agc ccg gta tta ctg ctg gcc       53
                                Met Ser Pro Val Leu Leu Leu Ala
                                -15                 -10
ctc ctg ggg ttc atc ctc cca ctg cca ggn agt gca rgc gct gss tck      101
Leu Leu Gly Phe Ile Leu Pro Leu Pro Gly Ser Ala Xaa Ala Xaa Ser
        -5                  1                   5
gcc agt ttg gga cag ttc agc atg tgt gga agg tgt ccg acm tgc ccc      149
Ala Ser Leu Gly Gln Phe Ser Met Cys Gly Arg Cys Pro Thr Cys Pro
10                  15                  20                  25
ggc aat gga ccc cta aga aca cca gct gcg aca sgg vtt rgg gtg cca      197
Gly Asn Gly Pro Leu Arg Thr Pro Ala Ala Thr Xaa Xaa Xaa Val Pro
```

```
               30                   35                   40
gga cac gtt gat gc                                                     211
Gly His Val Asp
          45

<210> 105
<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..490

<221> sig_peptide
<222> 29..97
<223> Von Heijne matrix
      score 9.10000038146973
      seq SLLLFSLMCETSA/FY

<400> 105
agtcattacg gcgacacgtg gatccaag atg gcg acg gcg atg gat tgg ttg          52
                               Met Ala Thr Ala Met Asp Trp Leu
                                           -20
ccg tgg tct tta ctg ctt ttc tcc ctg atg tgt gaa aca agc gcc ttc        100
Pro Trp Ser Leu Leu Leu Phe Ser Leu Met Cys Glu Thr Ser Ala Phe
-15                 -10                 -5                  1
tat gtg cct ggg gtc gcg cct atc aac ttc cac cag aac gat ccc gta        148
Tyr Val Pro Gly Val Ala Pro Ile Asn Phe His Gln Asn Asp Pro Val
            5                   10                  15
gaa atc aag gct gtg aag ctc acc agc tct cga acc cag cta cct tat        196
Glu Ile Lys Ala Val Lys Leu Thr Ser Ser Arg Thr Gln Leu Pro Tyr
        20                  25                  30
gaa tac tat tca ctg ccc ttc tgc cag ccc agc aag ata acc tac aag        244
Glu Tyr Tyr Ser Leu Pro Phe Cys Gln Pro Ser Lys Ile Thr Tyr Lys
    35                  40                  45
gca gag aat ctg gga gag gtg ctg aga ggg gac cgg att gtc aac acc        292
Ala Glu Asn Leu Gly Glu Val Leu Arg Gly Asp Arg Ile Val Asn Thr
50                  55                  60                  65
cct ttc cag gtt ctc atg aac agc gag aag aag tgt gaa gtt ctg tgc        340
Pro Phe Gln Val Leu Met Asn Ser Glu Lys Lys Cys Glu Val Leu Cys
                70                  75                  80
agc cag tcc aac aag cca gtg acc ctg aca gtg gag cag agc cga ctc        388
Ser Gln Ser Asn Lys Pro Val Thr Leu Thr Val Glu Gln Ser Arg Leu
            85                  90                  95
gtg gcc gag cgg atc aca gaa gac tac tac gtc cac ctc att gct gac        436
Val Ala Glu Arg Ile Thr Glu Asp Tyr Tyr Val His Leu Ile Ala Asp
        100                 105                 110
aac ctg cct gtg gcc acc ggc tgg agc tct act cca acc gag aca gcg        484
Asn Leu Pro Val Ala Thr Gly Trp Ser Ser Thr Pro Thr Glu Thr Ala
    115                 120                 125
atg aca ag                                                             492
Met Thr
130

<210> 106
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..124
```

```
<221> sig_peptide
<222> 41..94
<223> Von Heijne matrix
      score 9.10000038146973
      seq LISLLQCAHVSLG/LQ

<400> 106
tccatttgca gcccatggtt gtcacatcac gctgtttata atg ccc agc ccc tgc       55
                                            Met Pro Ser Pro Cys
                                                        -15
ctg atc tct ctt ctt caa tgt gct cat gtg tcc ctt ggc tta cag tat      103
Leu Ile Ser Leu Leu Gln Cys Ala His Val Ser Leu Gly Leu Gln Tyr
            -10                 -5                  1
cca tgc stt ctc ctt ctc cct cc                                       126
Pro Cys Xaa Leu Leu Leu Pro
    5                   10

<210> 107
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 82..240

<221> sig_peptide
<222> 82..132
<223> Von Heijne matrix
      score 9.10000038146973
      seq LVLAAFCLGIASA/VP

<400> 107
accagaccgc ggacgtctgt aatctcagag gcttgtttgc tgagggtgcc tgcgcastgc     60
gacggctgct ggttttgaaa c atg aat ctt tcg ctc gtc ctg gct gcc ttt      111
                        Met Asn Leu Ser Leu Val Leu Ala Ala Phe
                                -15                 -10
tgc ttg gga ata gcc tcc gct gtt cca aaa ttt gac caa aat ttg gat      159
Cys Leu Gly Ile Ala Ser Ala Val Pro Lys Phe Asp Gln Asn Leu Asp
        -5                  1               5
aca aag tgg tac cag tgg aag gca aca cac aga aga tta tat ggc gcg      207
Thr Lys Trp Tyr Gln Trp Lys Ala Thr His Arg Arg Leu Tyr Gly Ala
10                  15                  20                  25
aat gaa gaa gga tgg agg aga gca gcg tgg gag gg                       242
Asn Glu Glu Gly Trp Arg Arg Ala Ala Trp Glu
                30                  35

<210> 108
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..335

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
      score 9
      seq WVFLVAIFTGVHC/EV
```

<400> 108
```
agctctggga gaggagcccc agccgtgaga ttcccagaag tttccacttg gtgatcagca      60
ctgaacacag accaccaacc atg gag ttt ggc ctt aat tgg gtt ttc ctt gtt     113
                      Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val
                                          -15                 -10
gct att ttt aca ggt gtc cac tgt gag gtg cag ttg gtg gag tct ggg       161
Ala Ile Phe Thr Gly Val His Cys Glu Val Gln Leu Val Glu Ser Gly
            -5                  1               5
gga gac ctg gta cag cca ggg cgg tcc ctg aga ctc tcc tgt aca gct       209
Gly Asp Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala
    10                  15                  20
tct gga ttc acc ttt ggt gat tat gcc atg acc tgg ttc cgc cag gct       257
Ser Gly Phe Thr Phe Gly Asp Tyr Ala Met Thr Trp Phe Arg Gln Ala
25                  30                  35                  40
tca ggg aag cga ctg gag tgg cta ggt ttc att aga aat aga ggt tcs       305
Ser Gly Lys Arg Leu Glu Trp Leu Gly Phe Ile Arg Asn Arg Gly Ser
                45                  50                  55
ggt ggg tca gca gag tac ggc gcg tct gtg a                             336
Gly Gly Ser Ala Glu Tyr Gly Ala Ser Val
            60                  65
```

<210> 109
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..158

<221> sig_peptide
<222> 6..56
<223> Von Heijne matrix
score 9
seq LLILLMLLLFAIH/IN

<400> 109
```
cagct atg aaa aac tgc cta ctc ata ctc ctc atg ctt ctc tta ttt gca      50
      Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala
              -15                 -10                 -5
ata cac ata aac cgt atg aat gta agg aat gtg gga aat act tta gtc       98
Ile His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val
        1               5                   10
gta gtg caa atc tta ttc agc atc aga gta ttc ata ctg gag aga aac      146
Val Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn
15                  20                  25                  30
cct ttg aat gtg gg                                                   160
Pro Leu Asn Val
```

<210> 110
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..527

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
score 9
seq WIFLLAILKGVQC/EV

```
<221> misc_feature
<222> 307..308,466..467
<223> n=a, g, c or t


<400> 110
agctctggga gaggagcccc agccctgaga ttcccaggtg tttccattca gtgatcagca      60
ctgaacacag aggactcacc atg gag ttg gga ctg agc tgg att ttc ctt ttg     113
                      Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu
                                      -15                 -10
gct att tta aaa ggt gtc cag tgt gaa gtg cag ctg gtg gag tct ggg       161
Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly
            -5                  1               5
gga ggc ttg gta cag cct ggc agg tcc ctg aga ctc tcc tgt gca gcc       209
Gly Gly Leu Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala
    10                  15                  20
tct gga ttc acc ttt gat gat tac gcc atg cac tgg gtc cgg caa gct       257
Ser Gly Phe Thr Phe Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala
25                  30                  35                  40
cca ggg aag ggc ctg gag tgg gtc tca gga att act tgg aat agt ggt       305
Pro Gly Lys Gly Leu Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly
            45                  50                  55
ann ata ggc tac gcg gac tct gtg aag ggc cga ttc acc atc tcc aga       353
Xaa Ile Gly Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg
            60                  65                  70
gac aac gcc aag aac tcc ctg tat ttg caa atg aac agt ctg aga act       401
Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr
        75                  80                  85
gag gac acg gcc ttc tat ttc tgt gca aaa gct cgc ggg ctc ttt agc       449
Glu Asp Thr Ala Phe Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser
    90                  95                  100
gat acc tgg ccc tac vnn cac tac gct atg gac gtc tgg ggc caa ggg       497
Asp Thr Trp Pro Tyr Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly
105                 110                 115                 120
acc acg gtc acc gtc tcc tca gcc tcc acc                               527
Thr Thr Val Thr Val Ser Ser Ala Ser Thr
                125                 130

<210> 111
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..154

<221> sig_peptide
<222> 80..121
<223> Von Heijne matrix
      score 8.89999961853027
      seq LLVFFVLWTCSLA/LL

<400> 111
ctggaaaggg aggagccaaa aggggaacgc tttcttgatt gtcccagcct cattaggagc      60
taccacaggg ctctcctgc atg ctc ctt gtt ttc ttt gtg ctc tgg act tgc      112
                     Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys
                                         -10                 -5
tca ctt gca ctg ctt gct tct tcc cca atc gcm gcc yac cca               154
Ser Leu Ala Leu Leu Ala Ser Ser Pro Ile Ala Ala Xaa Pro
        1                   5                   10
```

```
<210> 112
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..439

<221> sig_peptide
<222> 59..115
<223> Von Heijne matrix
      score 8.89999961853027
      seq ILLLVAAATDASS/QM

<400> 112
atcacccatc aaccacatcc ctcctctaga gagtcccctg aaagcacagc tcctcacc        58
atg gac tgg acc tgg aga atc ctc ctc ttg gtg gca gca gcc aca gat      106
Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
                -15                 -10                 -5
gcc tcc tcc cag atg cag ctg ttg cag tct ggg cct gaa gtg aag aag      154
Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
            1               5                   10
act ggg tcc tca gtg aaa ctt tcc tgc acg gcc tcc ggc gac acc ctc      202
Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
    15                  20                  25
gcc tac cac tac ctg cac tgg gtg cga cag gcc ccc gga caa gcg ctt      250
Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
30                  35                  40                  45
gag tgg atg gga tgg atc aca cct ttc agt gga gac acc aac ttc gca      298
Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
                50                  55                  60
cag cga ttc cag gac aga ctc acc ttc acc agg gac agg tct atg agc      346
Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
            65                  70                  75
aca gtc tac atg acc ctg acc agc ctg ata tct gaa gac aca gcc atg      394
Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
        80                  85                  90
tat tac tgt gcc act gat gga cgt cgc acc aac cgt ctt ttt gaa ca       441
Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
    95                  100                 105

<210> 113
<211> 369
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 164..367

<221> sig_peptide
<222> 164..217
<223> Von Heijne matrix
      score 8.80000019073486
      seq LGCLLWLLTHIKA/QD

<221> misc_feature
<222> 290..292
<223> n=a, g, c or t

<400> 113
```

```
cagtttcagt ttctctccct tcctagtaga gacaaaaagg agacacattt tatccgtgca    60
tccaaagact ccgatgttgg tcatggactt gggaagacag tcttcccttg gcgtttgatc   120
actgcggaga tgccttcctt gatcattcac ccacattccc ttg atg gca ggt caa     175
                                                Met Ala Gly Gln
                                                            -15
ttg ctg gga tgc ctg ctt tgg ctg ctc acc cac att aaa gcc cag gac     223
Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile Lys Ala Gln Asp
                -10                 -5                  1
tca gtc agg gat gcc tac tgg aag act ggt agc tgc cca cct cca ttt     271
Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys Pro Pro Pro Phe
        5                   10                  15
ctc cat gtg tct acc ttc nnn kkt aaa ctt acc ttc tcc act aag ggc     319
Leu His Val Ser Thr Phe Xaa Xaa Lys Leu Thr Phe Ser Thr Lys Gly
    20                  25                  30
aac ctt ctg cat tcc att cct ctc tct tcc ccc tta gcc tgt gtt ctt     367
Asn Leu Leu His Ser Ile Pro Leu Ser Ser Pro Leu Ala Cys Val Leu
35                  40                  45                  50
ag                                                                  369
```

<210> 114
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..334

<221> sig_peptide
<222> 20..292
<223> Von Heijne matrix
score 8.80000019073486
seq LFLMLLGELGVFA/SY

<221> misc_feature
<222> 295
<223> n=a, g, c or t

<400> 114

```
agctctgaat tgggaaggg atg aag gag gct gtg cct ccg ggt tgc acg aag     52
                     Met Lys Glu Ala Val Pro Pro Gly Cys Thr Lys
                         -90                 -85
agt ccg agt cat ttc tca gaa ggt ttt gat agg tgg gcc tta gag gag    100
Ser Pro Ser His Phe Ser Glu Gly Phe Asp Arg Trp Ala Leu Glu Glu
-80                 -75                 -70                 -65
acg ccg ccg gaa aac ctg att ggc gcc ctc ttg gcg atc ttc ggg cac    148
Thr Pro Pro Glu Asn Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His
                -60                 -55                 -50
ctc gtg gtc agc att gca ctt aac ctc cag aag tac tgc cac atc cgc    196
Leu Val Val Ser Ile Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg
            -45                 -40                 -35
ctg gca ggc tcc aag gat ccc cgg gcc tat ttc aag acc aag aca tgg    244
Leu Ala Gly Ser Lys Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp
        -30                 -25                 -20
tgg ctg ggc ctg ttc ctg atg ctt ctg ggc gag ctg ggt gtg ttc gcm    292
Trp Leu Gly Leu Phe Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala
    -15                 -10                 -5
tcn tac gcc ttc gcg ccg ctg tca ctc atc gtg ccc ctc agc            334
Ser Tyr Ala Phe Ala Pro Leu Ser Leu Ile Val Pro Leu Ser
1               5                   10
```

<210> 115

```
<211> 153
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..152

<221> sig_peptide
<222> 21..74
<223> Von Heijne matrix
      score 8.80000019073486
      seq LLSCWALLGTTFG/CG

<400> 115
acacccctgc cagcggcacc atg gct ttc ctc tgg ctc ctc tcc tgc tgg gcc      53
                      Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala
                                  -15                 -10
ctc ctg ggt acc acc ttc ggc tgc ggg gtc ccc gcc atc cac cct ggc       101
Leu Leu Gly Thr Thr Phe Gly Cys Gly Val Pro Ala Ile His Pro Gly
        -5                  1               5
tgc caa ctg agc ccg cgg ctc cct ccg acc ctg ctc ccc aca gag cgc       149
Cys Gln Leu Ser Pro Arg Leu Pro Pro Thr Leu Leu Pro Thr Glu Arg
10                  15                  20                  25
ggg g                                                                 153
Gly

<210> 116
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..292

<221> sig_peptide
<222> 47..106
<223> Von Heijne matrix
      score 8.80000019073486
      seq LWLFFVLNLGSFA/FS

<400> 116
taccagtaac ttctttcatg gttcaataaa atcatagctt tagttt atg gca cct        55
                                                   Met Ala Pro
                                                   -20
ttt caa aac ttc ctt tgg ctt ttc ttt gtg ctt aat tta ggw agt ttt       103
Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu Gly Ser Phe
        -15                 -10                 -5
gct ttt agc tca mtt ccd aat tct ctt ttt tac aca att cat ttt ggt       151
Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile His Phe Gly
    1               5                   10                  15
cct aat ttc ttt act tta cta tat aaa caa ggt gct gaa atg tgt gtg       199
Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu Met Cys Val
                20                  25                  30
tat gta ttt aac ttc ctc tac cca ttt gct ctt ggt tat ttc ttc agt       247
Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr Phe Phe Ser
            35                  40                  45
tat gat att ctg gat ttg cca gtc akt gtc cgt cct cct agc ggg           292
Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro Ser Gly
        50                  55                  60

<210> 117
```

```
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 141..302

<221> sig_peptide
<222> 141..245
<223> Von Heijne matrix
      score 8.69999980926514
      seq LLLSVAFNQLVFA/LY

<400> 117
tttctcatca atttcttgct tctctggcaa cctcaacctc tgattcctga ggccaataaa      60
actgaaactt tctgcttgag ctcttgtttt gccaggctga tggggctgag gtgcaccctc     120
tgaggaaaag ctgtaaatac atg gat ttt acc caa tgc cat tcc ctt ctt tta     173
                      Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu
                      -35                 -30                 -25
agg gtt gaa tat tct cca gtg tct gtc tgc ttt tta tta ctt tcc gtt       221
Arg Val Glu Tyr Ser Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val
            -20                 -15                 -10
gcc ttc aat cag ttg gtt ttt gct ttg tat cca ata caa gct acw btc       269
Ala Phe Asn Gln Leu Val Phe Ala Leu Tyr Pro Ile Gln Ala Thr Xaa
            -5                  1               5
tgt ttc tct dda gtt tct ctc cct ttc ccc gct ca                        304
Cys Phe Ser Xaa Val Ser Leu Pro Phe Pro Ala
    10                  15

<210> 118
<211> 145
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..144

<221> sig_peptide
<222> 76..120
<223> Von Heijne matrix
      score 8.5
      seq LLLLACGVPSLWP/FA

<400> 118
gtgaaggtag gagtgttggg gccctgaccc ccgcaggagg gatgggcgga ttcgaggact      60
ggctgcctgc ccatc atg ctc ttg ctc ctg ctg gcc tgt ggt gtt ccc agc      111
                 Met Leu Leu Leu Leu Leu Ala Cys Gly Val Pro Ser
                 -15                 -10                 -5
ctg tgg ccc ttt gcw ctt gct ctc tta aag acc c                         145
Leu Trp Pro Phe Ala Leu Ala Leu Leu Lys Thr
            1               5

<210> 119
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..288
```

```
<221> sig_peptide
<222> 160..228
<223> Von Heijne matrix
      score 8.5
      seq SFLLLHLCQVLLS/RR

<400> 119
tctttagtcc tgtttatatg atgaatcaca tttattgatt tgcatatgtt gaaccatcct    60
tgtatcccag ggataaagcc tacttgattg taatggataa gcttcatgat gtgctgctga   120
atttggtttg ccagtatttt gttaaggatt tttacatca atg ttc att gag aat      174
                                           Met Phe Ile Glu Asn
                                                       -20
att ggv ctg aag ttt tct ttt ttg ttg ttg cat ctc tgc cag gtt ttg      222
Ile Gly Leu Lys Phe Ser Phe Leu Leu Leu His Leu Cys Gln Val Leu
            -15                 -10                 -5
cta tca aga cga gct ggt acc att cct act gaa aca att cca aaa aaa      270
Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu Thr Ile Pro Lys Lys
        1               5                   10
ttg agg agg aga gac ggg                                              288
Leu Arg Arg Arg Asp Gly
15                  20

<210> 120
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 71..385

<221> sig_peptide
<222> 71..142
<223> Von Heijne matrix
      score 8.5
      seq XALLMGFLMVCLG/AF

<400> 120
aattctcttg gagcaagcag ggaagcagag gagcagcagg gtcagggtgc tgggttccta    60
aggtgcaagg atg cag aac aga act ggc ctc att ctc tgt gct ytt gcc      109
           Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala
                           -20                 -15
ctc ctg atg ggt ttc ctg atg gtc tgc ctg ggg gcc ttc ttc att tcc      157
Leu Leu Met Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser
    -10                 -5                  1               5
tgg ggc tcc ata ttc gac tgt cag ggg agc ctg att gcg gcc tat ttg      205
Trp Gly Ser Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu
                10                  15                  20
ctt ctg cct ctg ggg ttt gtg atc ctt ctg agt gga att ttc tgg agc      253
Leu Leu Pro Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser
            25                  30                  35
aac tat cgc cag gtg act gaa agc aaa gga gtg ttg agg cac atg ctc      301
Asn Tyr Arg Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu
        40                  45                  50
cga caa cac ctt gct cat ggg gcc ctg ccc gtg gcc aca gta gac agt      349
Arg Gln His Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser
    55                  60                  65
gct gct ctt ctg aaa atc atg tgt aag car ttg ctt t                    386
Ala Ala Leu Leu Lys Ile Met Cys Lys Gln Leu Leu
70                  75                  80

<210> 121
<211> 190
```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..189

<221> sig_peptide
<222> 34..165
<223> Von Heijne matrix
score 8.5
seq LTCTSSLLSFALG/RS

<400> 121
```
atcttgaaaa cggaaaataa aaacagcaga cct atg aag gtc gaa ggg gaa gaa       54
                                     Met Lys Val Glu Gly Glu Glu
                                                         -40
aag ctg tat cga ttg ttg aga tct ggc gac ttg ttt aaa ttt cat cag      102
Lys Leu Tyr Arg Leu Leu Arg Ser Gly Asp Leu Phe Lys Phe His Gln
        -35                 -30                 -25
cct cac ttc tat gaa ctc tca ggc ctc acg tgt acc agc tct ctg ctc      150
Pro His Phe Tyr Glu Leu Ser Gly Leu Thr Cys Thr Ser Ser Leu Leu
    -20                 -15                 -10
tcc ttt gcc ttg gga cgt tcc atc cct gga agt ttc cca g                190
Ser Phe Ala Leu Gly Arg Ser Ile Pro Gly Ser Phe Pro
-5                  1               5
```

<210> 122
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..211

<221> sig_peptide
<222> 32..88
<223> Von Heijne matrix
score 8.5
seq LLLFSGAVALIQT/WA

<400> 122
```
agattctccc cagacgccaa ggttgcgggt c atg gag tcc cga acc ctc ctc         52
                                   Met Glu Ser Arg Thr Leu Leu
                                                       -15
ctg ctg ttc tcg gga gcc gtg gcc ctg atc cag acc tgg gca ggt gag      100
Leu Leu Phe Ser Gly Ala Val Ala Leu Ile Gln Thr Trp Ala Gly Glu
        -10                 -5                  1
tgc ggg gtc ggg agg gaa aag gcc tct gcg gga agg agc gag ggg ccc      148
Cys Gly Val Gly Arg Glu Lys Ala Ser Ala Gly Arg Ser Glu Gly Pro
5                   10                  15                  20
gcc cgg agg agt aaa tct gca cat ata kbt aat tac aga tta caa tta      196
Ala Arg Arg Ser Lys Ser Ala His Ile Xaa Asn Tyr Arg Leu Gln Leu
                25                  30                  35
caa tca agg cag ggg                                                  211
Gln Ser Arg Gln Gly
            40
```

<210> 123
<211> 353
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 249..353

<221> sig_peptide
<222> 249..296
<223> Von Heijne matrix
      score 8.39999961853027
      seq SVPLLCFWSLCYC/FA

<221> misc_feature
<222> 187
<223> n=a, g, c or t


<400> 123
agcgagtcct tgcctcccgg cggctcagga cgagggcaga tctcgttctg gggcaagccg    60
ttgacactcg ctccctgcca ccgcccgggc tccgtgccgc caagttttca ttttccacct   120
tctctgcctc cagtccccca gcccctggcc gagagaaggg tcttaccggc cgggattgct   180
ggaaacncaa gaggtggttt ttgtttttta aaacttctgt ttcttgggag ggggtgtggc   240
ggggcagg atg agc aac tcc gtt cct ctg ctc tgt ttc tgg agc ctc tgc     290
         Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys
             -15                 -10                 -5
tat tgc ttt gct gcg ggg agc ccc gta cct ttt ggt cca gag gga cgg     338
Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg
        1               5                   10
ctg gaa gat aag ctc                                                 353
Leu Glu Asp Lys Leu
15

<210> 124
<211> 249
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..248

<221> sig_peptide
<222> 93..134
<223> Von Heijne matrix
      score 8.39999961853027
      seq PWTILLFAAGSLA/IP

<400> 124
tttttccccg atctggcctc acaggaggag ttggcgggga gccttgggcc cctctggcct    60
cagccggatt tcccagccaa acgcagagag ag atg ccc tgg acc atc ttg ctc     113
                                    Met Pro Trp Thr Ile Leu Leu
                                                    -10
ttt gca gct ggc tcc ttg gcg atc cca gca cca tcc atc cgg gtg gtg     161
Phe Ala Ala Gly Ser Leu Ala Ile Pro Ala Pro Ser Ile Arg Val Val
        -5                  1               5
ccc ccg tac cca agc agc caa gag gac ccc atc cac atc gca tgc atg     209
Pro Pro Tyr Pro Ser Ser Gln Glu Asp Pro Ile His Ile Ala Cys Met
10                  15                  20                  25
gcc gct ggg aac ttc ccg ggg gcg aat ttc aca ctg tat c               249
Ala Ala Gly Asn Phe Pro Gly Ala Asn Phe Thr Leu Tyr
                30                  35

<210> 125
<211> 375
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 175..375

<221> sig_peptide
<222> 175..366
<223> Von Heijne matrix
      score 8.39999961853027
      seq GFLFFGFLFPVFS/FP

<400> 125
gtgctgcggc attcacgtga tctgcacggg cgcagatgta ggcaccggtc cgagtgcctg      60
ccctctgtcc ccgcggctgg gtctcgtctg ctccggttcc tgggctccta attcttggtc     120
cagcttcttc caggtcagtg tgcgggcctt ccacgctgcc agcggaacac tgga atg       177
                                                            Met
gcg gaa ggg gaa cgg gtc tgc gcg tct gtk gtt ccc agc gct ctg cga       225
Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu Arg
            -60                 -55                 -50
acg ctg aaa agg agg agc aac ctg tcc aga atc ccc gca gga cag gaa       273
Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln Glu
        -45                 -40                 -35
aag gag ggg aaa tct cga cat gtt gct ccc cct ttt cgc ttt ttc cct       321
Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe Pro
    -30                 -25                 -20
ttt tcc ggt ttt ttg ttt ttt ggt ttt ctt ttt ccc gtc ttt tct ttc       369
Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser Phe
-15                 -10                 -5                   1
ccc tcc                                                               375
Pro Ser

<210> 126
<211> 437
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..435

<221> sig_peptide
<222> 223..261
<223> Von Heijne matrix
      score 8.39999961853027
      seq MFCLAAILASASA/QR

<221> misc_feature
<222> 404
<223> n=a, g, c or t

<400> 126
tcaataccca tgtgaacagt ttcgtggagg gttttaagta ttttccactg gctggctttg      60
ggtataagta cctttccttc ttctgtcgtt aaccacgccg aggggagaaa actatgcccc     120
cgtgaaagtc cccactctgt ttcggttggg gaatactgga gcttaacctc ttggaggggg     180
ttgttccata ccaagggtcc ttccgtaggt atttctaatg gg atg ttc tgc ctg        234
                                               Met Phe Cys Leu
                                                           -10
gca gca att tta gcc tca gca tct gcc caa cgg ttt cct tct gcc ttt       282
Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe Pro Ser Ala Phe
                -5                   1                   5
```

```
tct cct tca cct tty yga tgg ctt yrg car tgt aas act gcc acc tcc      330
Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa Thr Ala Thr Ser
        10                  15                  20
ttg ggt ttt trc act gtg tgy art aac tcc ata att tcc ttg tgg tat      378
Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile Ser Leu Trp Tyr
    25                  30                  35
tta ayg ggr gtt ccc cca gag gtt ang gaa ctc cct ttc ttt cca tat      426
Leu Xaa Gly Val Pro Pro Glu Val Xaa Glu Leu Pro Phe Phe Pro Tyr
40                  45                  50                  55
tgc agc atg gg                                                       437
Cys Ser Met

<210> 127
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..302

<221> sig_peptide
<222> 24..74
<223> Von Heijne matrix
      score 8.39999961853027
      seq TLLLLLSEALALT/QT

<400> 127
ctcaggactc agaggctggg atc atg gta gat gga acc ctc ctt tta ctc ctc     53
                          Met Val Asp Gly Thr Leu Leu Leu Leu Leu
                                      -15                 -10
tcg gaa gcc ctg gcc ctt acc car acc tgg gcg ggc tcc cac tcc tkr      101
Ser Glu Ala Leu Ala Leu Thr Gln Thr Trp Ala Gly Ser His Ser Xaa
        -5                  1               5
aag tat ttc cac act tcc gtg tcc cgg mcc ggc cgc ggg gag ccc cgc      149
Lys Tyr Phe His Thr Ser Val Ser Arg Xaa Gly Arg Gly Glu Pro Arg
10                  15                  20                  25
ttc atc tct gtg ggc tac gtg gac gac acc cgg tca gag tat tgg gac      197
Phe Ile Ser Val Gly Tyr Val Asp Asp Thr Arg Ser Glu Tyr Trp Asp
                30                  35                  40
cgg gag aca cgg agc gcc agg gac acc gca cag att ttc cga gtg aac      245
Arg Glu Thr Arg Ser Ala Arg Asp Thr Ala Gln Ile Phe Arg Val Asn
            45                  50                  55
ctg cgg acg ctg cgc ggc tac tac aat cag agc gag gcc ggg tct cam      293
Leu Arg Thr Leu Arg Gly Tyr Tyr Asn Gln Ser Glu Ala Gly Ser Xaa
        60                  65                  70
acc ctg cag tg                                                       304
Thr Leu Gln
    75

<210> 128
<211> 244
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 19..243

<221> sig_peptide
<222> 19..99
<223> Von Heijne matrix
      score 8.39999961853027
```

seq LVLSLISLSIAWS/MV

<221> misc_feature
<222> 112
<223> n=a, g, c or t

<400> 128

```
gcgattaggt tttaatgt atg aat ttc agg ggg cca caa acg ttc agt ctt       51
                    Met Asn Phe Arg Gly Pro Gln Thr Phe Ser Leu
                            -25                 -20
tca cac agc ctt gtg tta tcc cta atc agt ctc tcc att gca tgg tct       99
Ser His Ser Leu Val Leu Ser Leu Ile Ser Leu Ser Ile Ala Trp Ser
    -15                 -10                 -5
atg gtc gaa atg nbc act tct gca agc tac aar caa aag ttt gcc ctt      147
Met Val Glu Met Xaa Thr Ser Ala Ser Tyr Lys Gln Lys Phe Ala Leu
1               5                   10                  15
aga atc cta gtt gtg cag ttg ccc aca tgg gtg gaa tgt cca gta aac      195
Arg Ile Leu Val Val Gln Leu Pro Thr Trp Val Glu Cys Pro Val Asn
            20                  25                  30
cac agg tgt gca cta ggg aga aag aat tgt tct att agg acc cag cca c    244
His Arg Cys Ala Leu Gly Arg Lys Asn Cys Ser Ile Arg Thr Gln Pro
        35                  40                  45
```

<210> 129
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 156..230

<221> sig_peptide
<222> 156..215
<223> Von Heijne matrix
score 8.39999961853027
seq SCICLFLPSLIHS/FP

<400> 129

```
ctacaggaag gaaaagtgtg acagctttga aaaagaaaga gggtaaaata ttttaaccac     60
ccttggtgtc atttgtggca gcctatagca ttagagcctt tgagaacaga tctttccaga    120
ttctgcttaa gtccagggat tctgtgaccg cagaa atg act ggc atc tcc atc      173
                                       Met Thr Gly Ile Ser Ile
                                       -20                 -15
tgc tcg tgc atc tgt ttg ttt ctt cct tca ttg att cac tca ttc ccc      221
Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser Leu Ile His Ser Phe Pro
                -10                 -5                  1
ccg ccc tgc gg                                                       232
Pro Pro Cys
        5
```

<210> 130
<211> 312
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..310

<221> sig_peptide
<222> 17..94

<223> Von Heijne matrix
      score 8.30000019073486
      seq FLLLVAAPRWVQL/QE

<400> 130
```
atgctttctg agagtc atg gac ctc ctg tgc aag aac atg aag cac ctg tgg      52
                  Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp
                      -25                 -20                 -15
ttc ttc ctc ctg ctg gtg gcg gct ccc aga tgg gtc cag ctg cag gag       100
Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu
                -10                 -5                  1
tcg ggc cca cgc ctg gtg agg cct ccg gag acc ctg aag cct tcg gag       148
Ser Gly Pro Arg Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu
        5                   10                  15
acc ctg tcc ctc acc tgc act att tct ggt gac tcc atg agc agt gct       196
Thr Leu Ser Leu Thr Cys Thr Ile Ser Gly Asp Ser Met Ser Ser Ala
    20                  25                  30
tct tac tat tgg gcc tgg atc cgc cag ccc cca ggc aag ggc ctg gaa       244
Ser Tyr Tyr Trp Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu
35                  40                  45                  50
ttc att ggg cgt gcc tta tat agt ggg acc acc gac tac aat ccg tcc       292
Phe Ile Gly Arg Ala Leu Tyr Ser Gly Thr Thr Asp Tyr Asn Pro Ser
                55                  60                  65
ctc agc agt cga atc acc ct                                            312
Leu Ser Ser Arg Ile Thr
            70
```

<210> 131
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 119..274

<221> sig_peptide
<222> 119..253
<223> Von Heijne matrix
      score 8.19999980926514
      seq PLSLSLCLSLCHT/HT

<400> 131
```
gccttcatct ctccatctct gcgctgctgc cggctgcgcc atccagcacc cagactccag      60
caccggccga ggaccccac tccggctgca gggaccctgt cccagcgaga ccgcaggc        118
atg tca tcc gaa aag tca gga ctc cca gac tca gtc cct cac act tct       166
Met Ser Ser Glu Lys Ser Gly Leu Pro Asp Ser Val Pro His Thr Ser
-45                 -40                 -35                 -30
ccg ccg ccc tac aat gcc cct cag cct cca gcc gaa ccc cca gcc ccg       214
Pro Pro Pro Tyr Asn Ala Pro Gln Pro Pro Ala Glu Pro Pro Ala Pro
                -25                 -20                 -15
cct ctc tct ctc tct ctc tgt ctc tct ctc tgt cac aca cac aca cac       262
Pro Leu Ser Leu Ser Leu Cys Leu Ser Leu Cys His Thr His Thr His
            -10                 -5                  1
aca cac aca cac ac                                                    276
Thr His Thr His
    5
```

<210> 132
<211> 174
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 35..172

<221> sig_peptide
<222> 35..118
<223> Von Heijne matrix
      score 8.19999980926514
      seq LVSLLMQPEGALG/EE

<400> 132
actctgctga gctcctctgc acctgcccag gacc atg acg cct gct ctg cgc tgc      55
                                      Met Thr Pro Ala Leu Arg Cys
                                                      -25
gca ttc gct ctg gcc ata gcg ggc ctc gtg tcg ctg ctg atg cag ccc       103
Ala Phe Ala Leu Ala Ile Ala Gly Leu Val Ser Leu Leu Met Gln Pro
    -20                 -15                 -10
gag ggc gcc ctc ggc gag gag gct gca agt gcc gca gcc cag ggc cgc       151
Glu Gly Ala Leu Gly Glu Glu Ala Ala Ser Ala Ala Ala Gln Gly Arg
-5                  1               5                   10
cag ttg gct gaa ctt agg ctc ca                                        174
Gln Leu Ala Glu Leu Arg Leu
            15

<210> 133
<211> 344
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..342

<221> sig_peptide
<222> 133..246
<223> Von Heijne matrix
      score 8.19999980926514
      seq LLLIFLSFPYTLC/IL

<400> 133
gcctttcact tgcacaaaca ctgttattat gatcacttat ccaactgaca tttttcagac      60
cttttaactt caactgttct tttttcctgt aaatcttaat tttctttttt tttctcccaa     120
tttttctcct ac atg tct gga ctc ttc cca gtt cct gtc aga gta aat gtt     171
              Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val
                          -35                 -30
gat att gcc cag aac ata act tgc tct tcc ttt tct ctc ctt ctc att       219
Asp Ile Ala Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile
-25                 -20                 -15                 -10
ttt ctt tct ttc ccc tac acc ctc tgt ata ctc tat aga gta aaa tca       267
Phe Leu Ser Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser
                -5                  1               5
tat aca ccc acg gag tca ata act gcc ttt aat cta aca att ggg wga       315
Tyr Thr Pro Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa
        10                  15                  20
ttc cca tat ctt taw wtt tcw acc ccg gg                                344
Phe Pro Tyr Leu Xaa Xaa Ser Thr Pro
    25                  30

<210> 134
<211> 244
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> 128..244

<221> sig_peptide
<222> 128..226
<223> Von Heijne matrix
score 8.19999980926514
seq HALSLCLCTCAFA/FL

<400> 134
aagcaagaga ggggtgttca ggatgataaa gtcctggttg atgaaggcag atgcctgcag 60
ctcttccctg ggcagggct ggcttccata gggtgcttgt ttgggccctt tggaaggggg 120
tgtgcgg atg tgc agg gct gct tgt atc att aga atg gct gtt aga att 169
Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile
-30 -25 -20
tca ttc ttt ctt tct tac cat gct ctg tct ctc tgc ctt tgt aca tgt 217
Ser Phe Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys
-15 -10 -5
gcg ttt gca ttt ctc tcc ctc ctc ggg 244
Ala Phe Ala Phe Leu Ser Leu Leu Gly
1 5

<210> 135
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..216

<221> sig_peptide
<222> 40..90
<223> Von Heijne matrix
score 8.19999980926514
seq LLXALGFLXQVNP/XP

<400> 135
attaaaccac caccagstcc ccaagccacc ccttcagcc atg aag ttc ctg ctc 54
Met Lys Phe Leu Leu
-15
ctg gma gcc ctc gga ttc ctg amc cag gtg aat ccc arc cca att sma 102
Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn Pro Xaa Pro Ile Xaa
-10 -5 1
ggd ggg tca aaa atg tgt gag twa cac ccc agg ata ctg cag gac atg 150
Gly Gly Ser Lys Met Cys Glu Xaa His Pro Arg Ile Leu Gln Asp Met
5 10 15 20
ttg cca ctg ggg gga gac agc att gtt cat gtg caa cgc tks cag aaa 198
Leu Pro Leu Gly Gly Asp Ser Ile Val His Val Gln Arg Xaa Gln Lys
25 30 35
atg ctg cat cag yta ctc c 217
Met Leu His Gln Leu Leu
40

<210> 136
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 114..428

<221> sig_peptide
<222> 114..239
<223> Von Heijne matrix
score 8.10000038146973
seq LFCFLLLCLSAAS/LL

<400> 136
```
aggcgtctgt gtgcgccgcc aagtcggtgg ggcggggacg cgaggtgtgg atggggggtc     60
gccttgacct ctgcctcagc cagtagcgca gtctcggcct cgccgttacg gag atg       116
                                                           Met
gtg ccc tgg gtg cgg acg atg ggg cag aag ctg aag cag cgg ctg cga      164
Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu Arg
    -40                 -35                 -30
ctg gac gtg gga cgc gag atc tgc cgc cag tac ccg ctg ttc tgc ttc      212
Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys Phe
-25                 -20                 -15                 -10
ctg ctg ctc tgt ctc agc gcc gcc tcc ctg ctt ctt aac agg tat att      260
Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr Ile
                -5                  1                   5
cat att tta atg atc ttc tgg tca ttt gtt gct gga gtt gtc aca ttt      308
His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr Phe
        10                  15                  20
tac tgc tca cta gga cct gat tct ctc tta cca aat ata ttc ttc aca      356
Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe Thr
    25                  30                  35
ata aaa tac aaa ccc aag cag tta gga ctt cag gaa tta ttt cct caa      404
Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro Gln
40                  45                  50                  55
ggt cat agc tgt gct gtt tgt ggt                                      428
Gly His Ser Cys Ala Val Cys Gly
                60
```

<210> 137
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 305..433

<221> sig_peptide
<222> 305..406
<223> Von Heijne matrix
score 8.10000038146973
seq LLCLFXLFFFSFL/KR

<400> 137
```
tttctgtcca ttctccctca ccaccctgac gcaggctctg ggaatgtgct gaaggtgcag     60
cagctgctcc acatttgtag cgaacacttt gactccaaag agaaggagga agacaaagac    120
aagaaggaaa agaaagacaa ggacaagaag gaagcccctg ctgacatggg agcacatcag    180
ggagtggctg ttctggggat tgcccttatt gctatggggg aggagattgg tgcagagatg    240
gcattacgaa cctttggcca cttggtgagt atagcatgaa gaaaattgga atatactggt    300
tttg atg gcc tgg ggt tcc cca ggg aag att ttt ctg atg ggt ttt ctt     349
     Met Ala Trp Gly Ser Pro Gly Lys Ile Phe Leu Met Gly Phe Leu
                 -30                 -25                 -20
ggt gga gag ctg gtc ttt ttg ctg tgc ctt ttc ttw ctt ttt ttc ttt      397
Gly Gly Glu Leu Val Phe Leu Leu Cys Leu Phe Xaa Leu Phe Phe Phe
                -15                 -10                 -5
tct ttt ttg aag cgg agt ttt gct cta gag tgc aat g                    434
Ser Phe Leu Lys Arg Ser Phe Ala Leu Glu Cys Asn
            1                   5
```

```
<210> 138
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..393

<221> sig_peptide
<222> 310..357
<223> Von Heijne matrix
      score 8.10000038146973
      seq SILLLLAPPLPSA/VS

<221> misc_feature
<222> 189
<223> n=a, g, c or t


<400> 138
aaaagctctg taaacatata ataaatggaa ttccattgac attcaagcct tacgtatttc    60
cagagcttct tcgacttatc ctgcctcccc tactttaatt ctgttaaagt agttgaacac   120
cattcttctc ataatagttc tccctcsatt cttcagtgat tyccttgtgt ttataggata   180
aagtccacnt gttattttgg cagtcagttc aagatccaca aatcagtctt taccccttaca   240
tccttatttc tcactgctgt tctaatatag tctttatacc agtcaggctg gtctgttcac   300
tattcctga atg ttt ttc tcc att ctt ttg tta ttg gca ccc ccg cta ccc   351
          Met Phe Phe Ser Ile Leu Leu Leu Leu Ala Pro Pro Leu Pro
              -15                 -10                 -5
tct gca gtg tct ttg cta cct ttc ttt ttc tac tgt gtg cag gg          395
Ser Ala Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln
        1               5                   10

<210> 139
<211> 268
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 141..266

<221> sig_peptide
<222> 141..206
<223> Von Heijne matrix
      score 8.10000038146973
      seq LLVCSWLSISLHA/HT

<400> 139
caactctgct gttttgtagg aagccacatg gaggtcattt acggttacta gttatcttag    60
tcagcttggg cagccattaa aaaataatac tgtagacgga gtggcccaaa cgagagaaat   120
ttatttctta tagttttggc atg gta gat ttc atc ctg agg tct ctt ctc ttg   173
                      Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu
                                  -20                 -15
gtt tgt agt tgg ctg tca atc tcc ctg cat gct cac acg acc gct ttt     221
Val Cys Ser Trp Leu Ser Ile Ser Leu His Ala His Thr Thr Ala Phe
    -10                 -5                  1                   5
tgt aca tac agt aag aaa ata cac act gtc atg tca ttt ttt tgt aa      268
Cys Thr Tyr Ser Lys Lys Ile His Thr Val Met Ser Phe Phe Cys
                10                  15                  20

<210> 140
```

<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..170

<221> sig_peptide
<222> 93..140
<223> Von Heijne matrix
score 8.10000038146973
seq LLYFLCVSSYVTS/FF

<400> 140
```
ttttgactga tatcaaattc taggtggacc gagattttct ttcagtcttt caaagatatt      60
actctattgc cttctatctt gcatagtttc tg atg aga agt ctg ttg tat ttc       113
                                    Met Arg Ser Leu Leu Tyr Phe
                                        -15                 -10
tta tgt gtt tct tca tat gta aca tct ttt ttc ttt ttt ttt ttt ttt       161
Leu Cys Val Ser Ser Tyr Val Thr Ser Phe Phe Phe Phe Phe Phe Phe
            -5                  1               5
ttt ttt ttt                                                           170
Phe Phe Phe
        10
```

<210> 141
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..395

<221> sig_peptide
<222> 192..236
<223> Von Heijne matrix
score 8
seq FISFLCLIALAGT/SS

<400> 141
```
gattctcagc ttagttgctg ttggtgtata ggagagctac tgatttgtgt acattaattt      60
tgtatccgga aactttgttg aattatttta tcagttctag gagctttttg gaggagtctt     120
tagggttctc taggtataca atcatatcat cagcaaacag tgacaattcg acttcctctt     180
tatggatttg t atg ccc ttt att tct ttc ctt tgt ctg att gct ctg gct      230
             Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala
             -15                 -10                 -5
ggg act tcc agt act atg ttg aga agt gct ctg gct ggg act tcc agt       278
Gly Thr Ser Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser
        1               5                   10
act atg tkg arg aga agt ggt gam agt ggg wat cct kgh ctk gty cma       326
Thr Met Xaa Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa
15                  20                  25                  30
gtc ctm aga ggg aat gct ttc agc ttt ttc cca ttc agt ctg atg twg       374
Val Leu Arg Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa
                35                  40                  45
gct atg ggt tgt cat aga tgg c                                         396
Ala Met Gly Cys His Arg Trp
            50
```

<210> 142
<211> 357

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 292..357

<221> sig_peptide
<222> 292..339
<223> Von Heijne matrix
      score 8
      seq FLLGAIFIALSSS/RI

<400> 142
```
cgtgcctgcg caatgggtgt cgggtccgct ttttcccaat ccggacgtaa tcgtggtttt     60
tgttctgcaa taggcggctt agagggaggg gctttttcgc ctatacctac tgtagcttct    120
ccacgtatgg accctaaagg ctactgctgc tactacgggg ctagacagtt actgtctcag    180
ctctaggatg tgcgttcttc cactagaagc tcttctgagg gaggtaatta aaaaacagtg    240
gaatggaaaa acagtgctgt agtcatcctg taatatgctc cttgtcaaca a atg tat     297
                                                         Met Tyr
                                                             -15
aca ttc ctg cta ggt gcc ata ttc att gct tta agc tca agt cgc atc      345
Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser Arg Ile
                -10                 -5                  1
tta cta gtg aag                                                      357
Leu Leu Val Lys
    5
```

<210> 143
<211> 159
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..157

<221> sig_peptide
<222> 26..151
<223> Von Heijne matrix
      score 7.90000009536743
      seq LVCVCVCVCVCXC/XR

<400> 143
```
tgtgtgtgtg tgtgtctgcg tgtgt atg tgt ttg tgt ccc tgc tgg gat gtg       52
                            Met Cys Leu Cys Pro Cys Trp Asp Val
                                    -40                 -35
ttt act gtg ttt gtg tgt gtc tct gtg tgt gtg tct gtg tct gtc cct      100
Phe Thr Val Phe Val Cys Val Ser Val Cys Val Ser Val Ser Val Pro
        -30                 -25                 -20
gtc ggg atg tat tta gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt stc      148
Val Gly Met Tyr Leu Val Cys Val Cys Val Cys Val Cys Val Cys Xaa
    -15                 -10                 -5
tgc gyg cgt gg                                                       159
Cys Xaa Arg
  1
```

<210> 144
<211> 433
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> 282..431

<221> sig_peptide
<222> 282..383
<223> Von Heijne matrix
      score 7.90000009536743
      seq LFSLLMLTQSPLA/GQ

<221> misc_feature
<222> 132,149
<223> n=a, g, c or t


<400> 144
aaaataaggt atctggcaaa agaatatatg aaagagtatg aagaactctc cttgaaagct      60
gtggccccca ttggccatgg ctgcagagcc gatgtcccgg ccaatccagg cgggatcccc     120
ttgaagcmgg knsmwhbtcy kragscwknc cmabtctccg ggggcaastc ttttcccttc     180
cctgtgaccc kcttcggaca gttgaccatc tcaacaccta gtggttaaaa agaagagcat     240
ggacggcctg ggcctgcac tggctgtgct gggagtttgt c atg ttg ata gct aag      296
                                             Met Leu Ile Ala Lys
                                                             -30
cag gcc cag ccc caa ggc ctc act gcc atc tgc ttc cct ctc aca cct       344
Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys Phe Pro Leu Thr Pro
                -25                 -20                 -15
ctc ttc tcc ctc ctc atg ctc act cag agc ccc ctt gca ggt cag gaa       392
Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro Leu Ala Gly Gln Glu
            -10                 -5                  1
gga aga gaa gga ggg aaa gaa cgg tac ttg ttg gtg att ca                433
Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu Val Ile
    5                   10                  15

<210> 145
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..200

<221> sig_peptide
<222> 15..92
<223> Von Heijne matrix
      score 7.90000009536743
      seq RVCLLSLSLFLWA/NR

<400> 145
aatacgccag gaac atg cta agg acc tgg agc tct cta ccc tgg acc cgt        50
                Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg
                    -25                 -20                 -15
ttt cgg gtt tgc ttg ctc tct ctc tct ctc ttt ctc tgg gct aat cgt        98
Phe Arg Val Cys Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg
                -10                 -5                  1
tta gag gac agt cgc tcc tgc caa cct aat ccc atg agc ctg act acc       146
Leu Glu Asp Ser Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr
        5                   10                  15
ttg ccg ggc cac agg ctc aaa gaa gca gtg tgg ctg cca gca ccc tca       194
Leu Pro Gly His Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser
    20                  25                  30
ctt ggg                                                               200
Leu Gly
35
```

```
<210> 146
<211> 297
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..295

<221> sig_peptide
<222> 80..166
<223> Von Heijne matrix
      score 7.90000009536743
      seq LVVXWLLPXQCSC/ER

<400> 146
aacaccccag cccaagttca tccccggtcc cttggcagca gtgcgcatcc acaaagccag    60
cggcacaatt taattactg atg gcc cct ttc cta cga cag gtg gat rtg tgg    112
                     Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp
                                     -25                 -20
gga gca cag gcc ggt ctg gtg gtb gsm tgg tta cta cca tgs caa tgc     160
Gly Ala Gln Ala Gly Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys
            -15                 -10                 -5
agc tgt gaa cga tca gag caa tat ctg agc acc tgt ctc cca cag cac     208
Ser Cys Glu Arg Ser Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His
        1               5                   10
tca agc atc aag cag tcg tgc atc aag cat cca gca ggc ccg atc ccc     256
Ser Ser Ile Lys Gln Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro
15                  20                  25                  30
gca ggc cac cta cag gga aag gcc aca gct gcg ccc ctg gg              297
Ala Gly His Leu Gln Gly Lys Ala Thr Ala Ala Pro Leu
                35                  40

<210> 147
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..298

<221> sig_peptide
<222> 80..136
<223> Von Heijne matrix
      score 7.90000009536743
      seq WLFLVAILKGVRC/EV

<400> 147
agctctgaga gaggagccca gccctgggat cttcaggtgt tttcactcgg tgatcaggac    60
tgcacagaga gaactcacc atg gag ttt ggg ctg aag tgg ctt ttt ctt gtg    112
                     Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val
                                     -15                 -10
gca att tta aaa ggt gtc cgg tgt gaa gtg aag ctg gtg gag tct ggg     160
Ala Ile Leu Lys Gly Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly
            -5                  1                   5
gga ggc ctg gtg cag ccg ggg ggg tcc ctg aga ctc tcc tgt gta gga     208
Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly
    10                  15                  20
tct gga ttc gtc ttc gat aaa tat ggc ata agt tgg gtg cgc cag gca     256
Ser Gly Phe Val Phe Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala
25                  30                  35                  40
```

cca gga aag ggc cta cag tgg gtc gcg ggg atc ggt ggc ggg gg 300
Pro Gly Lys Gly Leu Gln Trp Val Ala Gly Ile Gly Gly Gly
45 50

<210> 148
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..404

<221> sig_peptide
<222> 21..68
<223> Von Heijne matrix
score 7.90000009536743
seq AMLVLVVSPWSAA/RG

<400> 148
gcggtcttcc agcagggaaa atg gcg ctg gcc atg ctg gtc ttg gtg gtt tcg 53
Met Ala Leu Ala Met Leu Val Leu Val Val Ser
-15 -10
ccg tgg tct gcg gcc cgg gga gtg ctt cga aac tac tgg gag cga ctg 101
Pro Trp Ser Ala Ala Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu
-5 1 5 10
cta cgg aag ctt ccg cag agc cgg ccg ggc ttt ccc agt cct ccg tgg 149
Leu Arg Lys Leu Pro Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp
15 20 25
gga cca gca tta gca gta cag ggc cca gcc atg ttt aca gag cca gca 197
Gly Pro Ala Leu Ala Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala
30 35 40
aat gat acc agt gga agt aaa gag aat tcc agc ctt ttg gac agt atc 245
Asn Asp Thr Ser Gly Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile
45 50 55
ttt tgg atg gca gct ccc aaa aat aga cgc acc att gaa gtt aac cgg 293
Phe Trp Met Ala Ala Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg
60 65 70 75
tgt agg aga aga aat ccg cag aag ctt att aaa gtt aag aac aac ata 341
Cys Arg Arg Arg Asn Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile
80 85 90
gac gtt tgt cct gaa tgt ggt cac ctg aaa cag aaa srt gtc ctt tgt 389
Asp Val Cys Pro Glu Cys Gly His Leu Lys Gln Lys Xaa Val Leu Cys
95 100 105
gct act gct atg aaa a 405
Ala Thr Ala Met Lys
110

<210> 149
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..145

<221> sig_peptide
<222> 56..115
<223> Von Heijne matrix
score 7.80000019073486
seq LLLFPLSLLFTLG/FL

<400> 149

```
aaaccttctg actactaacc tgtagatccc tttagttcct tagcagtatt cacaa atg     58
                                                             Met
                                                             -20
ttt ttc tac tca cac ttt tta ctt ctt ttt ccc ctc tcg tta ctt ttc      106
Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu Phe
                -15                 -10                 -5
aca ctt gga ttt ttg ttt gtc ttt ttt ttt ttt ttt ttt t                146
Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe Phe
            1               5                   10
```

<210> 150
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..407

<221> sig_peptide
<222> 105..242
<223> Von Heijne matrix
score 7.80000019073486
seq LVLLGTRVPLSGG/GP

<400> 150

```
aaacagggcc attggcaaag ctggggtacc agtcacccag ccacgctcta gggtggtagc    60
caagaagacg gaccccgagt gggaggcaga gagacaagag gtgg atg aag cag agc     116
                                                 Met Lys Gln Ser
                                                     -45
aag cgt gas atg gtg aag aga aga cgg agc ccc gcg ctg gga gag gaa      164
Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala Leu Gly Glu Glu
        -40                 -35                 -30
cgc ttc agt ccg agt tcc att ctg cac cca agg ctc ccc ttg gtc ctc      212
Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu Pro Leu Val Leu
    -25                 -20                 -15
ctg gga acc agg gtg ccc ctt agt ggt ggt ggc cca gga gaa ccc gac      260
Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Gly Pro Gly Glu Pro Asp
-10                 -5                  1               5
caa ggc agg agc gcc ccc tcc tgg aag agc ctc gct tca acg cat mat      308
Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala Ser Thr His Xaa
            10                  15                  20
cat tcc cgg ccg gca gca ggg gcg acg cca gca agg cct gcg act cag      356
His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg Pro Ala Thr Gln
        25                  30                  35
agc cag ctt ggc ccg ttc gcc ccg ccc ctt ccc ggt gtc cgc ccc gcc      404
Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly Val Arg Pro Ala
    40                  45                  50
cca t                                                                408
Pro
55
```

<210> 151
<211> 166
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..164

<221> sig_peptide

<222> 69..122
<223> Von Heijne matrix
      score 7.80000019073486
      seq LCVLSLLVSFKSA/CL

<400> 151
```
cacattttct acttaaaagc aamgttacaa agcctgtgga attgctctga cttagaaaga     60
acttgatc atg ctt ttg gag tct cta tgt gtt ctc tct ctg ttg gtt agt     110
         Met Leu Leu Glu Ser Leu Cys Val Leu Ser Leu Leu Val Ser
                     -15                 -10                 -5
ttt aaa tca gcc tgc ctc aca agg gag cct gca ttt gat tcc caa gcc      158
Phe Lys Ser Ala Cys Leu Thr Arg Glu Pro Ala Phe Asp Ser Gln Ala
                1               5                  10
cgc ccg gg                                                           166
Arg Pro
```

<210> 152
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 99..380

<221> sig_peptide
<222> 99..236
<223> Von Heijne matrix
      score 7.80000019073486
      seq LLYLSFAALGVVA/LR

<400> 152
```
ttttacacac acacatacat acacacacac agctaattga gttttaaagt aatattcttg     60
ctaatcccta ctgaattgta gcttggtgtt gtttctga atg gtt ttt gga tat tgg    116
                                          Met Val Phe Gly Tyr Trp
                                              -45
aag cag ccg ctg att acc ctt gca aag aaa tct gta aaa tgt gca cgt      164
Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys Ser Val Lys Cys Ala Arg
-40                 -35                 -30                 -25
gaa tgt ctg aga tgc tct ctc agg cct cta gtc ctt ctg tat ctt tcc      212
Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu Val Leu Leu Tyr Leu Ser
                -20                 -15                 -10
ttt gca gcc ctg ggt gta gta gca ctc agg agt gtt gaa tca ccc ctg      260
Phe Ala Ala Leu Gly Val Val Ala Leu Arg Ser Val Glu Ser Pro Leu
            -5                   1               5
gcc gag acc cac tcc tgc tgg ctc agc ctg ggc atg tgt gtg ctc cag      308
Ala Glu Thr His Ser Cys Trp Leu Ser Leu Gly Met Cys Val Leu Gln
    10                  15                  20
tgt gaa cag cag tgg gtt cca acc cca gtc tcc ttt ctc tgt ggc ctc      356
Cys Glu Gln Gln Trp Val Pro Thr Pro Val Ser Phe Leu Cys Gly Leu
25                  30                  35                  40
tct ggc tcc agc acc atc atc gtt ag                                   382
Ser Gly Ser Ser Thr Ile Ile Val
                45
```

<210> 153
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..207

```
<221> sig_peptide
<222> 10..81
<223> Von Heijne matrix
      score 7.80000019073486
      seq CVYVVCLVSCVLC/VV

<400> 153
tgcaatgtc atg tgt gtt gtg tgc agt gtg cat ggt gtg tgt tgt gta tat      51
          Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr
                          -20                 -15
gtg gtg tgc ctg gtg tcg tgt gtt ttg tgt gtc gtg tgt cct gtg tgt        99
Val Val Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys
-10                 -5                  1               5
tgg gtt atg tgt tgt gtg tgg tgc atc tgt gtg tgt gtg tgg tgt gtc       147
Trp Val Met Cys Cys Val Trp Cys Ile Cys Val Cys Val Trp Cys Val
            10                  15                  20
tgt tgt atg tgt tgt gtg ttg tca tgt gtt gtg tca cat ggg ttg tgt       195
Cys Cys Met Cys Cys Val Leu Ser Cys Val Val Ser His Gly Leu Cys
        25                  30                  35
ggt gtg tca tgg g                                                     208
Gly Val Ser Trp
    40

<210> 154
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..249

<221> sig_peptide
<222> 73..129
<223> Von Heijne matrix
      score 7.80000019073486
      seq WVFLVAVLEVVQC/EI

<400> 154
agagaggagc ctcagcccta gactccaagg cctttccact tggtgatcag cactgagcac      60
agaggactca cc atg gaa ctg ggg ctg tcc tgg gtc ttc ctt gtt gct gtt     111
              Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Val
                              -15                 -10
tta gaa gtt gtc cag tgt gaa att caa ctg att gac gcc ggg gga ggc       159
Leu Glu Val Val Gln Cys Glu Ile Gln Leu Ile Asp Ala Gly Gly Gly
    -5                  1               5                   10
cac gtc cag gcg ggg ggg tca ctg aga ctc tcc tgt gtt gcc tct gac       207
His Val Gln Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Asp
                15                  20                  25
ttc ctg ttt aga agc tat tgg atg acc tgg gtc cgc cat ccg gg            251
Phe Leu Phe Arg Ser Tyr Trp Met Thr Trp Val Arg His Pro
            30                  35                  40

<210> 155
<211> 147
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 24..146
```

<221> sig_peptide
<222> 24..140
<223> Von Heijne matrix
score 7.80000019073486
seq ILLFLFLILFIWH/IR

<400> 155

```
ggattttgtc aaatgctttt tct atg tcg att ttg ctg agg gtt tta ggc ata      53
                          Met Ser Ile Leu Leu Arg Val Leu Gly Ile
                                          -35                 -30
aag gga tgc tgg att ttg tca aat cct ttt tct gca tgt att gag atg      101
Lys Gly Cys Trp Ile Leu Ser Asn Pro Phe Ser Ala Cys Ile Glu Met
            -25                 -20                 -15
atc ttg tta ttt ttg ttt tta att ctg ttt ata tgg cac att cgg g        147
Ile Leu Leu Phe Leu Phe Leu Ile Leu Phe Ile Trp His Ile Arg
        -10                  -5                   1
```

<210> 156
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..141

<221> sig_peptide
<222> 61..135
<223> Von Heijne matrix
score 7.69999980926514
seq LVPILLLIGWIVG/CT

<400> 156

```
gctggataac aaaagaaaga ggtaagcgtg gcctgaccta gccacccacc aacaggaata     60
atg gct gaa aaa gcg ggg tct aca ttt tca cac ctt ctg gtt cct att      108
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25                 -20                 -15                 -10
ctt ctc ctg att ggc tgg att gtg ggc tgc acc                          141
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
                -5                   1
```

<210> 157
<211> 115
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..113

<221> sig_peptide
<222> 12..68
<223> Von Heijne matrix
score 7.69999980926514
seq RLYLWMCLAAALA/SF

<400> 157

```
ctcaagaagc c atg gcg gaa tcc agg ggc cgt ctg tac ctt tgg atg tgc     50
             Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys
                             -15                 -10
ttg gct gct gcg ctg gca tct ttc ctg atg gga ttt atg gtg ggc tgg      98
Leu Ala Ala Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp
     -5                   1                   5                  10
```

```
ttt att aag cct ctg gg                                              115
Phe Ile Lys Pro Leu
                15

<210> 158
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..173

<221> sig_peptide
<222> 54..131
<223> Von Heijne matrix
      score 7.69999980926514
      seq FLLLLYFFXIAVT/HP

<400> 158
caattcaaca tgagatttag tggtgacaaa tatccaaact ctatcaacct cta atg      56
                                                        Met
ctg acc tca ctg cct ttc ctc ctg ccc acc atc agc ttt ctc ctc ctc     104
Leu Thr Ser Leu Pro Phe Leu Leu Pro Thr Ile Ser Phe Leu Leu Leu
-25                 -20                 -15                 -10
ttg tat ttt ttt cma att gct gtc acc cat ccg tca gtt ctc atc aac     152
Leu Tyr Phe Phe Xaa Ile Ala Val Thr His Pro Ser Val Leu Ile Asn
                -5                  1               5
ttc tct ttc tcc ttc ccc aga tc                                      175
Phe Ser Phe Ser Phe Pro Arg
        10

<210> 159
<211> 230
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 121..228

<221> sig_peptide
<222> 121..180
<223> Von Heijne matrix
      score 7.59999990463257
      seq LLFFTCGLPALHG/DS

<221> misc_feature
<222> 18
<223> n=a, g, c or t


<400> 159
aggaggggcc gtcagggngg gatacagcct ggaaggtgcg tgtggggctg ggtctcggag    60
tgggagacgt ggagtgcagg taatgcatgt ccatggtaca caaattcaca aggtttgtaa    120
atg aga aaa gac gtg agg ttc ctt ttg ttc ttt acc tgt ggc ctc cct     168
Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro
-20                 -15                 -10                 -5
gcc cta cac ggg gac tct agg gtg gaa tgt agc aaa gcc cat cca cca     216
Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro
                1                   5                   10
gcc atg tac tac cc                                                  230
Ala Met Tyr Tyr
```

15

<210> 160
<211> 346
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 202..345

<221> sig_peptide
<222> 202..282
<223> Von Heijne matrix
score 7.59999990463257
seq WTLLSISLSVFWS/EP

<400> 160
ttcttctaca tacagctacc caactagccc acaccattta ttgaatacag agtagtcttt 60
tccctgttgg ttatttttct taactttgtt aaagatcaga tatctgtagg tgtgcagctt 120
tatttctggg ttttctgttc cgttccattg gtctatgtgt ctgtttttgt accagtacca 180
tgctgttctg gcaccagtac c atg cta ttt tgg tta cca tct cca tct gag 231
Met Leu Phe Trp Leu Pro Ser Pro Ser Glu
-25 -20
acc act tca gcc tgg act tta ttg tcc ata tca cta tca gta ttt tgg 279
Thr Thr Ser Ala Trp Thr Leu Leu Ser Ile Ser Leu Ser Val Phe Trp
-15 -10 -5
tca gag cca ttc aat aag tct cta gga agt tcc aaa cta cca tgt cat 327
Ser Glu Pro Phe Asn Lys Ser Leu Gly Ser Ser Lys Leu Pro Cys His
1 5 10 15
ttt ttt tct ata aaa cgg g 346
Phe Phe Ser Ile Lys Arg
20

<210> 161
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 194..388

<221> sig_peptide
<222> 194..334
<223> Von Heijne matrix
score 7.59999990463257
seq LXLGEGLTFLCLC/QV

<221> misc_feature
<222> 352
<223> n=a, g, c or t

<400> 161
agtgagagct tagtcttggt actatttgtt tttgtttctt actgtttgtc tgtttatggt 60
tggttgcaag aaaattgtgt tgtaaattat cccttgcttt ctctattagt taatagcctt 120
ccccttctgt agtaaagtaa msagsctttt kcctgttcaa atattttagg cttgtttttt 180
gttttgattg tac atg cct gtg tgt ttt tat tcc tta att tgt ttc ttt 229
Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe
-45 -40
att tat ttc tgt ttg tta tct cca aga gaa aca ata gaa gag gtg gcc 277
Ile Tyr Phe Cys Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala

```
-35                 -30                 -25                 -20
ctc ttc cag ttt tct ctg cth mtc ttg gga gag ggt ctc acc ttt ctt     325
Leu Phe Gln Phe Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu
                -15                 -10                 -5
tgc ctc tgc cag gta atg acg aat aan atg caa ctg ctg ttc ttg agt     373
Cys Leu Cys Gln Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser
            1                   5                   10
ggg gta gtc tgt ggg                                                 388
Gly Val Val Cys Gly
    15
```

<210> 162
<211> 235
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 172..234

<221> sig_peptide
<222> 172..210
<223> Von Heijne matrix
      score 7.5
      seq MAPLLLSLSCSFS/CH

<400> 162

```
cccctccaaa tctcatgttg agatttgatc cctaatgttg gagatggggc ctggtgggag      60
atattcggat catgagggca gatccctcac taatggcctg gtgccctccc tgtggaaatg     120
agtaagttct cactcttttg gttcacctga gagctgtttg tttaaaagag c atg gca      177
                                                         Met Ala
ccc ctc ctt ctc tct ctg tct tgc tcc ttt tct tgc cat gtg aca ctc       225
Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val Thr Leu
    -10                 -5                  1               5
ctg ccc cgg g                                                         235
Leu Pro Arg
```

<210> 163
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 99..239

<221> sig_peptide
<222> 99..158
<223> Von Heijne matrix
      score 7.5
      seq LLWVLLLNLGPRA/AG

<400> 163

```
aaaacgaccc ggtgggtcta cagcggaagg gagggagcga aggtaggagg cagggcttgc      60
ctcactggcc accctcccaa ccccaagagc ccagcccc atg gtc ccc gcc gcc ggs     116
                                          Met Val Pro Ala Ala Gly
                                          -20                 -15
gcg ctg ctg tgg gtc ctg ctg ctg aat ctg ggt ccc cgg gcg gcg ggg       164
Ala Leu Leu Trp Val Leu Leu Leu Asn Leu Gly Pro Arg Ala Ala Gly
                -10                 -5                  1
gcc caa ggc ctg acc cag act ccg acc gaa atg cag cgg gtc agt tta       212
Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu Met Gln Arg Val Ser Leu
        5                   10                  15
```

```
cgc ttt ggg ggc ccc atg acc cgc agg g                                    240
Arg Phe Gly Gly Pro Met Thr Arg Arg
    20                  25

<210> 164
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..193

<221> sig_peptide
<222> 20..91
<223> Von Heijne matrix
      score 7.5
      seq LISELLLLRSVTS/HN

<400> 164
ttctgattat gatggtaat atg gta ttc tgg gaa ata tct gtc caa att atc      52
                     Met Val Phe Trp Glu Ile Ser Val Gln Ile Ile
                                     -20                 -15
ctg atc tct gaa ctc ctg ctg ttg agg tca gtc act tca cac aat acc      100
Leu Ile Ser Glu Leu Leu Leu Leu Arg Ser Val Thr Ser His Asn Thr
            -10                 -5                  1
atg atg aga gct tta tca agc cag atg ctt agt cag agc ttt cca aga      148
Met Met Arg Ala Leu Ser Ser Gln Met Leu Ser Gln Ser Phe Pro Arg
    5                   10                  15
ccc agc ttt ggt ttt atc agc aaa atc cat cct tcc cac ccc ccc aa       195
Pro Ser Phe Gly Phe Ile Ser Lys Ile His Pro Ser His Pro Pro
20                  25                  30

<210> 165
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..255

<221> sig_peptide
<222> 34..186
<223> Von Heijne matrix
      score 7.5
      seq VVSLTFLLGMTWG/FA

<221> misc_feature
<222> 18
<223> n=a, g, c or t


<400> 165
tatttatgtg acctgtgngg gtattttgga gtc atg ttt ttt ctg aac att gcc      54
                                      Met Phe Phe Leu Asn Ile Ala
                                              -50                 -45
atg ttc att gtg gta atg gtg cag atc tgt ggg agg aat ggc aag aga      102
Met Phe Ile Val Val Met Val Gln Ile Cys Gly Arg Asn Gly Lys Arg
                -40                 -35                 -30
agc aac cgg acc ctg aga gaa gaa gtg tta agg aac ctg cgc agt gtg      150
Ser Asn Arg Thr Leu Arg Glu Glu Val Leu Arg Asn Leu Arg Ser Val
            -25                 -20                 -15
```

```
gtt agc ttg acc ttt ctg ttg ggc atg aca tgg ggt ttt gca ttc ttt      198
Val Ser Leu Thr Phe Leu Leu Gly Met Thr Trp Gly Phe Ala Phe Phe
        -10                 -5                  1
gcc tgg gga ccc tta aat atc ccc ttc atg tac ctc ttc tcc atc ttc      246
Ala Trp Gly Pro Leu Asn Ile Pro Phe Met Tyr Leu Phe Ser Ile Phe
5                   10                  15                  20
aat tca tta c                                                        256
Asn Ser Leu
```

<210> 166
<211> 209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..209

<221> sig_peptide
<222> 36..86
<223> Von Heijne matrix
score 7.5
seq FLFLFLLXXLIVA/VT

<400> 166

```
cttttttdtc ckgcacaagg gatttccggg tcagg atg aac aaa cac ttc ttg        53
                                       Met Asn Lys His Phe Leu
                                                   -15
ttc ctc ttc ctc ctt dac kgc ctc att gtg gca gtg aca tca ctt cag      101
Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val Ala Val Thr Ser Leu Gln
    -10                 -5                  1                   5
tgc ata aca tgc cac ctt cgc aca cgg aca gac cgc tgt aga aga ggc      149
Cys Ile Thr Cys His Leu Arg Thr Arg Thr Asp Arg Cys Arg Arg Gly
                10                  15                  20
ttt ggt gdc tgt act gct cag aag ggc gag gca tgc atg ctc tta agg      197
Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu Ala Cys Met Leu Leu Arg
            25                  30                  35
att cac cag cgc                                                      209
Ile His Gln Arg
        40
```

<210> 167
<211> 184
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..184

<221> sig_peptide
<222> 44..148
<223> Von Heijne matrix
score 7.5
seq LLLTSHFLGESLG/GG

<400> 167

```
taaagtcctg tgtatgacat gacatagtat ttgcgtaatt taa atg tac ata aag       55
                                                Met Tyr Ile Lys
                                                -35
atg gag tct gtc acc ttg tca cca gcc cca gtc ttc ccc gtc cct gca      103
Met Glu Ser Val Thr Leu Ser Pro Ala Pro Val Phe Pro Val Pro Ala
    -30                 -25                 -20
```

```
car ctc ctt tta ctg aca tcc cat ttt cta ggc gag tcc ctt ggt gga      151
Gln Leu Leu Leu Leu Thr Ser His Phe Leu Gly Glu Ser Leu Gly Gly
-15                 -10                 -5                  1
ggc aca ctg ctt gtc cca ctc ctc ccc cca ggg                          184
Gly Thr Leu Leu Val Pro Leu Leu Pro Pro Gly
            5                   10

<210> 168
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 97..216

<221> sig_peptide
<222> 97..177
<223> Von Heijne matrix
      score 7.40000009536743
      seq ILLLTICAAGIXG/TR

<400> 168
ccttccctcc gcgcacaggc tgccggctca ccgcttgcta atggcagccg gggtctccct     60
gggacagcaa gacctccgct caggcccctc tttcga atg ckc cam gcm ctc ctg      114
                                        Met Xaa Xaa Ala Leu Leu
                                                -25
cga tct aga atg att cag ggc agg atc ctg ctc ctg acc atc tgc gct      162
Arg Ser Arg Met Ile Gln Gly Arg Ile Leu Leu Leu Thr Ile Cys Ala
    -20                 -15                 -10
gcc ggc att rgt ggg act cgt cag ttt ggc tat aac ctc tct atc atc      210
Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly Tyr Asn Leu Ser Ile Ile
-5                  1               5                   10
aat gac cc                                                           218
Asn Asp

<210> 169
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 317..478

<221> sig_peptide
<222> 317..457
<223> Von Heijne matrix
      score 7.40000009536743
      seq SCLFSXAWLXCXC/HG

<400> 169
gtctcgtggg ctggtcccca gcggctccct ccccgaacag ctgctgctcc agggaggaag     60
cggcgyrrgt gmtgtccagc ttcccggtgc tgaaaaccgg agggctcgtc atccaccact    120
accatgtaag ggccatgaga agggctcatc ctggcgcasg cggacatgga ggaggactta    180
ttccagctaa ggcagctgcc ggttgtgaaa ttccgtcgca caggcgagag tgcaaggtca    240
gaggacgaca cggcttcagg agagcatgaa gtccagattg aaggggtcca cgtgggccta    300
gaggctgtgg agctgg atg atg ggg cak ctg tgc cca agg agt ttg cca atc    352
                  Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile
                          -45                 -40
cca ccg atg ata ctt tca tgg tgg aag atg cag tgg aag cca ttg gct      400
Pro Pro Met Ile Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala
-35                 -30                 -25                 -20
```

```
ttg gaa aat ttc agt gga agc tgt ctg ttc tca mtg gct tgg ctt kga     448
Leu Glu Asn Phe Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa
                -15                 -10                 -5
tgc tsa tgc cat gga gat gat gat ctc agc at                          480
Cys Xaa Cys His Gly Asp Asp Asp Leu Ser
            1               5

&lt;210&gt; 170
&lt;211&gt; 280
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 135..278

&lt;221&gt; sig_peptide
&lt;222&gt; 135..179
&lt;223&gt; Von Heijne matrix
      score 7.40000009536743
      seq LLQLLAFSFLGNS/VE

&lt;221&gt; misc_feature
&lt;222&gt; 104
&lt;223&gt; n=a, g, c or t


&lt;400&gt; 170
ttctttgggc tcgggggctc ccggagcagg gcgagagctc gcgtcgccgg aaaggaagac    60
gggaagaaag ggcaggcggc tcggcgggcg tcttctccac tccntgccgc gccccgtggc   120
tgcagggagc cggc atg ggg ctt ctc cag ttg cta gct ttc agt ttc tta     170
                Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu
                -15                 -10                 -5
ggt aat tcc gtg gaa acg gtg cgg gga ggc gga cgg act tgg gca tgg     218
Gly Asn Ser Val Glu Thr Val Arg Gly Gly Gly Arg Thr Trp Ala Trp
            1               5                   10
gga agg aaa acc caa aag ctg ctt gct cac ctt cgt ggg atc ctg ggg     266
Gly Arg Lys Thr Gln Lys Leu Leu Ala His Leu Arg Gly Ile Leu Gly
    15                  20                  25
gct tgg gas agg ga                                                  280
Ala Trp Xaa Arg
30

&lt;210&gt; 171
&lt;211&gt; 103
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 28..102

&lt;221&gt; sig_peptide
&lt;222&gt; 28..69
&lt;223&gt; Von Heijne matrix
      score 7.40000009536743
      seq LVLVHSSLSKTLS/QK

&lt;400&gt; 171
actgggatgc agaggctgca gtgagcc atg ttg gtg ctg gtg cac tcc agc ctg    54
                              Met Leu Val Leu Val His Ser Ser Leu
                                                  -10
agc aag acc ttg tct cag aaa aaa aaa aag ttc aca aas ccc acc agg g   103
```

```
Ser Lys Thr Leu Ser Gln Lys Lys Lys Lys Phe Thr Xaa Pro Thr Arg
-5                  1                   5                   10

&lt;210&gt; 172
&lt;211&gt; 218
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 73..216

&lt;221&gt; sig_peptide
&lt;222&gt; 73..129
&lt;223&gt; Von Heijne matrix
      score 7.40000009536743
      seq LILVISCLLLAFE/CV

&lt;400&gt; 172
caattttgtt gatcttttca aaaaaccagc tcctggattc attaattttt tgaagggttt    60
tttgatgtct ct atg tcc ttc agt tct gct ctg att tta gtt att tct tgc   111
              Met Ser Phe Ser Ser Ala Leu Ile Leu Val Ile Ser Cys
                              -15                 -10
ctt ctg cta gct ttt gaa tgt gtt tgc tct tgc ttt tct ggt tct ttt      159
Leu Leu Leu Ala Phe Glu Cys Val Cys Ser Cys Phe Ser Gly Ser Phe
    -5                  1               5                   10
aat tgt gat gtt agg gtg tca att tcg gat ctt tcc tgc ttt ctc ttg      207
Asn Cys Asp Val Arg Val Ser Ile Ser Asp Leu Ser Cys Phe Leu Leu
                15                  20                  25
tgg ggc aag gg                                                       218
Trp Gly Lys

&lt;210&gt; 173
&lt;211&gt; 380
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 295..378

&lt;221&gt; sig_peptide
&lt;222&gt; 295..360
&lt;223&gt; Von Heijne matrix
      score 7.40000009536743
      seq CLXVFLLTDRTLS/CR

&lt;400&gt; 173
tattggttat tctagttata cattagtcta aatttttttc aaagttttca acttctttgc    60
ctttggtttg aatttcctcc tgtagcttgg agtagtttga tcatctgaag ctttcttctc   120
tcaactcatc aaagtcattc tccatccagc tttgttccat tgctggtgag gaactgtgtt   180
ccttcggagg aggagaggtg ctctgctttt ttgagtttcc agtttttctg ctctgttttt   240
tccccatctt tgtggtttta tctacttttg gtctttgatg ctggtgatgt acag atg      297
                                                            Met
ggt ttt tgg tgt gga tgt cct ttc tgt ttg twa gtt ttc ctt cta aca      345
Gly Phe Trp Cys Gly Cys Pro Phe Cys Leu Xaa Val Phe Leu Leu Thr
    -20                 -15                 -10
gac agg acc ctc agc tgc agg tct gtt gga gtt gc                       380
Asp Arg Thr Leu Ser Cys Arg Ser Val Gly Val
-5                  1                   5

&lt;210&gt; 174
&lt;211&gt; 139
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..139

<221> sig_peptide
<222> 59..103
<223> Von Heijne matrix
      score 7.30000019073486
      seq LLSLSLWGISTLS/ST

<400> 174
ataacagaat gatttacatt cctttgggta tatacccagt gatgggatat atgtgtca        58
atg gta tta ctg tct tta agt ctt tgg ggc atc tcc aca ctg tct tcc      106
Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser
-15                 -10                 -5                  1
aca aca att gaa cta att tac acc ccc atc ggg                          139
Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly
            5                   10

<210> 175
<211> 122
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..121

<221> sig_peptide
<222> 38..112
<223> Von Heijne matrix
      score 7.30000019073486
      seq LLHVHSFLPPVFS/TQ

<400> 175
ctacctgtcc ttgcgcacca cccttgtctg ggccttc atg gcc tct ctc ctg agt      55
                                         Met Ala Ser Leu Leu Ser
                                         -25                 -20
ggc ttt act agc ttc tgt ctt ttg cac gtt cac tct ttc ctc cct cca      103
Gly Phe Thr Ser Phe Cys Leu Leu His Val His Ser Phe Leu Pro Pro
                -15                 -10                 -5
gtg ttt tcc acc cag aat g                                            122
Val Phe Ser Thr Gln Asn
            1

<210> 176
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 175..300

<221> sig_peptide
<222> 175..264
<223> Von Heijne matrix
      score 7.30000019073486
      seq AILLXXWEAGSEA/VR
```

```
<221> misc_feature
<222> 51..52,63,239
<223> n=a, g, c or t


<400> 176
aaaaactcta aaagaaggac gcattttagg taagatctag tggctagatc nncagggtgg      60
gcnkcgttct tgtggaaatc agtcaagaaa gatcggattc gcggttattt atgcaaatca     120
tctgggtgga ttgtgtacgg agttaaactg cgccttctgg accgggtctg aaca atg       177
                                                            Met
                                                            -30
gag act gcg cta saa tka acg cca cag aaa agg caa gtt atg ttt ctt       225
Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe Leu
                -25                 -20                 -15
gct ata ttg ttg cnt twg tgg gag gct ggc tct gag gca gth agg tat       273
Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg Tyr
            -10                 -5                  1
tcc ata cca gaa gaa aca gaa agt ggc                                   300
Ser Ile Pro Glu Glu Thr Glu Ser Gly
    5                   10

<210> 177
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 268..465

<221> sig_peptide
<222> 268..372
<223> Von Heijne matrix
      score 7.30000019073486
      seq LDLLGSSSPPTSA/SQ

<400> 177
cttaaacttt attatgttgk kttcacaaag agcagccttt gttgactttg aaatcattgc      60
ttcagtattc tagaaaatct tgtttttgtt aaacatgggc agtaacttac tatttttgta     120
tagttgttgt wcatcktacc cccaccctgt tttaaaaata aaaagtagtt gtcagattac     180
tttggcttta gaagtacctt ttcacttgcc ttagaatctt cattactttg agcctacact     240
ccacctctta ttggaacttc atgaaga atg atg ttg gat ttc gct ctg tcg ccc     294
                              Met Met Leu Asp Phe Ala Leu Ser Pro
                              -35                 -30
agg cta gag cgc agt ggt ctg atc atg gct tgc tgt acc ctt gac ctc       342
Arg Leu Glu Arg Ser Gly Leu Ile Met Ala Cys Cys Thr Leu Asp Leu
    -25                 -20                 -15
ctg ggt tca agc agt cct ccc acc tca gcc tcc cag gtg gct ggg act       390
Leu Gly Ser Ser Ser Pro Pro Thr Ser Ala Ser Gln Val Ala Gly Thr
-10                 -5                  1               5
ggg cat gtg cca cca cac cca gct agt ttt ttt tac ttt ktt gta wga       438
Gly His Val Pro Pro His Pro Ala Ser Phe Phe Tyr Phe Xaa Val Xaa
            10                  15                  20
cag gtc tac tat gtt tcg cag ctg atc t                                 466
Gln Val Tyr Tyr Val Ser Gln Leu Ile
        25                  30

<210> 178
<211> 222
<212> DNA
<213> Homo sapiens

<220>
```

```
<221> CDS
<222> 30..221

<221> sig_peptide
<222> 30..95
<223> Von Heijne matrix
      score 7.19999980926514
      seq QVFFLVFPDGVRP/QP

<400> 178
acgtcggacc cggaggccct gaatgcccc atg cgc acc cca cag ctc gcg ctc        53
                                Met Arg Thr Pro Gln Leu Ala Leu
                                        -20                 -15
ctg caa gtg ttc ttt ctg gtg ttc ccc gat ggc gtc cgg cct cag ccc       101
Leu Gln Val Phe Phe Leu Val Phe Pro Asp Gly Val Arg Pro Gln Pro
                -10                 -5                  1
tct tcc tcc cca tca ggg gca gtg ccc acg tct ttg gag ctg cag cga       149
Ser Ser Ser Pro Ser Gly Ala Val Pro Thr Ser Leu Glu Leu Gln Arg
        5                   10                  15
ggg acg gat ggc gga acc ctc cag tcc cct tca gag gcg act gca act       197
Gly Thr Asp Gly Gly Thr Leu Gln Ser Pro Ser Glu Ala Thr Ala Thr
    20                  25                  30
cgc ccg gcc gtg ccc gga ctc cgg g                                     222
Arg Pro Ala Val Pro Gly Leu Arg
35                  40

<210> 179
<211> 171
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 33..170

<221> sig_peptide
<222> 33..95
<223> Von Heijne matrix
      score 7.19999980926514
      seq SWPLLAAVSGLRG/LE

<400> 179
cctttgcct tcaaccttcg agccgccacg ta atg cca cgt ccc cgc gca tgc        53
                                   Met Pro Arg Pro Arg Ala Cys
                                       -20                 -15
gca tct tgg ccg ctg ctg gcg gct gtt tcc ggg ctt aga ggg ctg gag       101
Ala Ser Trp Pro Leu Leu Ala Ala Val Ser Gly Leu Arg Gly Leu Glu
                -10                 -5                  1
tgg ccg ccg agt tgg agg cgg gtg gtg gca gca gta gga gtg tgt aga       149
Trp Pro Pro Ser Trp Arg Arg Val Val Ala Ala Val Gly Val Cys Arg
        5                   10                  15
gtg cgg gat tgg ggg ccc cgg g                                         171
Val Arg Asp Trp Gly Pro Arg
    20                  25

<210> 180
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 177..245
```

```
<221> sig_peptide
<222> 177..227
<223> Von Heijne matrix
      score 7.19999980926514
      seq FLLLISVLTVIWF/WK

<400> 180
tgtaattttc cttgccaaaa agcttagttt catcttttat aaatatccta taatgccaag     60
ttgattgcat ggtcagagtg aatctgtgct gtacccawat tcagtagcct tctcctatcc    120
aacaaagtgt tttgtaaata ggaggtaaat gaatgagtgg atggatggag ggatga atg    179
                                                              Met
aat gga att ttc ttg ctc ttg atc tct gtc tta aca gtg att tgg ttt      227
Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp Phe
    -15                 -10                 -5
tgg aag aca cac ccg ggg                                              245
Trp Lys Thr His Pro Gly
1               5

<210> 181
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..240

<221> sig_peptide
<222> 160..213
<223> Von Heijne matrix
      score 7.19999980926514
      seq XLLCIIXLYLIRG/SE

<400> 181
gttgactttt ctctctgctg aggcagaaaa atgcttccat agtccatgca gcaatgttta     60
aaacaaggga tttcgttccc ccctcvcctt ttgtgtaggc tggttaataa actctgtgtt    120
tywtagcatt gtcgtgaawa ttcagagtgc tccctgcga atg gtt ttc cta gta       174
                                           Met Val Phe Leu Val
                                                           -15
kct ctg ttg tgt atc att kct ctt tat ttg att cgt ggt tct gag tgg      222
Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile Arg Gly Ser Glu Trp
            -10                 -5                  1
amc cta cca ccg aac tgg g                                            241
Xaa Leu Pro Pro Asn Trp
    5

<210> 182
<211> 263
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..261

<221> sig_peptide
<222> 103..156
<223> Von Heijne matrix
      score 7.19999980926514
      seq LFFLLRIALASWA/LF

<400> 182
```

```
gggttatcta acctgttcca ttgttccgtg tatcagtttc tgtaccgata ccatgctgtt     60
ttggttactg tagtcttgta gtatagttta aagtcagata gc atg atg act cta       114
                                               Met Met Thr Leu
                                                           -15
gct ttg ttc ttt ttg ctt agg att gct ttg gct agt tgg gct ctc ttt      162
Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser Trp Ala Leu Phe
                -10                 -5                  1
tgg atc cat atg aat ttt aga aga gct ttt ttc cac tta cgg tgg ttt      210
Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His Leu Arg Trp Phe
            5                   10                  15
gat atc aat agc act gaa tct gta aat tgc ttt ggg cag tat ggc cta      258
Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly Gln Tyr Gly Leu
    20                  25                  30
gcg gg                                                               263
Ala
35

<210> 183
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 60..170

<221> sig_peptide
<222> 60..146
<223> Von Heijne matrix
      score 7.09999990463257
      seq SLLVFCLNDLSNA/VX

<400> 183
ttccatgtgg agatgrraag aatatatatt ctgtggttat tgggtagagt gttctatag      59
atg tct att agg tct aat tgg tct agt gtc gaa tct aag tct aga att      107
Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile
                -25                 -20                 -15
tct tta tta gtt ttc tgc ctc aat gat ctw tck aat gcw gtc arg wgg      155
Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa
            -10                 -5                  1
ggm att gaa rtc ccc                                                  170
Gly Ile Glu Xaa Pro
    5

<210> 184
<211> 443
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..442

<221> sig_peptide
<222> 83..130
<223> Von Heijne matrix
      score 7.09999990463257
      seq IPLFLGVLAYCTG/SV

<400> 184
ctttccagca aggggataag agaggcctgg aagaacctgc ccagcctggg cctcaggaag     60
cagcatcgga ggtgcctcag cc atg gca tgg atc cct ctc ttc ctc ggc gtc     112
                         Met Ala Trp Ile Pro Leu Phe Leu Gly Val
```

```
                              -15                 -10
ctt gct tac tgc aca gga tcc gtg gcc tcc tat gag ctg act cac cca      160
Leu Ala Tyr Cys Thr Gly Ser Val Ala Ser Tyr Glu Leu Thr His Pro
    -5                  1               5                   10
ccc tca gtg tcc gtg tcc cca gga cag aca gcc agc atc acc tgc tct      208
Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser
                15                  20                  25
gga gat aaa ttg ggg gat aaa tat gct tgc tgg tat cag cag aag cca      256
Gly Asp Lys Leu Gly Asp Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro
            30                  35                  40
ggc cag tcc cct gtg ctg gtc atc tat caa gat agc aag cgg ccc tca      304
Gly Gln Ser Pro Val Leu Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser
        45                  50                  55
ggg atc cct gag cga ttc tct ggc tcc aac tct ggg aac aca gcc act      352
Gly Ile Pro Glu Arg Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr
    60                  65                  70
ctg acc atc agc ggg acc cag gct atg gat gag gct gac tat tac tgt      400
Leu Thr Ile Ser Gly Thr Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys
75                  80                  85                  90
cag gcg tgg gac agc agc act gtg gta ttc ggc gga ggg acc a            443
Gln Ala Trp Asp Ser Ser Thr Val Val Phe Gly Gly Gly Thr
                95                  100
```

<210> 185
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 332..427

<221> sig_peptide
<222> 332..418
<223> Von Heijne matrix
score 7.09999990463257
seq FCFXLCFGRSSLC/CR

<400> 185

```
taagtttata yhtctgaatc tgaaatcaga atatatatat ttaatttttc aattttaaaa     60
atgttaccct gtgtgagaca aaacaaaaca gtgactagaa ccctccttgt gggctaaatt    120
tgagtttgct tcttcataat gttttaaatg cttcacaaac atttttcttt ggtatattga    180
gcaaaatgaa ttgaagtata tttactgagt gatgattatt gaggaaaaac tcaaagatct    240
gctgtaagca ctagagttga aggactagcc caacagctcc tcaggcacct ttgggtatat    300
tgagttgccc cccctgactt tgaacacatc t atg gtc tgt gtc atc ttc aaa       352
                                   Met Val Cys Val Ile Phe Lys
                                                       -25
gag ctc atg gaa ttt gaa ttc cct ggg ttt tgt ttt tgh ctt tgt ttt      400
Glu Leu Met Glu Phe Glu Phe Pro Gly Phe Cys Phe Xaa Leu Cys Phe
        -20                 -15                 -10
gga cgg agc tcg ctc tgt tgc cga rac                                  427
Gly Arg Ser Ser Leu Cys Cys Arg Xaa
    -5                  1
```

<210> 186
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 130..363

<221> sig_peptide
<222> 130..219
<223> Von Heijne matrix
score 7.09999990463257
seq SCLALXTLAVVYA/AL

<400> 186
```
aacgagtctt tgggaacgtg gtccacccag ggatgtaaaa ctgtgcttac cgatgcatcc    60
catacgaaat gcttatgtga tcgtctctct accttcgcca ttttggctca gcaacctaga   120
gaaataatc atg gaa tcc tct ggc aca cct tca gtt acc cta ata gta ggc   171
          Met Glu Ser Ser Gly Thr Pro Ser Val Thr Leu Ile Val Gly
          -30                 -25                 -20
agt ggt ctt tct tgc ttg gcc ttg atb acc cta gca gtt gtc tat gca     219
Ser Gly Leu Ser Cys Leu Ala Leu Xaa Thr Leu Ala Val Val Tyr Ala
    -15                 -10                 -5
gca tta tgg mgg tac ata cgc tct gag aga tcc ata ata cta att aac     267
Ala Leu Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile Ile Leu Ile Asn
1               5                   10                  15
ttc tgc ctg tct atc atc tca tcc aat atc ctc ata ctg gtt gga cag     315
Phe Cys Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile Leu Val Gly Gln
            20                  25                  30
act cag aca cat aat aaa gag tat ctg cac aac cac cac tgc att ttt     363
Thr Gln Thr His Asn Lys Glu Tyr Leu His Asn His His Cys Ile Phe
        35                  40                  45
gc                                                                  365
```

<210> 187
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 86..259

<221> sig_peptide
<222> 86..178
<223> Von Heijne matrix
score 7.09999990463257
seq LXFLASSFCFGEA/DS

<221> misc_feature
<222> 143
<223> n=a, g, c or t

<400> 187
```
ttttggaaca gggtaggcat tttgtttatt gtttgcttgc ttctaggtgt tttcgccatc    60
agggtgtatt ggaggctgac actta atg ggt gtg tgt tgc gcc cag aac tgc     112
                            Met Gly Val Cys Cys Ala Gln Asn Cys
                                -30                 -25
tcg gtg tcg ggg ktc waa agr aat gcg ctg ntg ttc ttg gct tca agt     160
Ser Val Ser Gly Xaa Xaa Arg Asn Ala Leu Xaa Phe Leu Ala Ser Ser
        -20                 -15                 -10
ttc tgc ttt gga gaa gca gat tca gga agt agg tgt tgc tta aaa ata     208
Phe Cys Phe Gly Glu Ala Asp Ser Gly Ser Arg Cys Cys Leu Lys Ile
    -5                  1               5                   10
att ctt ggt ttt tat cta atc aga tat tca ttg att acc tac cag gtg     256
Ile Leu Gly Phe Tyr Leu Ile Arg Tyr Ser Leu Ile Thr Tyr Gln Val
                15                  20                  25
cgt g                                                               260
Arg
```

<210> 188
<211> 172
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..171

<221> sig_peptide
<222> 52..105
<223> Von Heijne matrix
      score 7.09999990463257
      seq LFFFLKWSHPGWS/AT

<221> misc_feature
<222> 112
<223> n=a, g, c or t

<400> 188
```
ttaatggaat atattatagt acactagcat gctggaaaga atgaaaataa t atg aaa       57
                                                         Met Lys
att ctt tac ctt ttt ttc ttt ttg aaa tgg agt cac cca ggc tgg agt       105
Ile Leu Tyr Leu Phe Phe Phe Leu Lys Trp Ser His Pro Gly Trp Ser
    -15                 -10                 -5
gca acg ncg tgg tct tgg cac act gca acc tcc gcc tcc ctg att caa       153
Ala Thr Xaa Trp Ser Trp His Thr Ala Thr Ser Ala Ser Leu Ile Gln
1               5                   10                  15
gtg att ctc ccg cct tgg g                                             172
Val Ile Leu Pro Pro Trp
            20
```

<210> 189
<211> 150
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..148

<221> sig_peptide
<222> 47..124
<223> Von Heijne matrix
      score 7.09999990463257
      seq LFLSGCFLFLSXC/XI

<400> 189
```
tatcacwtct aagagatttc tggtgaaact tgtggatttt ctatac atg aca cca        55
                                                   Met Thr Pro
                                                       -25
tgt ttt ctg caa atg gac aat ttg act cct ctt ttc cta tct gga tgc       103
Cys Phe Leu Gln Met Asp Asn Leu Thr Pro Leu Phe Leu Ser Gly Cys
            -20                 -15                 -10
ttt tta ttt ctc tct cwt tgc wtg att tat ttg gct agg att ttg gg        150
Phe Leu Phe Leu Ser Xaa Cys Xaa Ile Tyr Leu Ala Arg Ile Leu
        -5                  1               5
```

<210> 190
<211> 339
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 195..338

<221> sig_peptide
<222> 195..314
<223> Von Heijne matrix
      score 7
      seq ITCKLCLCEQSXG/QD

<400> 190
agtcttgcaa agtgtaaagc tgtcagccgc agagcacgga ggaaagacgg agagaatgga      60
agagctcctg tccggtgtgc cagcagcccg gactggcggt gagcgcgagg gaggctackg     120
agaagcccgg cgacggagga acgcaggtct gctgccaggg attgaggaga ctgaagaacg     180
ctgaagacag gctg atg ggc tca gct ggt agg ctc cac tat ctc gsc atg       230
                Met Gly Ser Ala Gly Arg Leu His Tyr Leu Xaa Met
                -40                 -35                 -30
act gct gaa aat ccc act cct gga gac ctg gct ccg kcc ccc ctc atc       278
Thr Ala Glu Asn Pro Thr Pro Gly Asp Leu Ala Pro Xaa Pro Leu Ile
            -25                 -20                 -15
act tgc aaa ctc tgc ctg tgt gag cag tct crt gga caa gat gac cac       326
Thr Cys Lys Leu Cys Leu Cys Glu Gln Ser Xaa Gly Gln Asp Asp His
        -10                 -5                  1
act cca gga atg c                                                     339
Thr Pro Gly Met
5

<210> 191
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..359

<221> sig_peptide
<222> 96..242
<223> Von Heijne matrix
      score 7
      seq VTVLLSAAPCLLS/CF

<221> misc_feature
<222> 340
<223> n=a, g, c or t


<400> 191
tacaagagtt tttgctgaaa gttttaagtt gataagatgc agagaattgg gggaatgtat      60
aataaatcag gtttcattgt tatattattt accac atg aat cac ctt cct cct        113
                                       Met Asn His Leu Pro Pro
                                                           -45
aac cat tat agg mgc cat gtg ttc aca tgt cat gtg gac cag tat tta       161
Asn His Tyr Arg Xaa His Val Phe Thr Cys His Val Asp Gln Tyr Leu
            -40                 -35                 -30
act gtg gaa acc gcg ggt ggc atg gag aag gag gca gtg tcc gtg act       209
Thr Val Glu Thr Ala Gly Gly Met Glu Lys Glu Ala Val Ser Val Thr
        -25                 -20                 -15
gtg ctg ctc tcc gca gcc ccc tgc ctg ctg tcc tgt ttc ctc ggc tcc       257
Val Leu Leu Ser Ala Ala Pro Cys Leu Leu Ser Cys Phe Leu Gly Ser
    -10                 -5                  1               5
tcg gtg tct gga ctg gcg ttc tgg gtt tcc cag cag aaa act aaa ggg       305
```

```
Ser Val Ser Gly Leu Ala Phe Trp Val Ser Gln Gln Lys Thr Lys Gly
                10                  15                  20
cca gag agg tgt aaa aac aca cac cac tbg gca gnt aat aat ttc ccc      353
Pro Glu Arg Cys Lys Asn Thr His His Xaa Ala Xaa Asn Asn Phe Pro
            25                  30                  35
gcg agg                                                              359
Ala Arg

<210> 192
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..263

<221> sig_peptide
<222> 138..257
<223> Von Heijne matrix
      score 7
      seq FLFMLPLWCSIGT/CT

<400> 192
ttgagcttaa ggccaggtat atgggctcac acttgtaatc tcagtgcttt gggaggctga     60
gggaaaagga tagcttgagt ccaggagttc gagatcatcc tgggcaacat agcaagatcc    120
tgtctctaca aaaccta atg aac aaa att aaa gaa aac aca cac aca cac       170
                   Met Asn Lys Ile Lys Glu Asn Thr His Thr His
                   -40                 -35                 -30
aca cac aca cac aca cac aaa aac aac acc aaa cta gtg tca aac cta      218
Thr His Thr His Thr His Lys Asn Asn Thr Lys Leu Val Ser Asn Leu
                -25                 -20                 -15
ttc ctt ttt atg tta cct ctc tgg tgc tcc att ggc act tgc aca g        264
Phe Leu Phe Met Leu Pro Leu Trp Cys Ser Ile Gly Thr Cys Thr
            -10                  -5                   1

<210> 193
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..299

<221> sig_peptide
<222> 147..272
<223> Von Heijne matrix
      score 7
      seq LFLYSLFTENVLA/HP

<400> 193
tgtattgttt mmmttattta ctagtatgca gatctggttt tcattctttt catattgaat     60
ttcgttatgg gtagaatcat ttgcaaacat ttctagacat ttttaaagat ctatttaatt    120
tgtttaagaa tggaaaacat aaaata atg cat gat tct tca ggc aag aat aat     173
                             Met His Asp Ser Ser Gly Lys Asn Asn
                                         -40                 -35
ttc aga aag ata cct gtt gta aat tta att tat ctc tat gta gac ata      221
Phe Arg Lys Ile Pro Val Val Asn Leu Ile Tyr Leu Tyr Val Asp Ile
            -30                 -25                 -20
cat ata cat aaa tta ttt tta tat agt ctc ttt aca gaa aat gta ttg      269
His Ile His Lys Leu Phe Leu Tyr Ser Leu Phe Thr Glu Asn Val Leu
        -15                 -10                  -5
```

```
gca cat cct tgc att gtt cta cgc cgc cta tg                        301
Ala His Pro Cys Ile Val Leu Arg Arg Leu
    1               5

<210> 194
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..215

<221> sig_peptide
<222> 105..203
<223> Von Heijne matrix
      score 7
      seq LFFLFVGPFSCLG/SY

<400> 194
gctctgactg cagcctccca gggaatgcgc ggccgaggga atgcgcgcag tcacaggccc    60
tgggagtgag ctggtgcccg gcgacctggc acccgcgcct ggat atg ggg cgt cta    116
                                                 Met Gly Arg Leu
                                                             -30
cat cgt ccc agg agc agc acc agc tac agg aac ctg ccg cat ctg ttt     164
His Arg Pro Arg Ser Ser Thr Ser Tyr Arg Asn Leu Pro His Leu Phe
                -25                 -20                 -15
ctg ttt ttc ctc ttc gtg gga ccc ttc agc tgc ctc ggg agt tac agc     212
Leu Phe Phe Leu Phe Val Gly Pro Phe Ser Cys Leu Gly Ser Tyr Ser
            -10                  -5                   1
cgg                                                                 215
Arg

<210> 195
<211> 209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..209

<221> sig_peptide
<222> 78..158
<223> Von Heijne matrix
      score 7
      seq RLLLLLLLXLPLP/PP

<221> misc_feature
<222> 73..74
<223> n=a, g, c or t


<400> 195
tcattcactg attagatcca gcgctgagag gcagcactgc tccttctctc acgccaactg    60
agtctcttga tcnntac atg caa tcc cag gca gct cgc gaa cac aaa ccc     110
                   Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro
                                   -25                 -20
ggg ghc agc cgc cta ctg ctg ctg ctg ctg ctg cwg ctg ccg ctg cct     158
Gly Xaa Ser Arg Leu Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro
    -15                 -10                  -5
ccg ccg gkv ctg cga acc cgg gdy ttt tca wgc acc aca ctc acc gcm     206
Pro Pro Xaa Leu Arg Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala
```

1 5 10 15
ggg 209
Gly

<210> 196
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 287..361

<221> sig_peptide
<222> 287..331
<223> Von Heijne matrix
score 7
seq LWSLACLSPPAVQ/LG

<400> 196
ttacattgta atatataaat aattatacaa ctcaccataa cgtagaatca gtgggagccc 60
tgagcttgtt ttcctgcaac tagatggtcc caactagacc aggtgatggg agacaatgac 120
agatcattag gcattagatt atcataagga gcatacaacc tagatccctt gcatgtgcag 180
ttaataatag gttttgcact tctatgagga tctaatgcgg cctctgatct gacaaggggc 240
ggastcaggc agtaatggga gcaatgggga gcggttttca atacag atg agg ctt 295
Met Arg Leu
-15
tgg tca ctt gcc tgc ctt tca cct cct gct gtg cag ctt ggt tcc caa 343
Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu Gly Ser Gln
-10 -5 1
cag gcc acg gac tgg tgg tc 363
Gln Ala Thr Asp Trp Trp
5 10

<210> 197
<211> 155
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 58..153

<221> sig_peptide
<222> 58..132
<223> Von Heijne matrix
score 7
seq IFSFFFFITLVRG/SI

<400> 197
tagtgttatt catagtagta tctgaagacc ttttgtattc ttgtgggatc agttgta 57
atg tca cct ttg ttt att ctg att gtg ctt att tgg atc ttc tct ttc 105
Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe
-25 -20 -15 -10
ttt ttc ttt att act cta gtt agg ggg tct atc aat ctt ttt ttt ttt 153
Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe
-5 1 5
tt 155

<210> 198
<211> 135
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 60..134

<221> sig_peptide
<222> 60..125
<223> Von Heijne matrix
      score 7
      seq STFLFFLFFSVFC/FF

<400> 198
ttgcctctta aaaggccaca cttcttaata ctatcaaatt ggctattaag tttcaacaa      59
atg aat ttg ggg gga cat tca gat cat agc act ttt ctt ttc ttt ctt     107
Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu
        -20                 -15                 -10
ttt ttt tct gtt ttt tgt ttt ttt ttt t                               135
Phe Phe Ser Val Phe Cys Phe Phe Phe
    -5                  1

<210> 199
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..318

<221> sig_peptide
<222> 46..108
<223> Von Heijne matrix
      score 6.90000009536743
      seq VTFLLALVGAVLY/LY

<221> misc_feature
<222> 9
<223> n=a, g, c or t


<400> 199
gctggagcng ccgatccgag acgtggcthc ctgggcggca gaacc atg ttg gac ttc     57
                                                  Met Leu Asp Phe
                                                      -20
gcg atc ttc gcc gtt acc ttc ttg ctg gcg ttg gtg gga gcc gtg ctc     105
Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val Gly Ala Val Leu
        -15                 -10                 -5
tac ctc tat ccg gct tcc aga caa gct gca gga att cca ggg att act     153
Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile Pro Gly Ile Thr
    1               5                   10                  15
cca act gaa gaa aaa gat ggt aat ctt cca gat att gtg aat agt gga     201
Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile Val Asn Ser Gly
                20                  25                  30
agt ttg cat gag tbc ctg gtt aat ttg cat gag aga tat ggg cct gtg     249
Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg Tyr Gly Pro Val
            35                  40                  45
gtc tcc ttc tgg ttt ggc agg cgc ctc gtg gtt agt ttg ggc act gtt     297
Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser Leu Gly Thr Val
        50                  55                  60
gat gta ctg aag cag cat cgg gg                                      320
Asp Val Leu Lys Gln His Arg
    65                  70
```

<210> 200
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..123

<221> sig_peptide
<222> 40..93
<223> Von Heijne matrix
score 6.90000009536743
seq LELLGSSSPPISA/SQ

<400> 200
cttcctcagt cacccaggct ggagtacagt ggcataatc atg gct cac tgc agc 54
Met Ala His Cys Ser
-15
tta gaa ctc ttg ggc tca agc agt cct ccc atc tca gcc tcc caa agc 102
Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile Ser Ala Ser Gln Ser
-10 -5 1
act gga att aca agc gtg agc ca 125
Thr Gly Ile Thr Ser Val Ser
5 10

<210> 201
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..209

<221> sig_peptide
<222> 78..128
<223> Von Heijne matrix
score 6.90000009536743
seq LLLLSLSLFLFFW/RQ

<400> 201
tcaggttttc ctccttcccg ggtgctctga agtttcacca tgaatcacct tgcaggggct 60
ctttttattt tttattg atg ccc agc cag ttg ttg ttg ttg tct ctt tct 110
Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser
-15 -10
ctc ttt ttg ttt ttt tgg aga cag agt ctc gtt ttg tgg ccc agg ctg 158
Leu Phe Leu Phe Phe Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu
-5 1 5 10
gag tgc agt tgt gtc att gcg gct cac tgc agc ctg acc tcc cag gct 206
Glu Cys Ser Cys Val Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala
15 20 25
cgg g 210
Arg

<210> 202
<211> 338
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..337

<221> sig_peptide
<222> 89..226
<223> Von Heijne matrix
score 6.90000009536743
seq CLFCCXFISSCNS/VF

<221> misc_feature
<222> 291
<223> n=a, g, c or t

<400> 202
aattataata atatactaaa atatgtacga atatatacta ataattagta tataatgaat 60
cagtataaaa tatataatat acactaat atg tat act aat aaa tat aca cta 112
Met Tyr Thr Asn Lys Tyr Thr Leu
-45 -40
ata tat aac ata cta ata tat aat ata tgt btk drg tat atg tgg ttg 160
Ile Tyr Asn Ile Leu Ile Tyr Asn Ile Cys Xaa Xaa Tyr Met Trp Leu
-35 -30 -25
ata ctc att tat atg tac cta cat att tgc ctc ttt tgt tgc wct ttt 208
Ile Leu Ile Tyr Met Tyr Leu His Ile Cys Leu Phe Cys Cys Xaa Phe
-20 -15 -10
att tct tcc tgc aat tct gtg ttt ccc tgt gtg att atb ttt ctt ctg 256
Ile Ser Ser Cys Asn Ser Val Phe Pro Cys Val Ile Xaa Phe Leu Leu
-5 1 5 10
cct gaa gaa ctt ctt twt gtd twt ctd wdw dtg tnt tty wtt gtg aga 304
Pro Glu Glu Leu Leu Xaa Val Xaa Leu Xaa Xaa Xaa Phe Xaa Val Arg
15 20 25
tgg agt ctc amt cwg tcg tcc agg ctg gag tgc a 338
Trp Ser Leu Xaa Xaa Ser Ser Arg Leu Glu Cys
30 35

<210> 203
<211> 188
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..188

<221> sig_peptide
<222> 84..176
<223> Von Heijne matrix
score 6.90000009536743
seq LWSLIQAVHICLG/RK

<400> 203
tattctctga ttckctgtct tggaatgcat ttaaaatctc tgcctcgatt ctgacctacc 60
tggcatggga acaagaattt aca atg tta ctc acc cac aat gaa gat tac atg 113
Met Leu Leu Thr His Asn Glu Asp Tyr Met
-30 -25
cct ggc aat ttd grc ttw ard daw ttg tgg agc tta att cag gct gtt 161
Pro Gly Asn Xaa Xaa Xaa Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val
-20 -15 -10
cat atc tgc cta ggc agg aaa aaa aaa 188
His Ile Cys Leu Gly Arg Lys Lys Lys
-5 1

<210> 204
<211> 347
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 81..347

<221> sig_peptide
<222> 81..137
<223> Von Heijne matrix
score 6.90000009536743
seq WVFLVAIIKGVQC/QV

<400> 204

```
agctctggga gaagagcccc agccccagaa ttcccaggag tttccattcg gtgatcagca     60
ctgaacacag aggactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt    113
                      Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val
                                      -15                 -10
gct att ata aaa ggt gtc cag tgt cag gtg caa ctg gtg gag tct ggg      161
Ala Ile Ile Lys Gly Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly
            -5                  1               5
ggg ggc ttg gtc aag cct gga ggg tcc cta aga ctc tcc tgt gca gcc      209
Gly Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala
    10                  15                  20
tct gga ttc acc ttc agt gay tac waw atr act kgg att cgc mag gcc      257
Ser Gly Phe Thr Phe Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala
25                  30                  35                  40
cma ggg aag ggs ytg rak tgg att yca tam atw acg act agt ggg aat      305
Xaa Gly Lys Gly Leu Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn
                45                  50                  55
acc gca awy tac gca gwc tct gta aag gsc cga ttc acc atc              347
Thr Ala Xaa Tyr Ala Xaa Ser Val Lys Xaa Arg Phe Thr Ile
            60                  65                  70
```

<210> 205
<211> 440
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 276..440

<221> sig_peptide
<222> 276..326
<223> Von Heijne matrix
score 6.90000009536743
seq FLFVCLXFDESCS/VT

<400> 205

```
cagtaaattt ttttgwwcat tggttccttc dkcttggact ctctgttagc acacctgatc     60
agagttggcc gtgttgtaat tctttccctc tctgctgcaa tgttgtttac ttctacctgs    120
caactawkct ttatactttc cttttttgcc atgaagggaa tacatttttt ccttcttgtt    180
gggctataca gtgatcctca tcaacaaatt atcaaagaac tgtatgagga aaaggtctct    240
ttttttaaaa gtgaatcagg gctggggagt tagga atg aag agg ttt ttt ttg       293
                                       Met Lys Arg Phe Phe Leu
                                                   -15
ttt gtt tgt ttg tww ttt gac gag tct tgc tct gtc acc agg ctg ggg      341
Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys Ser Val Thr Arg Leu Gly
    -10                 -5                  1               5
tgc tgt ggc gcg atc tca gcc cac tgc aam ctc cga ctc cct ggt tca      389
Cys Cys Gly Ala Ile Ser Ala His Cys Xaa Leu Arg Leu Pro Gly Ser
                10                  15                  20
agc rat dyt cct gcc tca acc tcc cga gta gvy ggg att aca ggc atg      437
```

```
Ser Xaa Xaa Pro Ala Ser Thr Ser Arg Val Xaa Gly Ile Thr Gly Met
            25                  30                  35
cgc                                                                 440
Arg

<210> 206
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 162..281

<221> sig_peptide
<222> 162..275
<223> Von Heijne matrix
      score 6.90000009536743
      seq CMLFVSFLLLLLG/SR

<400> 206
aataactccc tttagcattt cttgtaggac aggtctgatg ttgatgaaat ctctcatctt    60
gtttgtcaga gaaagtcttt atttctcctt catgcttgaa ggatgtttcc accggatata   120
ctatcctagg gtaaaagttt ttttccttca gcactttaaa t atg tca tgc cac tct   176
                                              Met Ser Cys His Ser
                                                              -35
ctt ctg gcc tgt aag gtt ttc act gaa aag tct cct acc aaa cat att     224
Leu Leu Ala Cys Lys Val Phe Thr Glu Lys Ser Pro Thr Lys His Ile
            -30                 -25                 -20
aga gag cac cat tgt atg tta ttt gtt tct ttt ctc ttg ctg ctt tta     272
Arg Glu His His Cys Met Leu Phe Val Ser Phe Leu Leu Leu Leu Leu
        -15                 -10                 -5
gga tcc cgg gg                                                      283
Gly Ser Arg
    1

<210> 207
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 113..262

<221> sig_peptide
<222> 113..190
<223> Von Heijne matrix
      score 6.90000009536743
      seq LLSMLSCCQGACC/PS

<400> 207
gacggcggag agcagagagg gagcgcgcct tggctcgctg gccttggcgg cggctcctca    60
ggagagctgg ggcgcccacg agaggatccc tcacccgggt ctctcctcag gg atg aca   118
                                                          Met Thr
                                                              -25
tca tcc gtc cac ctc ctt gtc ttc aag gac cac ctc ctc tcc atg ctg     166
Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser Met Leu
            -20                 -15                 -10
agc tgc tgc caa ggg gcc tgc tgc cca tct aca cct cac gag ggc act     214
Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu Gly Thr
            -5                  1                   5
agg agc acg gtt tcc tgg atc cca cca aca tac aaa gca gcc aca cag     262
```

```
Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala Thr Gln
    10                  15                  20
gg                                                                  264

<210> 208
<211> 422
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 352..420

<221> sig_peptide
<222> 352..408
<223> Von Heijne matrix
      score 6.80000019073486
      seq LLSMFCVSHTVQT/AT

<221> misc_feature
<222> 289..290
<223> n=a, g, c or t


<400> 208
aaaataaaag tcttcttgat ttccagtgta ttcctcctgc acwttttggc ctgtttggac    60
cacagatttg tggcttttta tgaaatacac ctgtagatta atttwcagtt thtwhayggw   120
agtagacagt caaaggctag atcactgtra tgagtagggc ttccacattt aagaaaaagc   180
tgtaatgaag tgaattgaat cttgcttctt ttgggtcacc caaaagcagt gataagtgct   240
gagtgtgtta ggcacttatt aacaaaagta actcagaatt gctgtctann cctccatatc   300
tttttcttc tctccgtgta gttctaaaaa tgaccatatg atattccttg a atg gta     357
                                                      Met Val
aga gcg tct att ctt ctt agc atg ttc tgt gtg tca cac act gtg cag     405
Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr Val Gln
        -15                 -10                 -5
aca gca aca tac aca ca                                              422
Thr Ala Thr Tyr Thr
    1

<210> 209
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..194

<221> sig_peptide
<222> 39..89
<223> Von Heijne matrix
      score 6.80000019073486
      seq ALSSFTWWAPACC/AP

<400> 209
agccactgca cctgggctca cagtttaaat cttgagta atg gag aaa aca gcc ttg    56
                                          Met Glu Lys Thr Ala Leu
                                                      -15
tca tcc ttt acg tgg tgg gca cct gcc tgc tgt gct cca cgt aca tac     104
Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys Cys Ala Pro Arg Thr Tyr
    -10                 -5                  1               5
gtg gtg tct gca aca act ctg tca gct gtg caa ggt cac tgt cct cta     152
Val Val Ser Ala Thr Thr Leu Ser Ala Val Gln Gly His Cys Pro Leu
```

```
                10                  15                  20
cag agt aga aca tcg acc aaa gga aag tta tgg ccg ttt ggg g            195
Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu Trp Pro Phe Gly
            25                  30                  35
```

<210> 210
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..361

<221> sig_peptide
<222> 212..280
<223> Von Heijne matrix
score 6.80000019073486
seq KLLLSGLTQECLG/AL

<400> 210

```
taattttcat catctaaact gaatgcaaac agcgcttggc aattaaaatg aagctctcca     60
atgaagtata cttcatcagc tgctgtcaag tcatccattg atactgtttt gcggttttta    120
aattcctttt gtcactgtga ctgctcatca gcaggcaagg aagagcaggc aacaaaagtt    180
gaaaagtgca tgaaggaaaa ctttgaggaa t atg ata ttc aca ttc cag caa       232
                                   Met Ile Phe Thr Phe Gln Gln
                                                  -20
att ggg gga aaa ctg cta tta tct ggt tta aca cag gag tgc ctt ggt      280
Ile Gly Gly Lys Leu Leu Leu Ser Gly Leu Thr Gln Glu Cys Leu Gly
    -15                 -10                 -5
gcc ctg cct gag gct aat gtg ttc tgt agg ggt ggc tgc aca gcc aca      328
Ala Leu Pro Glu Ala Asn Val Phe Cys Arg Gly Gly Cys Thr Ala Thr
1               5                   10                  15
gtc ctg aaa cat ggg aaa gca tct cct gag tcc ag                       363
Val Leu Lys His Gly Lys Ala Ser Pro Glu Ser
            20                  25
```

<210> 211
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 230..367

<221> sig_peptide
<222> 230..322
<223> Von Heijne matrix
score 6.80000019073486
seq LLALSPDLQAARG/LM

<400> 211

```
acagagaacc ctgcttcaaa gcagaagtag cagttccgga gtccagctgg ctaaaactca     60
tccchyggat aatggcaacc catgccttag aaatcgctgg gctgtttctt ggtggtgttg    120
gmatgggtgg gsacmrgkwg ggbkgyvack gtcatgcctc agtggdrrag tgtcggcctt    180
cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgttg atg aat tgc    238
                                                      Met Asn Cys
                                                          -30
gtg agg cag gct aac atc agg atg cag tgc aaa atc tat gat tcc ctg      286
Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu
            -25                 -20                 -15
ctg gct ctt tct ccg gac cta cag gca gcc aga ggr ctg atg tgt gct      334
```

```
Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala
        -10                 -5                  1
gct tcc gtg atg tcc ttc ttg gct ttc atg atg g                      368
Ala Ser Val Met Ser Phe Leu Ala Phe Met Met
5                   10                  15
```

<210> 212
<211> 448
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 316..447

<221> sig_peptide
<222> 316..435
<223> Von Heijne matrix
      score 6.80000019073486
      seq LLKLLISLRSFWA/ET

<400> 212

```
ttgtcttggc tatacgggat ctttttttggt cccatatgaa atttaagtag cttttcctaa    60
ttctgtgaag gaagtcaatg gtagcttgat gggaatagca ttgaatctat aaattacttt    120
gggccgtatg gcatttgggc aatattgatt cttcctattc atgagcatgg aatgtttttc    180
catttgttca tgtcctctct tattttgttg agcagtggtt tgtagttctc cttgaagggg    240
ttcttcacat cccttgtaag ttgtattccc aggtatttta ttctctttgt agcaattttg    300
aatgggagtt cactc atg att tgg ctc tct ttt tgt cta tta ttg gtg tat     351
                 Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr
                 -40                 -35                 -30
agg aat gct tgt gat ttt tgc aca ttg act tta tat cct ggg act ttg      399
Arg Asn Ala Cys Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu
            -25                 -20                 -15
ctg aag ttg ctt atc agc tta agg agt ttt tgg gct gag acg acg ggg g    448
Leu Lys Leu Leu Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly
        -10                 -5                  1
```

<210> 213
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..156

<221> sig_peptide
<222> 28..102
<223> Von Heijne matrix
      score 6.69999980926514
      seq LVGSLHLFLSVLA/SK

<400> 213

```
gcgctgggag ttctcttttt cacttga atg ttt tct tct cca ggg ctg agg acg     54
                              Met Phe Ser Ser Pro Gly Leu Arg Thr
                              -25                 -20
ctc ttt gta ttg gta ggc agc ctg cac ttg ttc ctt tca gtc ctg gca      102
Leu Phe Val Leu Val Gly Ser Leu His Leu Phe Leu Ser Val Leu Ala
    -15                 -10                 -5
agt aaa agc agg aat tct aaa aag caa cga tta ttc ctc cta gtt cct      150
Ser Lys Ser Arg Asn Ser Lys Lys Gln Arg Leu Phe Leu Leu Val Pro
1               5                   10                  15
ttg tac ag                                                           158
```

Leu Tyr

<210> 214
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..191

<221> sig_peptide
<222> 39..107
<223> Von Heijne matrix
score 6.69999980926514
seq NVCSLPAPGLCSG/QP

<400> 214
aagaaaagct ttgggtcaac tcagcatcat gtttgcag atg ctg aca gac ggg atc 56
Met Leu Thr Asp Gly Ile
-20
cta atg aga gtc aat gtg tgc tca ctg cca gct cct ggg ctg tgc tct 104
Leu Met Arg Val Asn Val Cys Ser Leu Pro Ala Pro Gly Leu Cys Ser
-15 -10 -5
ggt cag cca ggt gtg agg gcc tgg cct ggg gtc aca cag ctg act car 152
Gly Gln Pro Gly Val Arg Ala Trp Pro Gly Val Thr Gln Leu Thr Gln
1 5 10 15
bta gag gaa tgc cca tgg ttc tca gca ttg gaa gga ctg gg 193
Xaa Glu Glu Cys Pro Trp Phe Ser Ala Leu Glu Gly Leu
20 25

<210> 215
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..213

<221> sig_peptide
<222> 67..165
<223> Von Heijne matrix
score 6.69999980926514
seq ILLLSLIFGPCIL/NS

<400> 215
aaagttcgag aaaatchaga taggcaccaa caagaacgag aaaataacat cccctggtat 60
caaagc atg ttt aac tgg aac cca tgg cta act act tta atc act ggg 108
Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly
-30 -25 -20
wta gch gga cct ctc ctc atc cta cta tta agt tta att ttt ggg cct 156
Xaa Ala Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro
-15 -10 -5
tgt ata tta aat tcg ttt ctk aat tkt ata aaa caa cgc ata gct tct 204
Cys Ile Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser
1 5 10
ggc aaa cgg g 214
Gly Lys Arg
15

<210> 216
<211> 327

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..327

<221> sig_peptide
<222> 22..108
<223> Von Heijne matrix
      score 6.69999980926514
      seq FCALLLSLXXXXP/XX

<400> 216
ctccgcgttc cagaatccaa g atg gcg gga tcc agg caa agg ggt ctc cgg       51
                        Met Ala Gly Ser Arg Gln Arg Gly Leu Arg
                                        -25                 -20
gcc aga gtt cgg ccg ctg ttc tgc gcc ttg ctg ctg tca ctm sgw hsv       99
Ala Arg Val Arg Pro Leu Phe Cys Ala Leu Leu Leu Ser Leu Xaa Xaa
            -15                 -10                 -5
mty ckt ccg rkg cka cgs cgt gkg agg aga ccc cgc ggt cgc gtt gcc      147
Xaa Xaa Pro Xaa Xaa Arg Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala
        1               5                   10
aca tcg ccg ttt cga gta saa ata cag ctt caa ggg gcc gca cct ggt      195
Thr Ser Pro Phe Arg Val Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly
    15                  20                  25
gca gag cga cgg gac cgt gcc ctt ctg ggm cca cgc ggg gaa tgc tat      243
Ala Glu Arg Arg Asp Arg Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr
30                  35                  40                  45
tcc aag ttc aga tca aat tcg agt agc acc atc ttt aaa aag cya aag      291
Ser Lys Phe Arg Ser Asn Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys
                50                  55                  60
agg ctc agt gtg gvm aam gac aav agc gga cct ggg                      327
Arg Leu Ser Val Xaa Xaa Asp Xaa Ser Gly Pro Gly
            65                  70

<210> 217
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..357

<221> sig_peptide
<222> 70..126
<223> Von Heijne matrix
      score 6.69999980926514
      seq WVFLVAILKGVHC/DV

<400> 217
aggagcccca gccctgggat tcccagctgt ttctgcttgc tgatcaggac tgcacacaga      60
gaactcacc atg gag ttt ggg ctg agc tgg gtt ttc ctt gtt gct att tta     111
          Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
                          -15                 -10
aaa ggt gtc cac tgt gac gtg cag ctg gtg gag tcc ggg gga ggt tta      159
Lys Gly Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu
-5                  1               5                   10
gtt cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tct gga ctc      207
Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu
            15                  20                  25
acc ctc agt aac gac tgg atg cac tgg gtc cgc caa gcc cca ggg aag      255
```

Thr Leu Ser Asn Asp Trp Met His Trp Val Arg Gln Ala Pro Gly Lys
30 35 40
ggg ctg gtg tgg gtc tca cac att gat agt tct rgg act atc aca aat 303
Gly Leu Val Trp Val Ser His Ile Asp Ser Ser Xaa Thr Ile Thr Asn
45 50 55
tac gcg gac tcc gtg aag ggc cga ttc acc atc tcc aga gac aac gcc 351
Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala
60 65 70 75
aag tgg 357
Lys Trp

<210> 218
<211> 189
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..187

<221> sig_peptide
<222> 74..118
<223> Von Heijne matrix
score 6.69999980926514
seq LFLGFLACSVAYQ/CH

<400> 218
ttatcaagga cactgtcttt tcgccatcat gtgttcttgg cccctctgtt gaaattcaat 60
ctatcataga caa atg ggt tta ttt ctg ggc ttt cta gcc tgt tct gtt 109
Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val
-15 -10 -5
gca tac cag tgc cat tct gct ttt gtt act gta gct tca cag tac act 157
Ala Tyr Gln Cys His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr
1 5 10
ttg aaa tca gag act ttg atg ccc gca gcg gg 189
Leu Lys Ser Glu Thr Leu Met Pro Ala Ala
15 20

<210> 219
<211> 353
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 41..352

<221> sig_peptide
<222> 41..187
<223> Von Heijne matrix
score 6.69999980926514
seq FLGLIFFLELATG/IL

<400> 219
agttgacttg ccatctgcct tgcaggatgg catccagccc atg tgg gag gac agc 55
Met Trp Glu Asp Ser
-45
agg aat aaa cgg ggt ggc cgc tgg ctg gtc agc ctg gcc aag cag cag 103
Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser Leu Ala Lys Gln Gln
-40 -35 -30
cgc cac att gag ctg gac cgg ctg tgg ctg gag acg ttc tcc gtg ttc 151
Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu Thr Phe Ser Val Phe
-25 -20 -15

```
ctc ggt ctc atc ttc ttc ctg gag ctg gca aca ggg atc ctg gcc ttt      199
Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr Gly Ile Leu Ala Phe
        -10                 -5                  1
gtc ttc aag gac tgg att cga gac cag ctc aac ctc ttc atc aac aac      247
Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn Leu Phe Ile Asn Asn
5                   10                  15                  20
aac gtc aag gcc tac cgg gac gac att gac ctc cag arc ctc att gac      295
Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu Gln Xaa Leu Ile Asp
                25                  30                  35
ttt gct cag gaa tac tgg tct tgc tgc gga scc gag gcc cca ata rdt      343
Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa Glu Ala Pro Ile Xaa
            40                  45                  50
gga acc ggg g                                                        353
Gly Thr Gly
        55
```

<210> 220
<211> 115
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..113

<221> sig_peptide
<222> 12..53
<223> Von Heijne matrix
score 6.59999990463257
seq FLSLSTAFWVVYA/MI

<400> 220

```
actagcattt c atg ttt tta tct ctc tct act gca ttc tgg gta gtt tat      50
             Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr
                                 -10                 -5
gcc atg ata att tat tca gct ctc tct gct gga ttt att att ttc ttt      98
Ala Met Ile Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe
    1               5                   10                  15
tta gtt gtg ttt aat ct                                               115
Leu Val Val Phe Asn
                20
```

<210> 221
<211> 142
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..142

<221> sig_peptide
<222> 29..130
<223> Von Heijne matrix
score 6.59999990463257
seq FFLFFCFETGSHS/VT

<400> 221

```
cctgcccatt gcttcaacct gcacctct atg tac att gtg atg gat cta cct      52
                               Met Tyr Ile Val Met Asp Leu Pro
                                                   -30
cta tgg ctc tcc cat gag gtc caa tct tat att cct tct ttc ttc ctt      100
Leu Trp Leu Ser His Glu Val Gln Ser Tyr Ile Pro Ser Phe Phe Leu
```

```
    -25                 -20                 -15
ttt ttt tgc ttt gag act ggg tct cac tct gtc acc cac ggg          142
Phe Phe Cys Phe Glu Thr Gly Ser His Ser Val Thr His Gly
-10                 -5                   1

<210> 222
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 209..370

<221> sig_peptide
<222> 209..289
<223> Von Heijne matrix
      score 6.59999990463257
      seq LAFSFSFFPSSFS/SF

<400> 222
ttttggatac atatgactca tgtgacatta gatcacagca tttttgtttt tattattaat     60
atattgcctt agaactacat tgctaaacct ggtctttgta tctgcgaagt tctaacatct    120
tgccacagct tagttagctt tgagagggaa agggtagaat ccatttaagg agacaggtta    180
aaaaatgata tatttaagca tataggca atg gta gca cat gat tac caa aac       232
                               Met Val Ala His Asp Tyr Gln Asn
                                       -25                 -20
ata att agc ctt ttc ttt ctt gct ttt tca ttt tct ttc ttt cct tct      280
Ile Ile Ser Leu Phe Phe Leu Ala Phe Ser Phe Ser Phe Phe Pro Ser
                -15                 -10                 -5
tca ttt tct tct ttc ttt ctt ktc ttt ctt tct ttt ttc tct tct ttc      328
Ser Phe Ser Ser Phe Phe Leu Xaa Phe Leu Ser Phe Phe Ser Ser Phe
            1               5                   10
ttt ctc tct ctt ctt tct ttc cct tcc ttc ctc ccc ccc ggr              370
Phe Leu Ser Leu Leu Ser Phe Pro Ser Phe Leu Pro Pro Gly
    15                  20                  25

<210> 223
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..429

<221> sig_peptide
<222> 22..66
<223> Von Heijne matrix
      score 6.59999990463257
      seq ALRALCGFRGVAA/QV

<400> 223
gcagtctgca gccggagtaa g atg gcg gcg ctg agg gct ttg tgc ggc ttc       51
                        Met Ala Ala Leu Arg Ala Leu Cys Gly Phe
                        -15                 -10
cgg ggc gtc gcg gcc cag gtg ctg cgg mct ggg gct gga gtc cga ttg       99
Arg Gly Val Ala Ala Gln Val Leu Arg Xaa Gly Ala Gly Val Arg Leu
-5                  1               5                   10
ccg att cag ccc agc aga ggt gtt cgg cag tgg cag cca gat gtg gaa      147
Pro Ile Gln Pro Ser Arg Gly Val Arg Gln Trp Gln Pro Asp Val Glu
            15                  20                  25
tgg gca cag cag ttt ggg gga gct gtt atg tac cca agc aaa gaa aca      195
```

```
Trp Ala Gln Gln Phe Gly Gly Ala Val Met Tyr Pro Ser Lys Glu Thr
        30                  35                  40
gcc cac tgg aag cct cca cct tgg aat gat gtg gac cct cca aag gac      243
Ala His Trp Lys Pro Pro Pro Trp Asn Asp Val Asp Pro Pro Lys Asp
    45                  50                  55
aca att gtg aag aac att acc ctg aac ttt ggg ccc caa cac cca gca      291
Thr Ile Val Lys Asn Ile Thr Leu Asn Phe Gly Pro Gln His Pro Ala
60                  65                  70                  75
gcg cat ggt gtc ctg cga cta gtg atg gaa ttg agt ggg gag atg gtg      339
Ala His Gly Val Leu Arg Leu Val Met Glu Leu Ser Gly Glu Met Val
                80                  85                  90
cgg aag tgt gat cct cac atc ggg ctc ctg cac cga ggc act gag aag      387
Arg Lys Cys Asp Pro His Ile Gly Leu Leu His Arg Gly Thr Glu Lys
            95                  100                 105
ctc att gaa tac aag rcc tat ctt cag gcc ctt cca tac ttt ga           431
Leu Ile Glu Tyr Lys Xaa Tyr Leu Gln Ala Leu Pro Tyr Phe
        110                 115                 120
```

<210> 224
<211> 282
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 132..281

<221> sig_peptide
<222> 132..215
<223> Von Heijne matrix
score 6.5
seq LVFLHLFLXVYLG/LV

<400> 224

```
attttaaagt gtttctgtta atgtattcta cttcagtccc ccaaaattcc aactaacgac     60
atacatgaat aacagatcat gactgctgtt tctacaagcc tttctgctca ctgtgcttcc    120
acttacaact c atg tta ata tgg tct tcc tct tct ttt cct gca ccc cct     170
             Met Leu Ile Trp Ser Ser Ser Ser Phe Pro Ala Pro Pro
                         -25                 -20
ctc ttt ctt gtc ttt ctt cat ctt ttc ctt mwt gtc tat ttg ggt ctt      218
Leu Phe Leu Val Phe Leu His Leu Phe Leu Xaa Val Tyr Leu Gly Leu
-15                 -10                 -5                  1
gtc atg ccc act caa cag tat ctc ctc ctg cag agt cca ttg atg ttc      266
Val Met Pro Thr Gln Gln Tyr Leu Leu Leu Gln Ser Pro Leu Met Phe
            5                   10                  15
aca gac aaa gcc cag c                                                282
Thr Asp Lys Ala Gln
        20
```

<210> 225
<211> 198
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..196

<221> sig_peptide
<222> 26..163
<223> Von Heijne matrix
score 6.5
seq WLFFLMLSLCTPP/DR

```
<400> 225
acttttgctt tatgttcagg ggtcc atg tgt agg atg tgc agg ttt gtt aca       52
                            Met Cys Arg Met Cys Arg Phe Val Thr
                                -45                 -40
tgg ata aac gtg tgc cat ggt gat ttg ctg cac aga tca tcc cgt cgc      100
Trp Ile Asn Val Cys His Gly Asp Leu Leu His Arg Ser Ser Arg Arg
        -35                 -30                 -25
ctg ggt gtg aag ccg agc acg cat tgg cta ttc ttc ctg atg ctc tcc      148
Leu Gly Val Lys Pro Ser Thr His Trp Leu Phe Phe Leu Met Leu Ser
    -20                 -15                 -10
ctt tgc acc cct cct gac aga ccc tgg tgt gtg ttg ttc ccc ccg ctg      196
Leu Cys Thr Pro Pro Asp Arg Pro Trp Cys Val Leu Phe Pro Pro Leu
-5                  1               5                   10
gg                                                                   198

<210> 226
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..140

<221> sig_peptide
<222> 21..113
<223> Von Heijne matrix
      score 6.5
      seq LSLSLPLSLXLLX/XP

<400> 226
gcagttgakr dsacttggta atg tsa acg caa gaa gca ggc ttg aty ttt ttt     53
                      Met Xaa Thr Gln Glu Ala Gly Leu Ile Phe Phe
                          -30                 -25
tct ccc ccc ttc tct ctc tct ctc tct ctc tct cty cct ctc tcc ctc      101
Ser Pro Pro Phe Ser Leu Ser Leu Ser Leu Ser Leu Pro Leu Ser Leu
-20                 -15                 -10                 -5
tyt ctc ctc tst sac cca cac tca cgc aca cct caa agg g                141
Xaa Leu Leu Xaa Xaa Pro His Ser Arg Thr Pro Gln Arg
                1               5

<210> 227
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..205

<221> sig_peptide
<222> 77..115
<223> Von Heijne matrix
      score 6.5
      seq MEFLLLWSLXSNG/KR

<400> 227
awcaartact tgttaagcrt ttacgatgtg ccaggttctg tgctaggtgc tgagtgtaca     60
ttgttgarcc aaacag atg gag ttc ctg cta ttg tgg agt ttg cmg tct aat    112
                  Met Glu Phe Leu Leu Leu Trp Ser Leu Xaa Ser Asn
                              -10                 -5
ggg aag aga ggc cag gca tgg cgg ctc atg cct gtw gtc cca gca gtt      160
```

```
Gly Lys Arg Gly Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val
    1               5                   10                  15
tgg gag cct gag gca ggt gga ttg ctt cag ctc ggg ggt tct agg g        206
Trp Glu Pro Glu Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg
                20                  25                  30
```

<210> 228
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 216..479

<221> sig_peptide
<222> 216..326
<223> Von Heijne matrix
score 6.5
seq LLVFFLIVRTLSC/RS

<400> 228

```
gcatccccck ktagctcaga gaagtttgtt rdgaccgatc ttctgaagcc tacttctgtc     60
aactcatcaa agtcattctc catccagctt tgttccatta tgggtgagga gctacgatcc    120
tttggaggag aagaggcact ctgattttta gaattttcag cttttctgct ctggtttcgc    180
cccatctttg tggttttatc taccttcggt ctttg atg atg gtg acc tac aga       233
                                       Met Met Val Thr Tyr Arg
                                                   -35
tgg ggt ttt ggt gtg gat gtc mtt ttt gtt gct gtt gat gct att cct      281
Trp Gly Phe Gly Val Asp Val Xaa Phe Val Ala Val Asp Ala Ile Pro
    -30                 -25                 -20
ttc tgt ttg tta gtt ttc ttt cta ata gtc agg acc ctc agc tgc agg      329
Phe Cys Leu Leu Val Phe Phe Leu Ile Val Arg Thr Leu Ser Cys Arg
-15                 -10                 -5                  1
tct gtt gga gta tgc tgg agg tcc act cca gac cct gtt tgc cta ggt      377
Ser Val Gly Val Cys Trp Arg Ser Thr Pro Asp Pro Val Cys Leu Gly
            5                   10                  15
atc acc agc aga ggc tgc aga aca gaa ata ttg cag aac agc aaa tgt      425
Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile Leu Gln Asn Ser Lys Cys
        20                  25                  30
tgc tcc ctg atc ctt cct ctg gaa gct tcg tct caa agg ggc act gaa      473
Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser Ser Gln Arg Gly Thr Glu
    35                  40                  45
tgt atg a                                                            480
Cys Met
50
```

<210> 229
<211> 144
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 43..144

<221> sig_peptide
<222> 43..99
<223> Von Heijne matrix
score 6.5
seq EIFLPFSLSPANA/QS

<400> 229

```
tccagatgtg atttggtatt tcatactttg ttgcttttgt aa atg ctg tac cca         54
                                                Met Leu Tyr Pro
ctg cct gag ata ttc tta cct ttt tct ttg tcc cca gca aat gcc cag       102
Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro Ala Asn Ala Gln
-15                 -10                 -5                  1
tca aaa ttt agc ctt tat ttt ttt ccc ttg gtg aag ccg ggg               144
Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys Pro Gly
            5                   10                  15
```

<210> 230
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 314..457

<221> sig_peptide
<222> 314..394
<223> Von Heijne matrix
score 6.40000009536743
seq RLLCLXFXRLLLG/TS

<221> misc_feature
<222> 118,258..259,303,440
<223> n=a, g, c or t

<400> 230

```
agctccgcgg taatggaggc tagggatggg tgctgaagta tcaggctctg gctctagctt      60
tagctctggc actggaactg cgtcggagtc tgggtctgag tctggcagcc cgaagccntg     120
grmcaccttt tcttgattct ctaaggcggg ggctgcctgc gtccaagcag ctggtttgca     180
gcgttccaac gctgggaggg agttcccta cctggggtcc agtctgtaaa gttgtcgccg      240
ctttctaggg acccgccnnd scggctggga ctcttccatg cgtgagtatt actgarstgc     300
tsnaaggtcc ggc atg tcc ctg gaa cct gcc tcg gsc ctc ttg ggt gtg        349
               Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val
                       -25                 -20
cgg cgg aga ctg ctt tgt cta mct ttc tsc cga ctt ctc tta ggr acc      397
Arg Arg Arg Leu Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr
-15                 -10                 -5                  1
agt ctg ttg aag ttt gtg gkc tcc tgs agy cca ccc ama ccg nat act      445
Ser Leu Leu Lys Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr
            5                   10                  15
ctc acc tct tcc                                                       457
Leu Thr Ser Ser
        20
```

<210> 231
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..110

<221> sig_peptide
<222> 12..83
<223> Von Heijne matrix
score 6.40000009536743
seq LSVLILCVCVCVC/VY

<400> 231
ctgattttkc t atg ytg att ttg tat ctk gca act tta cta aat tta tca 50
Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser
-20 -15
gtt cta ata ctt tgt gtg tgt gtg tgt gtg tgt gtg tat gat tta tat 98
Val Leu Ile Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr
-10 -5 1 5
ata waa agg gga gt 112
Ile Xaa Arg Gly

<210> 232
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..358

<221> sig_peptide
<222> 8..55
<223> Von Heijne matrix
score 6.40000009536743
seq LGTTVLLWSLLRS/SP

<221> misc_feature
<222> 326
<223> n=a, g, c or t

<400> 232
gataatc atg gcg ccc ctc gga aca act gta ttg ctg tgg agc ctc ttg 49
Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu
-15 -10 -5
agg agt tct ccg ggc gtg gaa cgg gtc tgt ttc cgg gct cga atc cag 97
Arg Ser Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln
1 5 10
ccc tgg cac ggt ggc ctg ctc caa ccg cta cct tgc tct ttc gag atg 145
Pro Trp His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met
15 20 25 30
ggg ctg cca cgc cgc cgg ttc agc tcc gag gcc gca gaa tct ggt agc 193
Gly Leu Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser
35 40 45
cca gag acc aag aaa cct aca ttt atg gat gag gaa gtt caa agc ata 241
Pro Glu Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile
50 55 60
ctc acg aaa atg aca ggc ttg aac ttg cag aag act ttt aag cca gct 289
Leu Thr Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala
65 70 75
ata caa gaa ctg aag cca cca acc tat aag cta atg nct cag gca cag 337
Ile Gln Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln
80 85 90
ttg gaa gag gct aca aga cag g 359
Leu Glu Glu Ala Thr Arg Gln
95 100

<210> 233
<211> 301
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 4..300

<221> sig_peptide
<222> 4..105
<223> Von Heijne matrix
score 6.40000009536743
seq LLFVVLLPPPPGS/VX

<221> misc_feature
<222> 124,129,162
<223> n=a, g, c or t

<400> 233

```
gcg atg ctc ctc act ttc agc tcc agc tcc cgc cac cgc cgc ctc tat        48
    Met Leu Leu Thr Phe Ser Ser Ser Ser Arg His Arg Arg Leu Tyr
                    -30                 -25                 -20
cgc cgc cgc cgc cac cac ctc ctc ttc gtt gtc ctc ctt cct cct ccg        96
Arg Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro
                -15                 -10                 -5
cct ggc agc gtt gkt ctc tgc agc sgg nrm grn smv raa gtg ctr vbg       144
Pro Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Xaa Val Leu Xaa
            1               5                   10
kma sga aag ttc cgg gan gga cta cat gga gcc atg ctc cct ggg ctc       192
Xaa Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu
    15                  20                  25
ttc cgc ggg cgc ccg cgc gct gcc ctt cgc ttg aga gtc tca ccg wgt       240
Phe Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa
30                  35                  40                  45
tgc cca ggc tgg aaa gtg gcg cga tct cgg ctc aca gca acc tcc gcc       288
Cys Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala
                50                  55                  60
tcm cgg gmc cgg g                                                     301
Ser Arg Xaa Arg
            65
```

<210> 234
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..247

<221> sig_peptide
<222> 152..190
<223> Von Heijne matrix
score 6.40000009536743
seq MLLLLQLNLKTLS/SS

<400> 234

```
acaagttggg tgctgtcgcc tgcgcatcgg cgggccggga ggctgagcag tactgttgag      60
agcggtgtga ggtgcttggt agcgcgccgt agctgcttcc acgtccttgc ttcacctcag     120
gtaaagagag aagtaatgga aggcctgtct g atg ttg ctt ctt ttg caa cta       172
                                   Met Leu Leu Leu Leu Gln Leu
                                                       -10
aac tta aaa aca ctc tca tcc agt acc ata gca ttg aag aag ata agt       220
Asn Leu Lys Thr Leu Ser Ser Ser Thr Ile Ala Leu Lys Lys Ile Ser
    -5                  1               5                   10
ggc gag ttg cta aga aaa cga aag agg g                                 248
Gly Glu Leu Leu Arg Lys Arg Lys Arg
                15
```

```
<210> 235
<211> 393
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 339..392

<221> sig_peptide
<222> 339..383
<223> Von Heijne matrix
      score 6.40000009536743
      seq LFVLLIITQLLYG/GI

<400> 235
gttccaaagt gagctgtctc tggcagcatt catatagaat agaatttgaa tggtgcaccc     60
agatttgaac aacatggtaa tcatgtgatg gacatggaaa agtgractaa cbtkrgggat    120
cwtggtargg tcaytaagaa taactckaat cawgatgtta aaaggctttc ctttacattc    180
acaaaacaat ttrsttccta gaagtagttt attcttgcct gtggtcattt ttgctccttt    240
ataatactac atctaaatca atttgttaaa tatagtagag aaatgaaata aatttcttcc    300
agttaaacca ctgcacttaa agagtagaaa ccctctct atg tca ctc ttt gtt ttg    356
                                          Met Ser Leu Phe Val Leu
                                          -15                 -10
ttg atc ata act caa ctg ctg tat ggt ggg ata ctc t                    393
Leu Ile Ile Thr Gln Leu Leu Tyr Gly Gly Ile Leu
                -5                  1

<210> 236
<211> 222
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 121..222

<221> sig_peptide
<222> 121..204
<223> Von Heijne matrix
      score 6.40000009536743
      seq ILFLGVLLSASDL/CV

<400> 236
ttttgagtta atttttgtat aagttgtaag gattaggtca gggttcttaa gaaaaatatt     60
gttttggtct atagatgtct cattgcttct gtgctatttg ttggaaaagc tgttcttcca    120
atg aat tgc ttt tgc aat ttt gtc aaa acc agt gag gca tat atg att      168
Met Asn Cys Phe Cys Asn Phe Val Lys Thr Ser Glu Ala Tyr Met Ile
            -25                 -20                 -15
ctg ttt cta ggt gtt cta ctc tct gca agt gat tta tgt gtc tat ccc      216
Leu Phe Leu Gly Val Leu Leu Ser Ala Ser Asp Leu Cys Val Tyr Pro
        -10                 -5                  1
atc ggg                                                              222
Ile Gly
5

<210> 237
<211> 154
<212> DNA
<213> Homo sapiens

<220>
```

```
<221> CDS
<222> 54..152

<221> sig_peptide
<222> 54..95
<223> Von Heijne matrix
      score 6.40000009536743
      seq SVILALWEAEAGG/SP

<400> 237
agtcttttgc tcctgtggtt aagattattc tgctaggctg ctcacggtgg ctg atg       56
                                                            Met
tct gta atc cta gca ctt tgg gag gcc gag gcg ggc gga tcg cct gag      104
Ser Val Ile Leu Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Pro Glu
            -10                 -5                  1
atc ggg agt tcg gga ccg gcc gca cca aca tgg aga agc ccc gtc cag      152
Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val Gln
    5                   10                  15
gg                                                                   154

<210> 238
<211> 439
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 255..437

<221> sig_peptide
<222> 255..341
<223> Von Heijne matrix
      score 6.30000019073486
      seq LGCLLLAVRSSAT/VN

<221> misc_feature
<222> 359..360,381
<223> n=a, g, c or t


<400> 238
tcaccacaat caattttaga acattttcat catcccgaaa ataagccctg ttccctttag     60
ctgtcactcc ccactcctac cccccagccc tgtgcaataa tctactttct gtctttgaag    120
ctttgcctat tctggacatt ttgtataaaa gggtttgtgg aggatgtggt cttttgtgac    180
tggcttcttg aacttggcat agtgttttca aggttcaacc atgttgtagc acgtacgttc    240
ctttttatgg ccaa atg tac gga gag tcc aca ttg ttt atc cat tca tca      290
                Met Tyr Gly Glu Ser Thr Leu Phe Ile His Ser Ser
                                -25                 -20
gtt cat ggg cat ttg ggt tgt ctc ctc ttg gct gtt agg agt agt gct      338
Val His Gly His Leu Gly Cys Leu Leu Leu Ala Val Arg Ser Ser Ala
        -15                 -10                 -5
act gtg aac att acg tac chn nkw gtk tgt gtg gac att cak ntt cat      386
Thr Val Asn Ile Thr Tyr Xaa Xaa Val Cys Val Asp Ile Xaa Xaa His
    1               5                   10                  15
ttc cat atg ctt atg tct gga att act ggg tca tat ggc aac tct ctt      434
Phe His Met Leu Met Ser Gly Ile Thr Gly Ser Tyr Gly Asn Ser Leu
                20                  25                  30
tca ct                                                               439
Ser

<210> 239
<211> 229
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 7..228

<221> sig_peptide
<222> 7..159
<223> Von Heijne matrix
score 6.30000019073486
seq WLYLLEVVAPLSG/IH

<400> 239
```
gtcaag atg gcg gcg tct gta tta aac acc gtg ctg agg cgg ctt cct        48
       Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro
           -50                 -45                 -40
atg cta tct ctc ttc cga ggt tct cac aga gtt cag gta act ctt cga       96
Met Leu Ser Leu Phe Arg Gly Ser His Arg Val Gln Val Thr Leu Arg
        -35                 -30                 -25
aag aca ttt tgc aca acc tca agt tgg tta tac ctt ctc gag gtt gtc      144
Lys Thr Phe Cys Thr Thr Ser Ser Trp Leu Tyr Leu Leu Glu Val Val
    -20                 -15                 -10
gct cca ctg tca gga atc cac gag tgg aga cct tcc cac gtg tgt ctt      192
Ala Pro Leu Ser Gly Ile His Glu Trp Arg Pro Ser His Val Cys Leu
-5                  1               5                   10
agc tgt cta ggc agt act tcc tgc aac ccc cct gag g                    229
Ser Cys Leu Gly Ser Thr Ser Cys Asn Pro Pro Glu
            15                  20
```

<210> 240
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 65..316

<221> sig_peptide
<222> 65..259
<223> Von Heijne matrix
score 6.30000019073486
seq LMVVAETSQGSWS/AP

<221> misc_feature
<222> 259
<223> n=a, g, c or t

<400> 240
```
ctcttcggtt gtccagccct tctcccagcc ctggtccctc agaaggaggg taactccctt      60
ccag atg tta cgg tcc gcc tgc gtc tct cag cac gcc ggt ggc att tgg      109
     Met Leu Arg Ser Ala Cys Val Ser Gln His Ala Gly Gly Ile Trp
     -65                 -60                 -55
gtt gac cgc gga ggc ccc cag tgc cag agg gtg ttc acg ttc tgc cgt      157
Val Asp Arg Gly Gly Pro Gln Cys Gln Arg Val Phe Thr Phe Cys Arg
-50                 -45                 -40                 -35
ggg ctc agc cca aac ttt gga cgc tca gag acc caa cgg gag cgc tgg      205
Gly Leu Ser Pro Asn Phe Gly Arg Ser Glu Thr Gln Arg Glu Arg Trp
                -30                 -25                 -20
ata agg cca gga cag ctg atg gtt gtg gca gaa aca tct caa ggt agc      253
Ile Arg Pro Gly Gln Leu Met Val Val Ala Glu Thr Ser Gln Gly Ser
            -15                 -10                 -5
```

```
tgg tcn gcc ccc act tcc cca tst acc tct tgt cct ccc ccc aac acc      301
Trp Ser Ala Pro Thr Ser Pro Xaa Thr Ser Cys Pro Pro Pro Asn Thr
        1               5                   10
asc acc aca ccg gyt cc                                               318
Xaa Thr Thr Pro Xaa
15

<210> 241
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 123..404

<221> sig_peptide
<222> 123..257
<223> Von Heijne matrix
      score 6.30000019073486
      seq GFVSLLVVHAADA/WV

<400> 241
tagctggacc cgtctgggag gtaggtttgt gagcgtgaga gaksgatctg taccgcgggg     60
atccgaagta tgcttatcca ggtggctgc ctcaagcctc gatcccaccc ccgcgctdvt     120
ag atg gtg tca agg tcc ttg cgt ggg aga agg act tgg gtg aga tgc      167
   Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys
   -45                 -40                 -35
atg cgg aga ttg ccc cca att ccg gcc tgg agc caa ggg aaa ggg atg      215
Met Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met
-30                 -25                 -20                 -15
cct gga ttt gtg tct cta ttg gtg gtc cac gct gcg gat gcc tgg gta      263
Pro Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val
                -10                 -5                  1
gcc cag agg ttr tct acg cca tac ttc tca ctg ttt ttg agc ata cct      311
Ala Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro
        5                   10                  15
aga tgt tcc ttt cct agg cgg agt ata gat cgc acg tgt tct agc stc      359
Arg Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa
    20                  25                  30
tta gac tca gag ggt tcg agc tct ata asc ccc tcc act ccc ttc a        405
Leu Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe
35                  40                  45

<210> 242
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..242

<221> sig_peptide
<222> 129..191
<223> Von Heijne matrix
      score 6.30000019073486
      seq SLLPCSLISDCCA/SN

<400> 242
cttttgtttt gcaatgccct gcccccagag gtggagtcta cagaggcagg caggcctcct     60
tgagctgagg tgggctccac ccagttcgag cttcccagct gctttgttta cctactcaag    120
cctgggca atg gtg ggc gcc ctt ccc cca gcc tcg ctt ctg cct tgc agt     170
```

```
        Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser
            -20                 -15                 -10
ttg atc tca gac tgc tgt gct agc aat gag cga ggc tcc atg ggc gta      218
Leu Ile Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val
        -5                  1                   5
gga ccc tct gag cca cgg cgy ggg                                      242
Gly Pro Ser Glu Pro Arg Arg Gly
10                  15
```

<210> 243
<211> 363
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 298..363

<221> sig_peptide
<222> 298..357
<223> Von Heijne matrix
score 6.30000019073486
seq LGSLIASLAPSTG/LG

<400> 243

```
accactctga ggagacgcgt gacagataag aagggctggt gggatcagtc ctggtggtag     60
ctcaggaagc agagcctgga gcatctccac tatggcctgg gctccactac ttctcaccct    120
cctcgctcac tgcacaggtt cttgggccaa ctttatgctg actcagccgc actctgtgtc    180
ggagtcgccg gssgaagacg gtaaccatct cctgcacccg cagcagtggc agctttgtca    240
gcaactatgt tcagtggtac cagcggcgcc cggacagtgc ccccaccact gtgatct       297
atg agg atg aca aaa gac cct ctg ggg tct ctg atc gct tct ctg gct      345
Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala
-20                 -15                 -10                 -5
cca tcg aca ggt ctt ggg                                              363
Pro Ser Thr Gly Leu Gly
                1
```

<210> 244
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..323

<221> sig_peptide
<222> 153..236
<223> Von Heijne matrix
score 6.30000019073486
seq FFLFLFFXEXXXX/XX

<400> 244

```
aattgatact gctttagatg tttctgtctc attttacaaa aatgtaagaa aaaagaaaaa     60
tcaaactata ctgttaccta tttcttgtat attcttaaca gaatgttctg tacacataag    120
tgtatgtgtg ttaatcctct tgtttaaatg cc atg aaa ctt cag ttt gcc ttt      173
                                    Met Lys Leu Gln Phe Ala Phe
                                                    -25
tgt tat ttt ctt tat tta gat acc ttt ttt ctt ttt ctt ttt ttt ttk      221
Cys Tyr Phe Leu Tyr Leu Asp Thr Phe Phe Leu Phe Leu Phe Phe Xaa
    -20                 -15                 -10
gag ama gyc tkg cyc kgt kgc hta ggm agg agt gca gtg gca maa cct      269
Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Arg Ser Ala Val Ala Xaa Pro
```

```
-5                    1                   5                   10
cag ctc ayt gca gcc tcc acc ttc kgg tty caa gca att tty ctg ccc       317
Gln Leu Xaa Ala Ala Ser Thr Phe Xaa Phe Gln Ala Ile Phe Leu Pro
            15                  20                  25
cag ckg g                                                             324
Gln Xaa
```

<210> 245
<211> 280
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..278

<221> sig_peptide
<222> 27..233
<223> Von Heijne matrix
score 6.30000019073486
seq GILKVLLFSVVSG/LE

<400> 245

```
gttgcggggc ggggccttcg cagagc atg gcg gcg ggc gag ctt gag ggt ggc       53
                             Met Ala Ala Gly Glu Leu Glu Gly Gly
                                             -65
aaa ccc ctg agc ggg ctg ctg aat gcg ctg gcc cag gac act ttc cac       101
Lys Pro Leu Ser Gly Leu Leu Asn Ala Leu Ala Gln Asp Thr Phe His
-60                 -55                 -50                 -45
ggg tac ccc ggc atc aca gag gag ctg cta cgg agc cag cta tat cca       149
Gly Tyr Pro Gly Ile Thr Glu Glu Leu Leu Arg Ser Gln Leu Tyr Pro
                -40                 -35                 -30
gag gtg cca ccc gag gag ttc cac ccc ttt ctg gca aag atg agg ggg       197
Glu Val Pro Pro Glu Glu Phe His Pro Phe Leu Ala Lys Met Arg Gly
            -25                 -20                 -15
att ctt aag gta ctg ctc ttt tct gta gtc tcc ggc ttg gag cag aac       245
Ile Leu Lys Val Leu Leu Phe Ser Val Val Ser Gly Leu Glu Gln Asn
        -10                 -5                  1
ccc ttg gcc gct ggc ttc aga ctc tcc cac ccg gg                        280
Pro Leu Ala Ala Gly Phe Arg Leu Ser His Pro
5                   10                  15
```

<210> 246
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..210

<221> sig_peptide
<222> 70..162
<223> Von Heijne matrix
score 6.30000019073486
seq SLILSPSPRPVLG/FF

<400> 246

```
tttggctggg gagacccatc tggactacca aggagaagct atagactact tctactccac      60
caggaaggt atg atg atg tca aac gtg atg ctg atg cta cag tta cag ccc      111
          Met Met Met Ser Asn Val Met Leu Met Leu Gln Leu Gln Pro
              -30                 -25                 -20
ctg ctg gcg cas tct ctg att ctc tct ccc tct ccg cgt cca gtg ctg       159
```

```
Leu Leu Ala Xaa Ser Leu Ile Leu Ser Pro Ser Pro Arg Pro Val Leu
        -15                 -10                 -5
ggc ttt ttc aga caa gtg cat ctc cta acc agg tca cat ttc agc cgc      207
Gly Phe Phe Arg Gln Val His Leu Leu Thr Arg Ser His Phe Ser Arg
    1               5                   10                  15
tgg g                                                                211
Trp

<210> 247
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 249..359

<221> sig_peptide
<222> 249..308
<223> Von Heijne matrix
      score 6.19999980926514
      seq LLFICPPPPPISA/SS

<400> 247
tttcagaatt ttgtgcagga atatctgagt atttctaatt agattagaat gtcagaatac     60
attcatggac atatgagggg ttttttaaaa tttttttag atatccttca ccttgaacat     120
ttattatttc tttgtgttgg gaacaatcca aatctctcct agatgttttg aaatgtgcaa    180
tgtattgtta gctgtagtca ccctactgtg ctattgaata ctagagcttg ttccttctgt    240
ctaactgt atg att ata ctc att aac caa ctt ctc ttc atc tgt ccc cca     290
         Met Ile Ile Leu Ile Asn Gln Leu Leu Phe Ile Cys Pro Pro
         -20                 -15                 -10
cct cca ccc atc tca gcc tct agt aac tac cat ttt act ctc tac ctc      338
Pro Pro Pro Ile Ser Ala Ser Ser Asn Tyr His Phe Thr Leu Tyr Leu
    -5                  1               5                   10
cat gac att aac ttt ttt agc                                          359
His Asp Ile Asn Phe Phe Ser
                15

<210> 248
<211> 236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 182..235

<221> sig_peptide
<222> 182..226
<223> Von Heijne matrix
      score 6.19999980926514
      seq DVLLQLLLRVCSP/RT

<400> 248
attgggttaa tttcactgca ctgactattt ttagatatat attctttgtg ccttcactag     60
aactcctctt acttcatgat atcttaacta taaaatcatc caaccatgaa aacaagcaca    120
caagaaacag aaacaaaaca gtcacaaaaa agcataaact gttagcattg atccatgatg    180
a atg act gat gta tta ctt caa ttg cta tta aga gtg tgt tct ccc agg    229
  Met Thr Asp Val Leu Leu Gln Leu Leu Leu Arg Val Cys Ser Pro Arg
  -15                 -10                 -5                  1
acc agg g                                                            236
Thr Arg
```

```
<210> 249
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 266..340

<221> sig_peptide
<222> 266..304
<223> Von Heijne matrix
      score 6.19999980926514
      seq MGLFLCCSLLIFC/LV

<400> 249
taggctattt cttaattttc cttctaggat tcttatagtt tgaagtttta catttagatc      60
gtcaatccat cttgagttca tttttgtata tgatgaaaag taggggtctg attttattct     120
tctgcataag accagttatc ccagaaccgt ttgttgaata ggaagttctt ttctcattgc     180
ttgtttgtgg ggactttgtc aaagatcaaa tagttatagg tgtgtggctg tatttcaggg     240
tttctttatt ccatttcact gatct atg ggt ctg ttt ttg tgc tgc tct tta      292
                            Met Gly Leu Phe Leu Cys Cys Ser Leu
                                        -10                 -5
ctg ata ttc tgt ctg gtt gtt cta atc ata act gaa ctg ggc tat ggg      340
Leu Ile Phe Cys Leu Val Val Leu Ile Ile Thr Glu Leu Gly Tyr Gly
                1               5                   10
gg                                                                    342

<210> 250
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 291..380

<221> sig_peptide
<222> 291..332
<223> Von Heijne matrix
      score 6.19999980926514
      seq GSWALTWLHPAEA/GT

<221> misc_feature
<222> 264..265,279..280
<223> n=a, g, c or t


<400> 250
atacagcggc ctctgacacc agcacagcaa acccgccggg atcaaagtgt accagtcggc      60
agcatgggta aggagagggg tttccaatca cccattgcct gctctgtctg cccctaattt     120
ggaaaggccc tcctccagaa aatgctagaa aacctgagtg gggagctggg gagggagtag     180
tggactctgc ttcattgtcc ccagtctgca cacccccctcc cccaccaccc cactgcattt     240
cccagctcag ccaaactttc tgannaagac gggcagagnn ctgctgggag atg gga        296
                                                      Met Gly
tcc tgg gcc ctg act tgg ctc cat cca gca gag gct ggg acc agg gtg      344
Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr Arg Val
        -10                 -5                  1
cct ttc tgc agc tgg gaa aaa tca gat ggg cgc tct ta                   382
Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser
5                   10                  15

<210> 251
```

```
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 108..302

<221> sig_peptide
<222> 108..233
<223> Von Heijne matrix
      score 6.19999980926514
      seq LSVLSLVINFSWS/RK

<221> misc_feature
<222> 279
<223> n=a, g, c or t


<400> 251
aaaagctgtg aggttgtaac tcagttcagt agtatttata aatatttgtt ttccactttt      60
gtgcatatta tacaaatgat ggatataaaa tttgtttwga ccatwta atg atg ctt       116
                                                    Met Met Leu
                                                            -40
rmw wwr rra aga gga tat cct cat aga act gaa cgt tat gat gga ttt       164
Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr Asp Gly Phe
            -35                 -30                 -25
tta aaa tat tct gac cca aat gat att gca ttg tca gta ctg tcc ctg       212
Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val Leu Ser Leu
        -20                 -15                 -10
gtt att aat ttc tcc tgg agt aga aaa tgc ttt gtt cct tac tat atc       260
Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro Tyr Tyr Ile
    -5                   1               5
cca ttt aaa cct tac cgv nta cct tac ccc acc gcg gcc cgg g             303
Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala Arg
10                  15                  20

<210> 252
<211> 259
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..258

<221> sig_peptide
<222> 106..222
<223> Von Heijne matrix
      score 6.19999980926514
      seq CFVCXLFVFLLSG/LN

<221> misc_feature
<222> 134
<223> n=a, g, c or t


<400> 252
atttaaaagg attttttaaa ggacctctat agttataagt cagcttaatt aaaaatggat      60
attccatagt catatttata tatatataca cacacatata tatgt atg tat gtg tgt     117
                                                  Met Tyr Val Cys
ata tat ata trt tta ana gac ctg tat gat ttt ttt ctt ctt gga act       165
Ile Tyr Ile Xaa Leu Xaa Asp Leu Tyr Asp Phe Phe Leu Leu Gly Thr
```

```
-35                 -30                 -25                 -20
tat ttt ttt gag aga aag tgt ttt gtg tgt ktg ttg ttt gtt ttt ctt       213
Tyr Phe Phe Glu Arg Lys Cys Phe Val Cys Xaa Leu Phe Val Phe Leu
                -15                 -10                 -5
ctc agt gga ctg aat tat ttc tcc att ctg tct ttt tac ccc cgg g         259
Leu Ser Gly Leu Asn Tyr Phe Ser Ile Leu Ser Phe Tyr Pro Arg
            1               5                   10

<210> 253
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..163

<221> sig_peptide
<222> 14..133
<223> Von Heijne matrix
      score 6.19999980926514
      seq FITFIFSFSFCEC/IV

<400> 253
atattttata cac atg tgc ata ttc tgc ctt ttt cat tta cta tat cat         49
               Met Cys Ile Phe Cys Leu Phe His Leu Leu Tyr His
               -40                 -35                 -30
aaa ctt ctt tct aga tca tta ttt ttc tgc tgc att ttt tca gga ttt        97
Lys Leu Leu Ser Arg Ser Leu Phe Phe Cys Cys Ile Phe Ser Gly Phe
            -25                 -20                 -15
atc acc ttt att ttt agt ttt agt ttt tgt gag tgt ata gta ggt atg       145
Ile Thr Phe Ile Phe Ser Phe Ser Phe Cys Glu Cys Ile Val Gly Met
        -10                 -5                  1
tat att tat ggg gca cga ag                                            165
Tyr Ile Tyr Gly Ala Arg
5                   10

<210> 254
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..326

<221> sig_peptide
<222> 207..287
<223> Von Heijne matrix
      score 6.19999980926514
      seq LLIFLYLSLNLFC/IF

<400> 254
aaacgttttc ttttatctaa tttatattaa atttaattaa aataagccag gaggctagtg      60
gctaccatgt tagcagcaca gtcctatata ttctttcact tttgttacat ttgttatcaa     120
ttttaactac tattattatt acatacaata caattttaac aataggagat tgctattaga     180
tgaggcttta acagaaaarv attaav atg ara ata tgc tat aac att ttt caa      233
                             Met Xaa Ile Cys Tyr Asn Ile Phe Gln
                                     -25                 -20
aac att ctc ggc ctc ttg ctt att ttc ctg tat ctt tct ttg aat ctt       281
Asn Ile Leu Gly Leu Leu Leu Ile Phe Leu Tyr Leu Ser Leu Asn Leu
            -15                 -10                 -5
ttt tgt att ttc ttt tct gtc cct gcc ctt caa cct aga aga ctg gg        328
```

```
Phe Cys Ile Phe Phe Ser Val Pro Ala Leu Gln Pro Arg Arg Leu
        1               5                   10

<210> 255
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 233..319

<221> sig_peptide
<222> 233..310
<223> Von Heijne matrix
      score 6.09999990463257
      seq MLTLLGFPSKALT/FI

<221> misc_feature
<222> 129
<223> n=a, g, c or t


<400> 255
caagttgtct cctgcgtagt gtctattagc tcttgaattt cttcaagatc catatactga     60
aacacttcac tctccaactt ttttgccata ttgacaatca ctttcataat ttcacttatt    120
gacyctgynw haaatcmtgt gaagyhatgc agahcatctg gacacagctt tctccagcag    180
ggatyyatdg ttttgggctt gaaggggttt cacggctttt tctataacaa cg atg gca    238
                                                          Met Ala
                                                              -25
tct tca atg ctg waa tcc ttc cag act ttc atg atg ttg act cta ttg      286
Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr Leu Leu
                -20                 -15                 -10
ggt ttc cct tcc aaa gct ttg aca ttc att tcc a                        320
Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser
            -5                  1

<210> 256
<211> 305
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 205..303

<221> sig_peptide
<222> 205..264
<223> Von Heijne matrix
      score 6.09999990463257
      seq LLSLPGSFIPGNC/RP

<400> 256
tttgttttat ttggttattt gttttgtttt gtttctctga ggccaatggg tgggaggaag     60
tataaagaag tgtaaacagg aaagccagct gggcctggag ttccaagtgc ccatatttca    120
tcagcttcct ctccataact gtggcaggga cacttaaccc ttccctggct gtgagaagtt    180
attctctgag ggctggtgag caga atg gga aga tct aag agg cag ctc ctt       231
                           Met Gly Arg Ser Lys Arg Gln Leu Leu
                           -20                 -15
tcc ttg cct ggt tcc ttt atc cct ggg aat tgc agg cca agg att ctg      279
Ser Leu Pro Gly Ser Phe Ile Pro Gly Asn Cys Arg Pro Arg Ile Leu
    -10                 -5                  1               5
agc aat ggw gaa gwc aga agg aag gg                                   305
```

```
Ser Asn Gly Glu Xaa Arg Arg Lys
                10

<210> 257
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..180

<221> sig_peptide
<222> 37..111
<223> Von Heijne matrix
      score 6.09999990463257
      seq CFFLIFLLPPLPA/MI

<400> 257
tttctaatgc tattatcctg mtagtgamta agtctc atg aga tct gat ggg ttt       54
                                        Met Arg Ser Asp Gly Phe
                                        -25                 -20
atc agg ggt ttc tgc ttc tgc ttc ttc cta att ttt ctc ctg cca ccg      102
Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu Ile Phe Leu Leu Pro Pro
                -15                 -10                 -5
ctt cct gcc atg ata ctg agg cct ctg cag cca tgt gga att ata agt      150
Leu Pro Ala Met Ile Leu Arg Pro Leu Gln Pro Cys Gly Ile Ile Ser
            1               5                   10
cca att aaa cct ctt ttt cct ttt ttt ttt t                            181
Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe
    15                  20

<210> 258
<211> 236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 119..235

<221> sig_peptide
<222> 119..166
<223> Von Heijne matrix
      score 6.09999990463257
      seq LWTASSLPLSTHS/QR

<400> 258
caaaaaaatc agtctttaag catttgcttg gtaaggtttc ttaagattag gtttataata     60
caaccatctg taatgtatct stcgtttgag cttgtgggcc atacaattca ttaactag      118
atg aat aca ttg tgg aca gca tcc tca cta ccc ctc tct act cac tca      166
Met Asn Thr Leu Trp Thr Ala Ser Ser Leu Pro Leu Ser Thr His Ser
    -15                 -10                 -5
caa aga acc atg ata cac tgg aat gtt ttt ctc tgg aat tct ttc tac      214
Gln Arg Thr Met Ile His Trp Asn Val Phe Leu Trp Asn Ser Phe Tyr
1               5                   10                  15
tct tgt att aaa att ttt ccc c                                        236
Ser Cys Ile Lys Ile Phe Pro
            20

<210> 259
<211> 265
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 128..265

<221> sig_peptide
<222> 128..220
<223> Von Heijne matrix
score 6.09999990463257
seq CLIGLLVPLLGWG/NQ

<400> 259
gacttaggat ttgagcatct ttctgttatg ctgttgcccc actcctattg caatactccc 60
cttcttaaga aagtttttct agactaatgt ctagattaaa cttcttttct ttgacaataa 120
tgatgcc atg act tgg aca aaa tgc cca ttg cct ctg ggt cct gct ttc 169
Met Thr Trp Thr Lys Cys Pro Leu Pro Leu Gly Pro Ala Phe
-30 -25 -20
ttc acc cag tgc tgc ctt att gga ctc ctt gtg cct ctc ctt ggc tgg 217
Phe Thr Gln Cys Cys Leu Ile Gly Leu Leu Val Pro Leu Leu Gly Trp
-15 -10 -5
gga aat cag aat aca cag tgg tat ccc act tct aag atg cct gat ggg 265
Gly Asn Gln Asn Thr Gln Trp Tyr Pro Thr Ser Lys Met Pro Asp Gly
1 5 10 15

<210> 260
<211> 272
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 162..272

<221> sig_peptide
<222> 162..257
<223> Von Heijne matrix
score 6.09999990463257
seq IVYFLVLLRVLYT/LQ

<400> 260
cacaaggttg atttaaaatt cttaaaaaat ttttcaaaat ctttccaaat gaaacaagat 60
ttattgttaa tctacagaaa tatcctccat tcactttgat atttaaatga catcgtacat 120
tttaggtaga gcatttttat gaccactcat tgcttagtct g atg ggg agg agc aat 176
Met Gly Arg Ser Asn
-30
gat ttt agg ttt gcc ttt cta aca tgc ttt ctt gga tgg gaa ata gta 224
Asp Phe Arg Phe Ala Phe Leu Thr Cys Phe Leu Gly Trp Glu Ile Val
-25 -20 -15
tat ttc ttg gtg ctt ctt cgt gtt tta tac act tta caa tgg ggt ggg 272
Tyr Phe Leu Val Leu Leu Arg Val Leu Tyr Thr Leu Gln Trp Gly Gly
-10 -5 1 5

<210> 261
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..97

<221> sig_peptide

<222> 26..79
<223> Von Heijne matrix
score 6.09999990463257
seq LTSFLTYMPLISS/SC

<400> 261
```
tttctaggta tacaatcata ttata atg aaa aca gat aat ttg act tct ttt       52
                            Met Lys Thr Asp Asn Leu Thr Ser Phe
                                            -15                 -10
ctt aca tat atg cct ctt att tct tcc tct tgc tca att gct ccc t         98
Leu Thr Tyr Met Pro Leu Ile Ser Ser Ser Cys Ser Ile Ala Pro
                -5                  1               5
```

<210> 262
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..417

<221> sig_peptide
<222> 28..264
<223> Von Heijne matrix
score 6.09999990463257
seq ATVAVLSFILSSA/AK

<400> 262
```
attcccgggc cctggcttct tggcgcg atg agg ttc cgg ttc tgt ggt gat ctg     54
                              Met Arg Phe Arg Phe Cys Gly Asp Leu
                                                  -75
gac tgt ccc gac tgg gtc ctg gca gaa atc agc acg ctg gcc aag atg      102
Asp Cys Pro Asp Trp Val Leu Ala Glu Ile Ser Thr Leu Ala Lys Met
-70                 -65                 -60                 -55
tcc tct gtg aag ttg cgg ctg ctc tgc agc cag gta cta aag gag ctg      150
Ser Ser Val Lys Leu Arg Leu Leu Cys Ser Gln Val Leu Lys Glu Leu
                -50                 -45                 -40
ctg gga cag ggg att gat tat gag aag atc ctg aag ctc acg gct gac      198
Leu Gly Gln Gly Ile Asp Tyr Glu Lys Ile Leu Lys Leu Thr Ala Asp
            -35                 -30                 -25
gcc aag ttt gag tca ggc gat gtg aag gcc aca gtg gca gtg ctg agt      246
Ala Lys Phe Glu Ser Gly Asp Val Lys Ala Thr Val Ala Val Leu Ser
        -20                 -15                 -10
ttc atc ctc tcc agt gcg gcc aag cac agt gtc gat ggc gaa tcc ttg      294
Phe Ile Leu Ser Ser Ala Ala Lys His Ser Val Asp Gly Glu Ser Leu
    -5                  1               5                   10
tcc agt gaa ctg cag cag ctg ggg ctg ccc aaa gag cac gcg gcc agc      342
Ser Ser Glu Leu Gln Gln Leu Gly Leu Pro Lys Glu His Ala Ala Ser
                15                  20                  25
ctg tgc cgc tgt tat gag gag aag caa agc ccc ttg cag aag cac ttg      390
Leu Cys Arg Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln Lys His Leu
            30                  35                  40
cgg gtc tgc agc cta cgc atg aat agg tt                               419
Arg Val Cys Ser Leu Arg Met Asn Arg
        45                  50
```

<210> 263
<211> 371
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> 133..369

<221> sig_peptide
<222> 133..174
<223> Von Heijne matrix
score 6.09999990463257
seq FLAALFTVAKIWK/QP

<400> 263
```
cactatggag aactgtatgg cgggtcctca aaaaactaaa aatagaactc ccatatgatc      60
cagcaatccc attgctaggt atataccccc ccaaaaaagg aaatcagtat atgaaagaga     120
tatctgaatc cc atg ttt ctt gca gca ctg ttt aca gta gct aag att tgg     171
              Met Phe Leu Ala Ala Leu Phe Thr Val Ala Lys Ile Trp
                              -10                 -5
aag caa cct aag tgt tca tca aca aac aaa tgg aca aag aaa atg tgg      219
Lys Gln Pro Lys Cys Ser Ser Thr Asn Lys Trp Thr Lys Lys Met Trp
    1               5                  10                  15
tac ata tac aca atg gag tac tat tca gcc ata aaa aaa gat gat atc      267
Tyr Ile Tyr Thr Met Glu Tyr Tyr Ser Ala Ile Lys Lys Asp Asp Ile
                20                  25                  30
ctg tca ttt gca aca ata tgg atg gaa ctg gag agc att aca tta agt      315
Leu Ser Phe Ala Thr Ile Trp Met Glu Leu Glu Ser Ile Thr Leu Ser
            35                  40                  45
gaa ata agt ggg sca cca aaa gac aaa ctt ctc atg ttc tca ctc att      363
Glu Ile Ser Gly Xaa Pro Lys Asp Lys Leu Leu Met Phe Ser Leu Ile
        50                  55                  60
tgt gga ag                                                           371
Cys Gly
    65
```

<210> 264
<211> 283
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 194..283

<221> sig_peptide
<222> 194..274
<223> Von Heijne matrix
score 6.09999990463257
seq LSILQSLVPAAGA/XS

<400> 264
```
ctcattccct gtcctcggat cacagtctct tctcactaca gtgtcgccgc ctctgcctgc      60
gtascccggc catggctctg tagcctcgac ccctttgtgc ccccggcccg tctccgcgct     120
caccacgcct gcgctctccg ctcccacctt ctttcttcag ccgaggccgc cgccgcctct     180
ccttgctgca gcc atg gag tct tcc act ttc gcc ttg gtg cct gtc ttc       229
               Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe
                           -25                 -20
gcc cac ctg agc atc ctc cag agc ctc gtg cca gct gct ggt gca gyc      277
Ala His Leu Ser Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa
-15                 -10                 -5                  1
tct cct                                                              283
Ser Pro
```

<210> 265
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 117..368

<221> sig_peptide
<222> 117..350
<223> Von Heijne matrix
score 6.09999990463257
seq LLWFLQTFFFGIA/SL

<400> 265
aaagcgcgct cccggggagg tgttgcagcc atggctacgg cagccggcgc gacctacttt 60
cagcgaggca gtctgttctg gttcacagtc atcaccctca gctttggcta ctacac atg 119
Met
ggt tgt ctt ctg gcc tca gag tat ccc tta tca gaa cct tgg gcc cct 167
Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala Pro
-75 -70 -65
ggg ccc ttc act cag tac ttg gtg gac cac cat cac acc ctc ctg tgc 215
Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu Cys
-60 -55 -50
aat ggg tat tgg ctt gcc tgg ctg att cat gtg gga gag tcc ttg tat 263
Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu Tyr
-45 -40 -35 -30
gcc ata gta ttg tgc aag cat aaa ggc atc aca agt ggt cgg gct cag 311
Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala Gln
-25 -20 -15
cta ctc tgg ttc cta cag act ttc ttc ttt ggg ata gcg tct ctc asc 359
Leu Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu Xaa
-10 -5 1
atc ttg att gc 370
Ile Leu Ile
5

<210> 266
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 178..273

<221> sig_peptide
<222> 178..225
<223> Von Heijne matrix
score 6.09999990463257
seq WIWVASILLRIFA/SV

<400> 266
tatcgtgaaa gaatattgaa ttttatcaaa tctttttttg tatctgttga gatgattaca 60
tggttattat ccttcattct gttgatgtga tgtatcacat ttattgattt gcatatgttg 120
aaccctcctt gcatccctgg aatgattcct acttcattat agtgtataat ctttttg 177
atg tgc tgt tgg att tgg gtt gct agt att ttg ttg aga att ttt gca 225
Met Cys Cys Trp Ile Trp Val Ala Ser Ile Leu Leu Arg Ile Phe Ala
-15 -10 -5
tct gtg tta atc agg gat att tac ctg tgg ttt tct ttt ttt ttt ttt t 274
Ser Val Leu Ile Arg Asp Ile Tyr Leu Trp Phe Ser Phe Phe Phe Phe
1 5 10 15

<210> 267
<211> 342
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 232..342

<221> sig_peptide
<222> 232..300
<223> Von Heijne matrix
score 6.09999990463257
seq LLFFXLWLRYKES/GR

<221> misc_feature
<222> 158
<223> n=a, g, c or t

<400> 267

```
caagttatct caatttcttc tgagaagaaa tatagtttca aaatcaatca ataaagataa      60
tcctctgata aagtaagatc tgaatataca aatcatggtt acagtaatct taccattata     120
tataaattac ctctcaaaca aatgggccat tcagaarnrg gctcagagtg aattagctgg     180
aggggttgtc aagggtcata gtttttactg ctttgaagag attatcactg g atg att      237
                                                         Met Ile
tcc tca cat tta tat aac ttc agt ctc ctg ttc ttt kta ctc tgg ctg       285
Ser Ser His Leu Tyr Asn Phe Ser Leu Leu Phe Phe Xaa Leu Trp Leu
    -20                 -15                 -10
agg tac aag gaa tca gga aga gag ggc aac tgt gag gaa gga gca ttc       333
Arg Tyr Lys Glu Ser Gly Arg Glu Gly Asn Cys Glu Glu Gly Ala Phe
-5                  1               5                   10
tcc agg tgg                                                           342
Ser Arg Trp
```

<210> 268
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 62..427

<221> sig_peptide
<222> 62..112
<223> Von Heijne matrix
score 6.09999990463257
seq RLLLLPRPPASTG/AS

<400> 268

```
agttgagtgg aaatgggcaa cggcgggcgg agcggcctgc agcaggggaa ggggaacgtg      60
g atg ggg tgg cag cga ctc cta ctg ctg cct cgg cct cct gcc agt aca    109
  Met Gly Trp Gln Arg Leu Leu Leu Leu Pro Arg Pro Pro Ala Ser Thr
          -15                 -10                 -5
ggt gca tcg aat gca acc agg rrg cca aag agk ttg tac cga grc tat      157
Gly Ala Ser Asn Ala Thr Arg Xaa Pro Lys Xaa Leu Tyr Arg Xaa Tyr
    1               5                   10                  15
aac cac ggt gtg ctg aag ata acc atc tgt aaa tcc tgc cag aaa cct      205
Asn His Gly Val Leu Lys Ile Thr Ile Cys Lys Ser Cys Gln Lys Pro
                20                  25                  30
gta gac aaa tat atc gag tat gat cct gtt atc atc ttg awk aat gct      253
Val Asp Lys Tyr Ile Glu Tyr Asp Pro Val Ile Ile Leu Xaa Asn Ala
            35                  40                  45
ata ttg tgc aaa gct cad gcc tac agr cat att ctt ttc aat act caa      301
Ile Leu Cys Lys Ala Xaa Ala Tyr Arg His Ile Leu Phe Asn Thr Gln
```

```
        50                          55                          60
ata aat aac aaa ctg cct att tta ttg gca ttt tta cct tcc tgt ggv      349
Ile Asn Asn Lys Leu Pro Ile Leu Leu Ala Phe Leu Pro Ser Cys Gly
    65                      70                      75
dga acg gcc cat gac ggc aaa aaa aag ccc aac ttc att ttg ctg ctg      397
Xaa Thr Ala His Asp Gly Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu
80                      85                      90                  95
aaa sat tat tat tat cta gct acg gaa aac                              427
Lys Xaa Tyr Tyr Tyr Leu Ala Thr Glu Asn
                100                 105
```

<210> 269
<211> 143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..142

<221> sig_peptide
<222> 20..76
<223> Von Heijne matrix
score 6
seq LLALVVRVILSTA/IL

<400> 269

```
ctttctttgc ggaatcacc atg gcg gct ggg gta agt ttg ctg gct ctg gtg      52
                     Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val
                                     -15                 -10
gtt cgg gtc atc cta tcc acc gcc atc ctt tgc ccg agt ggg gcc agt      100
Val Arg Val Ile Leu Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser
            -5                      1               5
cgg cgc cag agg agt tct gag gtt gag tgg gga act gat tcg g            143
Arg Arg Gln Arg Ser Ser Glu Val Glu Trp Gly Thr Asp Ser
    10                  15                  20
```

<210> 270
<211> 79
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..79

<221> sig_peptide
<222> 23..67
<223> Von Heijne matrix
score 6
seq PLFWLILCSGLLC/NK

<221> misc_feature
<222> 2..3
<223> n=a, g, c or t

<400> 270

```
tnngctaatc ttgcttgtac tt atg aat cct tta ttc tgg ttg att ctc tgc      52
                         Met Asn Pro Leu Phe Trp Leu Ile Leu Cys
                         -15                 -10
tct ggg tta tta tgt aac aag tca ttt                                  79
Ser Gly Leu Leu Cys Asn Lys Ser Phe
```

-5 1

<210> 271
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..120

<221> sig_peptide
<222> 61..114
<223> Von Heijne matrix
score 6
seq ISIFLSSLSLSLS/LF

<400> 271
```
cttccttaag aagcggtttc tctcccctct tttctctctc tcacctgggt ttgtttgtcc   60
atg aga ggg gct tgg ata agt ata ttt ctt tct tct cta tct ctc tct    108
Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
            -15                 -10                 -5
ctc tct ctt ttt t                                                  121
Leu Ser Leu Phe
        1
```

<210> 272
<211> 292
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..291

<221> sig_peptide
<222> 196..267
<223> Von Heijne matrix
score 6
seq LFVLLPHFFLSFL/SP

<400> 272
```
ctcatggact gtggctgtct tattttatgt ctctaatacc agattatgaa aatcacagaa   60
aaaaggaaaa aatattattt ccaaagagta agttatgaag ccatgttaga aacccatatg  120
acaatatgaa tttcttttat ctgtcaatct caaggtagaa ttcctcatat ttctgataat  180
gccaaatacc atgaa atg tct caa aaa aga ctt gac ttt ata tac cag ttg   231
                 Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu
                                 -20                 -15
ttt gtc ttg ctg cct cac ttc ttc ctt tct ttt ctt tct ccc ttt tat    279
Phe Val Leu Leu Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr
        -10                 -5                  1
ctg cac cca tgg g                                                  292
Leu His Pro Trp
5
```

<210> 273
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..157

<221> sig_peptide
<222> 2..100
<223> Von Heijne matrix
score 6
seq LAHFLIGLTVCFG/EG

<400> 273
```
c atg tac ctg tac ctg ttg tcc att tgt atg tct tct ttg aag aaa tgt      49
  Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
              -30                 -25                 -20
cta ttc aag ttc tta gcc cac ttt tta atc ggg tta aca gtt tgt ttt        97
Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
        -15                 -10                 -5
ggt gag ggr wgg cta atg agt tat agg agt tct tat tta tta ctt aaa       145
Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
    1               5                  10                  15
gga cca ccg ggg g                                                     158
Gly Pro Pro Gly
```

<210> 274
<211> 113
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..111

<221> sig_peptide
<222> 31..96
<223> Von Heijne matrix
score 6
seq CLLVFLLTEWTSS/KL

<400> 274
```
cctttggtct ttgatgatgg tgacatacag atg ggg ttt tgg tgt gaa tgt cct       54
                                 Met Gly Phe Trp Cys Glu Cys Pro
                                             -20                 -15
ttc tgt ttg tta gtt ttc ctt cta aca gag tgg acc tct agc aaa ctc       102
Phe Cys Leu Leu Val Phe Leu Leu Thr Glu Trp Thr Ser Ser Lys Leu
                -10                 -5                   1
caa aag acg gg                                                        113
Gln Lys Thr
        5
```

<210> 275
<211> 254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 182..253

<221> sig_peptide
<222> 182..247
<223> Von Heijne matrix
score 6
seq VLHLFPLTPASTG/HW

<400> 275
```
cccatctgcc tgctcccact aggggtctga gtagcaggca ccgaagaagt gagccacgcc      60
```

```
ctcttcacac accctttgag gaggacaagg gaacttttcc tgtttcagaa agttgtgttg    120
agaagaatgg caaggctaac agggcaggtg tccgggcgga ggggcggaac tggctgttgg    180
c atg tgg tgg ggg aga tgc ttc atc cgg gtc ttg cat ttg ttc cct ctg    229
  Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu
          -20                 -15                 -10
aca cca gcc tcg aca gga cac tgg g                                    254
Thr Pro Ala Ser Thr Gly His Trp
    -5                  1
```

<210> 276
<211> 364
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 189..362

<221> sig_peptide
<222> 189..275
<223> Von Heijne matrix
score 6
seq LFMALPPVLSSHG/SR

<400> 276

```
acttgcactt gcttgttggt gtcagagccc gtccctaaac cagggctcca tatgggctgc     60
ctgtctgccg caacacagcc tagcggggaa acagtagaaa tgccacttct atgtatttat    120
catatttatt ttgagataat taacgaagac gttaaataaa gccagactgc actgacccct    180
ggggcgcc atg cga gac ccc ctc gcg gac atg gta cac agt tat tta tca     230
         Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser
                         -25                 -20
tcg tct ttg ttc atg gcc ctt cca cca gtg ctg agc tca cat ggc agc      278
Ser Ser Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser
-15                 -10                 -5                   1
agg aac ctg aga atc tgg ggg agt cca ttt ggt gga gcg ctg act aag      326
Arg Asn Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys
            5                   10                  15
ggc aaa gca ccc cca acc cca gca caa cca gcc ctg gg                   364
Gly Lys Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu
        20                  25
```

<210> 277
<211> 130
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..129

<221> sig_peptide
<222> 46..96
<223> Von Heijne matrix
score 6
seq WLCLPCSLCVSQL/LP

<400> 277

```
gtctttgcag gmvtgtttgt gctccaacag ggagctgagt ttgtc atg agc agt gcc     57
                                                  Met Ser Ser Ala
                                                          -15
tgg ctg tgt ctg cca tgc tcc ctg tgt gtg tcc cag ctc ctt ccc tct      105
Trp Leu Cys Leu Pro Cys Ser Leu Cys Val Ser Gln Leu Leu Pro Ser
            -10                 -5                  1
```

```
tat tcc ctg ttg atc cca gcc ccg g                                  130
Tyr Ser Leu Leu Ile Pro Ala Pro
    5                   10

<210> 278
<211> 184
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..183

<221> sig_peptide
<222> 103..165
<223> Von Heijne matrix
      score 5.90000009536743
      seq LSLLGPLXPPMRA/CS

<400> 278
cattatgttg acatttctag ctacaaggcc agtattttac aaaataaggc cttttccctt    60
aattaaggtt gtgacagata aaagtatatt cccagctgac tc atg tca ccc atg      114
                                               Met Ser Pro Met
                                                   -20
tgg gca ggc cta tta tcc cta ctt ggc ccg ctc wgt ccg cct atg agg      162
Trp Ala Gly Leu Leu Ser Leu Leu Gly Pro Leu Xaa Pro Pro Met Arg
        -15                 -10                 -5
gct tgc tct gtg tgc gta ctc t                                        184
Ala Cys Ser Val Cys Val Leu
    1               5

<210> 279
<211> 265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..265

<221> sig_peptide
<222> 149..202
<223> Von Heijne matrix
      score 5.90000009536743
      seq LSIADLLPSSSFA/NP

<400> 279
tgagcatttc ccaacatatc tgttgagttt ttaactcttt ttatgatctt ttttatttct    60
aggagttcta tttggttctt ttccaagtca gctatgtcat gttttaawag tttccwgtcc   120
ttdgcrrtwc twttctawct tgaggttt atg tct tta aac gag tta agc ata      172
                               Met Ser Leu Asn Glu Leu Ser Ile
                                               -15
gct gat tta tta ccc agc tca tcc ttt gct aat ccc aag ctg agt ggg      220
Ala Asp Leu Leu Pro Ser Ser Ser Phe Ala Asn Pro Lys Leu Ser Gly
-10                 -5                  1               5
ccg att tct atc tcg gtc act tca gct ggt tct cct ccc ggg gcg          265
Pro Ile Ser Ile Ser Val Thr Ser Ala Gly Ser Pro Pro Gly Ala
            10                  15                  20

<210> 280
<211> 188
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 110..187

<221> sig_peptide
<222> 110..154
<223> Von Heijne matrix
      score 5.90000009536743
      seq DLLGTAFLEGSLA/AY

<400> 280
taataataat aataataaat ttttctgtta gattagtaga tgttaagatt atggacaaaa      60
tccaacgtag attggagtat agagaagtgg acctttctgt gtggtcttg atg aaa gac     118
                                                      Met Lys Asp
                                                      -15
tta ctt ggc act gcc ttt ctg gag gga agt tta gca gca tat ctc acc       166
Leu Leu Gly Thr Ala Phe Leu Glu Gly Ser Leu Ala Ala Tyr Leu Thr
        -10                 -5                  1
atg gcc aat ata acc cat gtg g                                         188
Met Ala Asn Ile Thr His Val
5                   10

<210> 281
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..177

<221> sig_peptide
<222> 91..147
<223> Von Heijne matrix
      score 5.90000009536743
      seq HLFMCLLTICISS/LE

<400> 281
gccaacttgt tttttgctgt agttttgatt agagccattc tactgggtgt gaagtgatat      60
tttgatgttg ttttgatttg catttccttg atg gct aat gac att aag cat ctt      114
                                 Met Ala Asn Asp Ile Lys His Leu
                                                 -15
ttc atg tgc tta ttg acc ata tgt ata tct tct ttg gag aaa ctt cca      162
Phe Met Cys Leu Leu Thr Ile Cys Ile Ser Ser Leu Glu Lys Leu Pro
    -10                 -5                  1               5
ttc ttt ttt ttt ttt                                                  177
Phe Phe Phe Phe Phe
                10

<210> 282
<211> 336
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..335

<221> sig_peptide
<222> 42..113
<223> Von Heijne matrix
      score 5.90000009536743
```

```
      seq ATLVGFTVGSVLG/QI

<400> 282
ttgcctatta ctcttatatc tacagtgtgg tggacctggg c atg tac cag aaa gtc      56
                                              Met Tyr Gln Lys Val
                                                              -20
aca agt tac tgt cga agt gcc act ttg gtg ggc ttt aca gtg ggc tct       104
Thr Ser Tyr Cys Arg Ser Ala Thr Leu Val Gly Phe Thr Val Gly Ser
                -15                 -10                 -5
gtc cta ggg caa atc ctt gtc tca gtg gca ggc tgg tcg ctg ttc agc       152
Val Leu Gly Gln Ile Leu Val Ser Val Ala Gly Trp Ser Leu Phe Ser
            1               5                   10
ctg aat gtc atc tct ctt acc tgt gtt tca gtg gct ttt gct gtg gcc       200
Leu Asn Val Ile Ser Leu Thr Cys Val Ser Val Ala Phe Ala Val Ala
    15                  20                  25
tgg ttt tta cct atg cca cag aag agc ctc ttc ttt cac cac att cct       248
Trp Phe Leu Pro Met Pro Gln Lys Ser Leu Phe Phe His His Ile Pro
30                  35                  40                  45
tct acc tgc cag aga gtg aat ggc atc aag gta caa aat ggt ggc att       296
Ser Thr Cys Gln Arg Val Asn Gly Ile Lys Val Gln Asn Gly Gly Ile
                50                  55                  60
gtt act gac acc cag ctt cta aca cct tcc tgg ctg gga g                 336
Val Thr Asp Thr Gln Leu Leu Thr Pro Ser Trp Leu Gly
            65                  70

<210> 283
<211> 294
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 238..294

<221> sig_peptide
<222> 238..288
<223> Von Heijne matrix
      score 5.90000009536743
      seq ALFFLLRIAWLLG/LF

<221> misc_feature
<222> 227
<223> n=a, g, c or t


<400> 283
acatacacgt caattaatct gattcatccc ataaacaaaa ctaaagataa aaaccatgtg      60
attatctcaa tatatgcaga aaaggctttc aataaaattc aaggcctctc catattaaaa     120
actctaaaaa atctgggtat tgaggaarca tagctcaaaa gtgatgrgct gtttttgtac     180
cagtatcatg ctgttttggt tactgtagcc ctgtagtata gtttgangtt gggtaac        237
atg atg cct cca gct ttg ttc ttt ttg ctg agg att gct tgg cta tta       285
Met Met Pro Pro Ala Leu Phe Phe Leu Leu Arg Ile Ala Trp Leu Leu
        -15                 -10                 -5
ggg ctc ttt                                                           294
Gly Leu Phe
    1

<210> 284
<211> 203
<212> DNA
<213> Homo sapiens

<220>
```

<221> CDS
<222> 90..203

<221> sig_peptide
<222> 90..152
<223> Von Heijne matrix
score 5.90000009536743
seq ALSLWASVSPSWM/CR

<400> 284
catctttcgg cctagatgga ggaaccgtgt gctggctggg caggctgctg gcagaggtca 60
ggagggctct tccctgagcc ctgccatcc atg aac tgt gta act ttg atc cag 113
Met Asn Cys Val Thr Leu Ile Gln
-20 -15
gcc ttg tcc ctc tgg gcc tca gtt tcc cca agc tgg atg tgt cgt ccc 161
Ala Leu Ser Leu Trp Ala Ser Val Ser Pro Ser Trp Met Cys Arg Pro
-10 -5 1
cct gct tca ttc ata atc acc acc acc acc acc acc tgc ggg 203
Pro Ala Ser Phe Ile Ile Thr Thr Thr Thr Thr Thr Cys Gly
5 10 15

<210> 285
<211> 297
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 240..296

<221> sig_peptide
<222> 240..287
<223> Von Heijne matrix
score 5.90000009536743
seq LLSLMARTDLVFC/SP

<221> misc_feature
<222> 107
<223> n=a, g, c or t

<400> 285
aggcattgtc taggctgctg ggcacatgag ctccgggatg cccatgtcct ctggccaggc 60
agacacagac ctggggcagc accagctttc tgatggcagc ctgctcnttc caacagttcc 120
ctaccagaat cctgcctcac tggagcagag gatgccagca tcagccggga accactcctg 180
tgctaaaacc gccttggtgg cctgtggctt gaggtcttga tgcggatgaa gccggagga 239
atg ttg tct ctc ctc agt ctc atg gca agg act gat ctt gtt ttc tgt 287
Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys
-15 -10 -5
tcc cca cgg g 297
Ser Pro Arg
1

<210> 286
<211> 774
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..772

<221> sig_peptide

```
<222> 8..109
<223> Von Heijne matrix
      score 5.90000009536743
      seq MAVLAPLIALVYS/VP

<221> misc_feature
<222> 486,565
<223> n=a, g, c or t


<400> 286
agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca        49
        Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala
                        -30                 -25
gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct        97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-20                 -15                 -10                 -5
ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac       145
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
                1               5                   10
tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa       193
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
        15                  20                  25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac       241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn
    30                  35                  40
ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt       289
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
45                  50                  55                  60
gcc att gtg atg atg aag aac cgc aga tcc atc act gtg gag caa cat       337
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His
                65                  70                  75
ata ggc aac att ttc atg ttt agt aaa gtg gcc aac aca att ctt ttc       385
Ile Gly Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe
            80                  85                  90
ttc cgc ttg gat att cgc atg ggc cta ctt tac atc aca ctc tgc ata       433
Phe Arg Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile
        95                  100                 105
gtg ttc ctg atg acg tgc aaa ccc ccc cta tat atg ggc cct gag tat       481
Val Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr
    110                 115                 120
atc ang tac ttc aat gat aaa acc att gat gag gaa cta gaa cgg gac       529
Ile Xaa Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp
125                 130                 135                 140
aag agg gtc act tgg att gtg gag ttc ttt gcc aan tgg tct aat gac       577
Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Xaa Trp Ser Asn Asp
                145                 150                 155
tgc caa tca ttt gcc cct atc tat gct gac ctc tcc ctt aaa tac aac       625
Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn
            160                 165                 170
tgt aca ggg cta aat ttt ggg aag gtg gat gtt gga cgc tat act gat       673
Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg Tyr Thr Asp
        175                 180                 185
gtt agt acg cgg tac aaa gtg agc aca tca ccc ctc acc aag caa ctc       721
Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr Lys Gln Leu
    190                 195                 200
cct acc ctg atc ctg ttc caa ggt ggc aag gag gca atg cgg cgg cca       769
Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met Arg Arg Pro
205                 210                 215                 220
cag at                                                                774
Gln

<210> 287
```

<211> 614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 155..613

<221> sig_peptide
<222> 155..205
<223> Von Heijne matrix
score 5.80000019073486
seq LWLKLLAFGFAFL/DT

<400> 287
aaaaaccgaa tctgacatca tcacctagca gttcatgcag ctagcaagtg gtttgttctt 60
agggtaacag aggaggaaat tgttcctcgt ctgataagac aacagtggag aaaggacgca 120
tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
Met Thr Met Tyr Leu Trp Leu
-15
aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
-10 -5 1 5
aca ggg caa agc cca aca cct tcc ccc act gga ttg act aca gca aag 271
Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Leu Thr Thr Ala Lys
10 15 20
atg ccc agt gtt cca ctt tca agt gac ccc tta cct act cac acc act 319
Met Pro Ser Val Pro Leu Ser Ser Asp Pro Leu Pro Thr His Thr Thr
25 30 35
gca ttc tca ccc gca agc acc ttt gaa aga gaa aat gac ttc tca gag 367
Ala Phe Ser Pro Ala Ser Thr Phe Glu Arg Glu Asn Asp Phe Ser Glu
40 45 50
acc aca act tct ctt agt cca gac aat act tcc acc caa gta tcc ccg 415
Thr Thr Thr Ser Leu Ser Pro Asp Asn Thr Ser Thr Gln Val Ser Pro
55 60 65 70
gac tct ttg gat aat gct agt gct ttt ark acc aca ggt gtt tca tca 463
Asp Ser Leu Asp Asn Ala Ser Ala Phe Xaa Thr Thr Gly Val Ser Ser
75 80 85
gta cag acg cct cas ctt ccc acg cac gca gac tcg cag acg ccc tct 511
Val Gln Thr Pro Xaa Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser
90 95 100
gct gga act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac 559
Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn
105 110 115
tca acc cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga 607
Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg
120 125 130
gga gta c 614
Gly Val
135

<210> 288
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..249

<221> sig_peptide
<222> 124..174
<223> Von Heijne matrix

score 5.80000019073486
seq LWLKLLAFGFAFL/DT

<400> 288
atttttattt acttttacat ttttgattcg tttttacaga gaaaaacttc tacagagata 60
acaattattt tgcttttcag aaggacgcat gctgtttctt agggacacgg ctgacttcca 120
gat atg acc atg tat ttg tgg ctt aaa ctc ttg gca ttt ggc ttt gcc 168
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala
-15 -10 -5
ttt ctg gac aca gaa gta ttt gtg aca ggg caa agc cca aca cct tcc 216
Phe Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser
1 5 10
ccc act ggt gtt tca tca gta cag acg ccc cag gg 251
Pro Thr Gly Val Ser Ser Val Gln Thr Pro Gln
15 20 25

<210> 289
<211> 416
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 155..415

<221> sig_peptide
<222> 155..205
<223> Von Heijne matrix
score 5.80000019073486
seq LWLKLLAFGFAFL/DT

<400> 289
aaaaaccgaa tctgacatca tcacctagca gttcatgcag ctagcaagtg gtttgttctt 60
agggtaacag aggaggaaat tgttcctcgt ctgataagac aacagtggag aaaggacgca 120
tgctgtttct tagggacacg gctgacttcc agat atg acc atg tat ttg tgg ctt 175
Met Thr Met Tyr Leu Trp Leu
-15
aaa ctc ttg gca ttt ggc ttt gcc ttt ctg gac aca gaa gta ttt gtg 223
Lys Leu Leu Ala Phe Gly Phe Ala Phe Leu Asp Thr Glu Val Phe Val
-10 -5 1 5
aca ggg caa agc cca aca cct tcc ccc act ggt gtt tca tca gta cag 271
Thr Gly Gln Ser Pro Thr Pro Ser Pro Thr Gly Val Ser Ser Val Gln
10 15 20
acg cct cac ctt ccc acg cac gca gac tcg cag acg ccc tct gct gga 319
Thr Pro His Leu Pro Thr His Ala Asp Ser Gln Thr Pro Ser Ala Gly
25 30 35
act gac acg cag aca ttc agc ggc tcc gcg sca atg caa aac tca acc 367
Thr Asp Thr Gln Thr Phe Ser Gly Ser Ala Xaa Met Gln Asn Ser Thr
40 45 50
cta ccc cag gca gca atg cta tct cag atg tcc cag gag aga gga gta c 416
Leu Pro Gln Ala Ala Met Leu Ser Gln Met Ser Gln Glu Arg Gly Val
55 60 65 70

<210> 290
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 183..308

<221> sig_peptide

<222> 183..290
<223> Von Heijne matrix
score 5.80000019073486
seq LFLLSGTIWIAIC/KP

<400> 290
```
gaggcctttt ggtcacttag aagaggtgcc aaagatcaag gagaggaaag tggtgggcta     60
caaatgtaaa ttctgtgtgg aagtgcaccc aacgctccga gccatctgca atcacctccg    120
wwagcacgtc cagtatggca atgtcccagc tgtgtcagct gctgtgaagg ggctgcgttc    180
tc atg aga gga gcc acc tgg ccc tgg cca tgt tta ccc gcg agg aca       227
   Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr
       -35                 -30                 -25
agt aca gct gcc agt att gct cgt ttg ttt ctg ctt tca ggc aca att      275
Ser Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile
    -20                 -15                 -10
tgg atc gcc ata tgc aaa ccc acc acg aac ggg g                        309
Trp Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
-5                  1               5
```

<210> 291
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 142..357

<221> sig_peptide
<222> 142..333
<223> Von Heijne matrix
score 5.80000019073486
seq SALLRSLLLPXLX/QI

<221> misc_feature
<222> 282..283
<223> n=a, g, c or t

<400> 291
```
caagtccaca gcgctgggtg cagtacctcc ggcttcttca ggagtccatc tggcctggtg     60
gagttttgcc taagtttcca cggcccsgta aggacccaag agcagaaact ggctgctgag    120
aaacaggctt tgcagagcct g atg gga gtc ctc cca gat ctc gta gta gaa      171
                        Met Gly Val Leu Pro Asp Leu Val Val Glu
                                        -60                 -55
att ttt ggg gtg aac aaa tgc cgg ctg agc tgg ggt cta gtc ctg gag      219
Ile Phe Gly Val Asn Lys Cys Arg Leu Ser Trp Gly Leu Val Leu Glu
                -50                 -45                 -40
tca cta caa caa ccc ctc atc aac agg cat ttg att tac tgc ctt ggg      267
Ser Leu Gln Gln Pro Leu Ile Asn Arg His Leu Ile Tyr Cys Leu Gly
            -35                 -30                 -25
gac atc atc ctg grn ntc ttg gat ctc agt gct ctg ttg agg agt ctg      315
Asp Ile Ile Leu Xaa Xaa Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu
        -20                 -15                 -10
ctg cta cca sct ctg sct cag ata ccc cag gca act cta aga gg           359
Leu Leu Pro Xaa Leu Xaa Gln Ile Pro Gln Ala Thr Leu Arg
    -5                  1               5
```

<210> 292
<211> 254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..254

<221> sig_peptide
<222> 129..173
<223> Von Heijne matrix
score 5.80000019073486
seq ALGFVLLAPRGWG/SL

<400> 292
gtttttcagc tcgccattca cttcgctgtg aagatggcgt cgggcagcgg gacaaaaaac 60
ttggactttc gccgaaagtg ggatgtggga aggtgggcag ggaccagatc aaaggagaca 120
gccaggag atg aca gca ctg ggg ttt gtt ctg tta gct cca cgt ggc tgg 170
Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp
-15 -10 -5
ggg agc ctc aca gtc atg gtg gaa ggc aag gaa gag caa gtc acg tct 218
Gly Ser Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser
1 5 10 15
tac acg gat ggc agc agg caa aga gac agc aat ttt 254
Tyr Thr Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe
20 25

<210> 293
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..412

<221> sig_peptide
<222> 221..337
<223> Von Heijne matrix
score 5.80000019073486
seq LISFLHTLQVVCS/VI

<400> 293
gtcagagcac atccggtgtt agaagcgctg gtaggccttg gagaggcggg ttaggaagag 60
tggagactgc tgcacggact ctggaaccat gaacatattt gatcgaaaga tcaactttga 120
tgcgctttta aaattttctc atataacccc gtcaacgcag cagsrcctga agaagatttc 180
attactgtct tcagaaaact catgatgatc ctggccatga atg aaa agg ata aga 235
Met Lys Arg Ile Arg
-35
aga aag aga aga aat gaa gtg acc atc cag cct ttc cca att aga ctt 283
Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro Phe Pro Ile Arg Leu
-30 -25 -20
cct ctc ctt cca ccc ctc att tcc ttt ttg cac aca tta cag gtg gtg 331
Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His Thr Leu Gln Val Val
-15 -10 -5
tgt tct gtg ata atg aaa agc atc aga aaa gct ttt gta ctt tgt ggt 379
Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala Phe Val Leu Cys Gly
1 5 10
ttc ctc tat ttt gaa ttt ttt gat caa aaa ctg at 414
Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu
15 20 25

<210> 294
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 156..332

<221> sig_peptide
<222> 156..221
<223> Von Heijne matrix
score 5.80000019073486
seq XVXLFXXVXVXXA/AL

<400> 294
catgtgtttc tcatctttca accaccaaac ttacataaaa ttcatccacc ttcccattct 60
tcctattata gtacaggaaa ggtccttcct gtcaaaggca aaatcactta tgattgtgtc 120
cccatctctc ttgccttttc aaggactttg agcct atg ctg cca ctg ctt cat 173
Met Leu Pro Leu Leu His
-20
tgt ttt ttt ttk gtt kgt ttg ttt kgt ttk gtt ttk gtt twa ama gca 221
Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa Val Xaa Val Xaa Xaa Ala
-15 -10 -5
gct tta ttg aga tat aat yca agt ata cag kgt ggc cgg gca cag kgg 269
Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln Xaa Gly Arg Ala Gln Xaa
1 5 10 15
ctc ama cct gwa atc cca gma ctt tgg gag act aag gma ggc aga tta 317
Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu Thr Lys Xaa Gly Arg Leu
20 25 30
ctt gag cct agg aat tt 334
Leu Glu Pro Arg Asn
35

<210> 295
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 284..373

<221> sig_peptide
<222> 284..346
<223> Von Heijne matrix
score 5.80000019073486
seq EMCLSQLFLQVEA/AY

<400> 295
ataacgctac ctgccgagca agccgagtgg agggaggcaa aggccaggct gaggatcagg 60
gtggcccggg tggcagcggg gaggcgctgc atgctggagg ctgtgctgag tgcccggtgc 120
aggtgagccg gtcctgcgga gttgtgccga gtgcctgctg cagtctcatt tccagttcct 180
ccatgacgtg gcaagtgaag acaggaatga aaggratgta aagcagcttt tctctgaaga 240
gaagaagaga gagagacaca gccaagaccg aggctgggcc aag atg gtg tct gtg 295
Met Val Ser Val
-20
ttt cga agc gag gag atg tgt ttg tca caa ctg ttt ctc cag gtg gaa 343
Phe Arg Ser Glu Glu Met Cys Leu Ser Gln Leu Phe Leu Gln Val Glu
-15 -10 -5
gct gca tat tgc tgt gtg gct gag ctc gga ga 375
Ala Ala Tyr Cys Cys Val Ala Glu Leu Gly
1 5

<210> 296
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 104..226

<221> sig_peptide
<222> 104..187
<223> Von Heijne matrix
score 5.80000019073486
seq WWSVASLLSDVAA/WW

<400> 296
tggattgaaa taaattccta gctccacggt caggtcagta ggctgccatg atgaaatttg 60
aagaagagtc tgttatgatg tgtaatacca atttctggag ggc atg gct gct ctc 115
Met Ala Ala Leu
-25
cga agt act cta aca tgg aca gaa gtc gtg ggc tgg tgg agt gtt gcg 163
Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp Trp Ser Val Ala
-20 -15 -10
tcg ctg ctt agt gat gtg gca gca tgg tgg cca ccg cac tcc acc tca 211
Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro His Ser Thr Ser
-5 1 5
aca cgg gga ggg gta 226
Thr Arg Gly Gly Val
10

<210> 297
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..230

<221> sig_peptide
<222> 90..221
<223> Von Heijne matrix
score 5.80000019073486
seq LVCVFTCSLLAFF/SP

<400> 297
ctgaactttt tatttttcta tttttataac caggagaaag taaacacata cacacacatg 60
gatggagaga gggacagagg gatggacgg atg aat gca ttr gta gat ggg aaa 113
Met Asn Ala Leu Val Asp Gly Lys
-40
cgg ctt asa krg tgc ata cgc tat ttc gat tct atc tca cta tat tct 161
Arg Leu Xaa Xaa Cys Ile Arg Tyr Phe Asp Ser Ile Ser Leu Tyr Ser
-35 -30 -25
aag gca agt tta agt tgt tgt tta gtg tgt gtg ttt act tgt tca ttg 209
Lys Ala Ser Leu Ser Cys Cys Leu Val Cys Val Phe Thr Cys Ser Leu
-20 -15 -10 -5
cta gct ttc ttc agc cca tgc ac 232
Leu Ala Phe Phe Ser Pro Cys
1

<210> 298
<211> 258
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 7..258

<221> sig_peptide
<222> 7..63
<223> Von Heijne matrix
score 5.80000019073486
seq WVFLVAILKGVQC/EL

<400> 298
```
ccaacc atg gag ttt ggg ctt agc tgg gtt ttc ctt gtt gct att ttg      48
       Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu
                       -15                 -10
aaa ggt gtc caa tgt gaa ctg cag gtg gtg gag tct ggg gga ggc ttg      96
Lys Gly Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu
-5                  1               5                  10
gta cag cca ggg cgg tcc ctc aga ctc tcc tgt cga act tct gga ttc     144
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe
            15                  20                  25
gcc ttt gat gat tat aat ttg agt tgg gtc cgc cag gct cca ggg aag     192
Ala Phe Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys
        30                  35                  40
ggg ctg gag tgg gta ggt ttc att aga agc aaa cct tat ggt gag aca     240
Gly Leu Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr
    45                  50                  55
aca acg tac gcc gcg tgg                                             258
Thr Thr Tyr Ala Ala Trp
60                  65
```

<210> 299
<211> 139
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..139

<221> sig_peptide
<222> 83..124
<223> Von Heijne matrix
score 5.80000019073486
seq SLFXLXXLRQSFT/XX

<400> 299
```
tttgggagct ccagtgttag gcgcatatat atttyagaat tgtgacaatt tcctgttggt    60
ttagtcctyt tatcattata ta atg tcc ctc ttt gwc ctt yyt yyt ttg aga   112
                         Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg
                                         -10                 -5
cag agt ttc act cht gwt gcc cag gca                                139
Gln Ser Phe Thr Xaa Xaa Ala Gln Ala
                1               5
```

<210> 300
<211> 286
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..285

<221> sig_peptide
<222> 196..252

<223> Von Heijne matrix
      score 5.80000019073486
      seq SFYFLASSSLSTS/AS

<221> misc_feature
<222> 16,286
<223> n=a, g, c or t

<400> 300
```
asatcgcgct ggggganasgc cacgtcgcta tgagtgtgtt tcagtctacc tggattaaac    60
gtttgcttct cttcgtctac cttgattaaa cgtgcacttc gcagtcctcg gttctccata   120
cccgtgacct ggggatcgct acggacctta aaatacccgc aacasccccct tcgtsccaag   180
ctggagagca gtggc atg atc tcg gct cac tgc agc ttc tac ttc ctg gcc    231
                 Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala
                                 -15                 -10
tca agc agt ctt tcc acc tca gcs tct saa cgc act gga att aca gat    279
Ser Ser Ser Leu Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp
        -5                  1               5
gtg agc n                                                          286
Val Ser
10
```

<210> 301
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 113..241

<221> sig_peptide
<222> 113..184
<223> Von Heijne matrix
      score 5.69999980926514
      seq CLFVFLYTTPCNC/FG

<400> 301
```
tgcaatgggt ggtgttttat aatgctctct tccctaatca tgttaatcag gagattttcc    60
ttttggaact cctgactgaa agcttcttag tttacacaca tgttcctcca gg atg aac   118
                                                          Met Asn
gct gaa aat aac ttt ttc ggt ttt gtt tgt ttg ttt gtt ttc ctc tat    166
Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe Leu Tyr
        -20                 -15                 -10
aca acc cct tgc aat tgc ttt ggt tta gaa cac ctt tgg att cta agt    214
Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile Leu Ser
    -5                  1               5                   10
ttc atg gtt gtt ctg gga gwy acc agg g                              242
Phe Met Val Val Leu Gly Xaa Thr Arg
                15
```

<210> 302
<211> 136
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..134

<221> sig_peptide
<222> 42..110

```
<223> Von Heijne matrix
      score 5.69999980926514
      seq LPCCCHLLTCVSS/LR

<400> 302
agtcacagtg acacagcctt ccaaccaggc cgccccctgg c atg acc atg gct gtg     56
                                              Met Thr Met Ala Val
                                                          -20
ggt gca gct gmy cam ctc ccc tgc tgc tgc cat ttr ctc acc tgc gtm      104
Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His Leu Leu Thr Cys Val
            -15                 -10                 -5
tcc agc ctt cgc amt gac att tac cca cat gg                           136
Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His
        1               5

<210> 303
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..174

<221> sig_peptide
<222> 73..147
<223> Von Heijne matrix
      score 5.69999980926514
      seq SILLAALSRNISP/GQ

<400> 303
aagaggaagc ggaakdgcct caggtgggcg gtagtgccaa aagcccaggg cgtccgcgca     60
aaccgaggcg tc atg cgg aga aaa agg cga gaa aga aaa gag agg aag agc    111
              Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser
              -25                 -20                 -15
atc ctc ctg gcc gcc ctt tcg agg aac ata agt cct ggt cag aca tac      159
Ile Leu Leu Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr
    -10                 -5                  1
cga aca tcc ccc gcg g                                                175
Arg Thr Ser Pro Ala
5

<210> 304
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 402..491

<221> sig_peptide
<222> 402..470
<223> Von Heijne matrix
      score 5.69999980926514
      seq LELLTSSDPPSLA/SQ

<400> 304
ttaggtgttc tgatagttaa gtggtagtat catggtctta atttttcctt gaagtggctt      60
ttgatttgca tttccttaat gactaattag gttgagcatc ttttcatgta cttactggcc     120
ttctttggag aaataccttt tccaaatcca atgggttgtc ttttttttatt gttgatctta     180
agggttctta ggtgttctgg gtaccagttt cttgtgagat gtgtgacttg taaatacttt     240
cttccattct ccatgttgtc tttttattct cttgatggta ttctttgaaa tacaaaartk     300
```

```
tttatatttg acaaagttca gtttatttat ttatttattg ccattcgtgc ttttggtttt   360
gataatccat ttttwttgtt tttattttta tttacttaga g atg ggg tct ccc tat   416
                                              Met Gly Ser Pro Tyr
                                                          -20
gtt gcc cac gtt ggt ctt gaa ctc ttg acc tca agt gat cct ccc tcc     464
Val Ala His Val Gly Leu Glu Leu Leu Thr Ser Ser Asp Pro Pro Ser
        -15                 -10                 -5
ttg gcc tcc caa gtg ctg gga ata cat tm                              493
Leu Ala Ser Gln Val Leu Gly Ile His
    1               5

<210> 305
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..213

<221> sig_peptide
<222> 79..135
<223> Von Heijne matrix
      score 5.69999980926514
      seq VCWLTLTLAHSHS/LT

<400> 305
cacacacgca ccaaatacac acagasaccc tggccctcac tcacgcacav tctctcacac    60
tcgtggacac acccccag atg cat ctt tac act cat gta tgc tgg ctc act    111
                    Met His Leu Tyr Thr His Val Cys Trp Leu Thr
                                    -15                 -10
ctc aca ctg gca cac tca cac agc ttg acc cac acg cac aca ctc aca    159
Leu Thr Leu Ala His Ser His Ser Leu Thr His Thr His Thr Leu Thr
            -5                  1               5
ccc agt cac aca cgt aca cac tca cat acg tgt gct tgc cta cac gca    207
Pro Ser His Thr Arg Thr His Ser His Thr Cys Ala Cys Leu His Ala
    10                  15                  20
cac aag g                                                          214
His Lys
25

<210> 306
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 306..458

<221> sig_peptide
<222> 306..350
<223> Von Heijne matrix
      score 5.69999980926514
      seq LSLTFYHFPLCWG/HQ

<221> misc_feature
<222> 286,448
<223> n=a, g, c or t


<400> 306
atcagagagc gccggaagcg gtccgagaat gaagcagtgt gatctaccat gcattgtctc    60
```

```
agaaagaggc gaatgactcc gatgtccagg tcagttcttg gcagggagtc caggagcaac    120
agaggtgatg gcaaagatgg ctcagtagct tctgagcccc cagcactgat tgagatgtcc    180
tttcccacat catactcctc atttttctgg cagacatcta aggctggatc aaagtctgta    240
gttctcatta cctgttccca cgtgccagcc tccttttctg ttgtgnmmaa gtcaagtttg    300
gtaaa atg agg ctt tcc tta acc ttt tat cat ttc cca ctg tgt tgg gga    350
      Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly
      -15                -10                 -5
cac cag gct gtg ccc acg tgg tgg saa rgc atc att caa cct tgt cac      398
His Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His
1               5                   10                  15
tgt gcc ctc tgc act tct gca gaa ggt gtg caa tca cat atc ata agt      446
Cys Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser
            20                  25                  30
gna att tac aga                                                      458
Xaa Ile Tyr Arg
        35
```

<210> 307
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..326

<221> sig_peptide
<222> 87..128
<223> Von Heijne matrix
score 5.69999980926514
seq NVLIIVFVAFAFG/FL

<400> 307

```
tatcttctct ccagtctaaa gcctcactga acaaactgtc cttgactgtc agtgctcagg     60
gaactgctct gccacccttc tcctca atg aat gtg tta atc att gtt ttt gtt     113
                             Met Asn Val Leu Ile Ile Val Phe Val
                                                     -10
gca ttt gct ttt ggg ttc ytg gtc atg aag tct ttg ctt aag cca atg      161
Ala Phe Ala Phe Gly Phe Leu Val Met Lys Ser Leu Leu Lys Pro Met
-5                  1               5                   10
tcg aga agg gtt ttt ctg atg tta tct tct agg att ttt atg gtt tca      209
Ser Arg Arg Val Phe Leu Met Leu Ser Ser Arg Ile Phe Met Val Ser
            15                  20                  25
ggt ctt aga ttt aag tcc ttg atc cat ctt gag ttg att ttt gta tat      257
Gly Leu Arg Phe Lys Ser Leu Ile His Leu Glu Leu Ile Phe Val Tyr
        30                  35                  40
aag ttg aga gat gag gat cca gtt tca ttc ttc tac atg tgg ctt gcc      305
Lys Leu Arg Asp Glu Asp Pro Val Ser Phe Phe Tyr Met Trp Leu Ala
    45                  50                  55
aat tat ccc agc acc att tgt tg                                       328
Asn Tyr Pro Ser Thr Ile Cys
60                  65
```

<210> 308
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 33..380

<221> sig_peptide

```
<222> 33..92
<223> Von Heijne matrix
      score 5.69999980926514
      seq LAWALPSLLRLGA/AQ

<221> misc_feature
<222> 326
<223> n=a, g, c or t


<400> 308
agcggtctcc cggcccctgc cgccctgcca ct atg tcc cgc cgc tct atg ctg        53
                                    Met Ser Arg Arg Ser Met Leu
                                    -20                 -15
ctt gcc tgg gct ctc ccc agc ctc ctt cga ctc gga gcg gct cag gag       101
Leu Ala Trp Ala Leu Pro Ser Leu Leu Arg Leu Gly Ala Ala Gln Glu
            -10                 -5                  1
aca gaa gac ccg gcc tgc tgc agc ccc ata gtg ccc cgg aac gag tgg       149
Thr Glu Asp Pro Ala Cys Cys Ser Pro Ile Val Pro Arg Asn Glu Trp
    5                   10                  15
aag gcc ctg gca tca gag tgc gcc cag cac ctg agc ctg ccc tta cgc       197
Lys Ala Leu Ala Ser Glu Cys Ala Gln His Leu Ser Leu Pro Leu Arg
20                  25                  30                  35
tat gtg gtg gta tcg cac acg gcg ggc agc agc tgc aac acc scc gcc       245
Tyr Val Val Val Ser His Thr Ala Gly Ser Ser Cys Asn Thr Xaa Ala
                40                  45                  50
tcg tgc cag cag cag gcc cgg aat gtg cag cac tac cac atg aag aca       293
Ser Cys Gln Gln Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr
            55                  60                  65
ctg ggc tgg tgc gac gtg ggc tac aac tkc ctn gat tgg aga aga cgg       341
Leu Gly Trp Cys Asp Val Gly Tyr Asn Xaa Leu Asp Trp Arg Arg Arg
        70                  75                  80
gct cgt ata cra ggg ccg tgg mtg gaa ctt cac ggg tsc                   380
Ala Arg Ile Xaa Gly Pro Trp Xaa Glu Leu His Gly Xaa
    85                  90                  95


<210> 309
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 228..284

<221> sig_peptide
<222> 228..269
<223> Von Heijne matrix
      score 5.69999980926514
      seq VFLFLMISVFAGC/QI

<400> 309
aaaagaagaa agctgaatca tactcgatga ttattgatca tttgtataca gctcaagccc    60
tcaagtagcc tgctgtaata tttactagtt acaaagaaaa gattcgtttt gtcacagtta   120
catgaaaggt gcttatattt gcaaatatgg agacaaagtt catcttaaaa gattaaaatg   180
agaatctcct aaatgaagca tttggaatat tgattagtat accagaa atg gtt ttt     236
                                                    Met Val Phe
ctt ttt ctt atg atc agc gtt ttt gcc ggt tgt caa atc cct tcc ggg     284
Leu Phe Leu Met Ile Ser Val Phe Ala Gly Cys Gln Ile Pro Ser Gly
    -10                 -5                  1                   5

<210> 310
<211> 357
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 243..356

<221> sig_peptide
<222> 243..305
<223> Von Heijne matrix
      score 5.59999990463257
      seq AGLELLASSNSSA/LP

<400> 310
ttgagatcac ctgaggcaac atagtgaaac cctgtatcta gaataaatta gagaaagaaa      60
aatagtctgg gcatgatggt gtgcacctat agtctccagc tabtcasgag cctgaggcag     120
gaggwtcact tgagctkagg agttcaagga tgcagtsacc tgtgattgca ccactgcatt     180
ccagcttgga caacagagtg agaccctgtc ttaaaattta aattttktgt yttwggtag      240
ag atg ggg tct cgc cct gtt tcc gak gct ggt ctc gaa ctc ctg gcc        287
   Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala
       -20                 -15                 -10
tcg agc aat tct tct gcc ttg ccc ttc caa tgt tct ggg att aca ggc       335
Ser Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly
    -5                  1               5                  10
atg agc crc cac acc cta gcg g                                         357
Met Ser Xaa His Thr Leu Ala
                15

<210> 311
<211> 470
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 413..469

<221> sig_peptide
<222> 413..451
<223> Von Heijne matrix
      score 5.59999990463257
      seq MLCHLSLVFLGXG/QF

<221> misc_feature
<222> 30
<223> n=a, g, c or t


<400> 311
ccgttaacgg gattctggaa tttgttaggn taattgcttt tcaatatcaa gagatctggc      60
aatcaaattt aataatatca agcttgcttg gtgagcatgg atttataaga tagaatggtt     120
tgtgggggrg artatagtka cgaaaaagrk tattgtttcc cataatgcct ggtattgtat     180
taagtacttt gcatacagta gggcatttca ttgtcccagt gatcctcctg caaagtaggt     240
acaattatct tcaatttaca aatgaggaaa ccaagctctc ttcaagctga taagatgctg     300
aactgagatt tgaaccaagt ccctctgccc ctaagagccc ctacccctag ctgctactat     360
atgctgtacc catctaagct ttgtgaaata rccttgttcc actgcagaga ag atg ttg     418
                                                          Met Leu
tgt cac cta tct cta gta ttt ctt ggc ktt ggg cag ttc tgg agt caa       466
Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp Ser Gln
    -10                 -5                  1               5
aat g                                                                 470
Asn
```

<210> 312
<211> 187
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..187

<221> sig_peptide
<222> 98..148
<223> Von Heijne matrix
score 5.59999990463257
seq FMCLFAICISSNA/KC

<400> 312
```
aagtttgttt ttgttggtgg tggtgatagt ttcttatatt ctattccata aagtatgaaa      60
tggaggctcc ttgtgatttt taatttgcac ttctgta atg act aat ctt ttc atg     115
                                         Met Thr Asn Leu Phe Met
                                                 -15
tgc ttg ttt gcc atc tgt ata tct tct aat gcg aag tgt ctg ttt agt     163
Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn Ala Lys Cys Leu Phe Ser
    -10                 -5                  1               5
ctt ttt cct ttt ttt att gag ggg                                     187
Leu Phe Pro Phe Phe Ile Glu Gly
                10
```

<210> 313
<211> 237
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..236

<221> sig_peptide
<222> 93..173
<223> Von Heijne matrix
score 5.59999990463257
seq CVLFTLLVSTRSG/RS

<221> misc_feature
<222> 111
<223> n=a, g, c or t

<400> 313
```
ttgcttagga ttttctaaaa gattacataa aatactgttg aaaagatgat tgcatacaaa      60
acataatctg ttcattgtta aacgtatacg aa atg ttg gga tac atc tgg naa      113
                                    Met Leu Gly Tyr Ile Trp Xaa
                                                -25
caa gac aaa gtc ttt gct aat tgt gtt cta ttt acg ctc tta gtg tct     161
Gln Asp Lys Val Phe Ala Asn Cys Val Leu Phe Thr Leu Leu Val Ser
-20                 -15                 -10                 -5
aca aga tcc ggg aga tcg cgs gcg ggt tgt gcc tgg agg tgg agg gga     209
Thr Arg Ser Gly Arg Ser Arg Ala Gly Cys Ala Trp Arg Trp Arg Gly
                1               5                   10
aga tgg tca gta gga cag aag ggc hgg g                               237
Arg Trp Ser Val Gly Gln Lys Gly Xaa
        15                  20
```

<210> 314

<211> 356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 272..355

<221> sig_peptide
<222> 272..316
<223> Von Heijne matrix
score 5.59999990463257
seq LILSLQVCRPATL/DQ

<221> misc_feature
<222> 275..276
<223> n=a, g, c or t

<400> 314
```
ggatttgctt tctttttctc caaaagggga ggaaattgaa actgagtggc ccacgatggg     60
aagaggggaa agcccagggg tacaggaggc ctctgggtga aggcagaggc taacatgggg    120
ttcggagcga ccttggccgt tggcctgacc atctttgtgc tgtctgtcgt cactatcatc    180
atctgcttca cctgctcctg ctgctgcctt tacaagacgt gccgccgacc acgtccggtt    240
gtcaccacca ccacatccac cactgtggtg c atg nnc ctt atc ctc agc ctc       292
                                   Met Xaa Leu Ile Leu Ser Leu
                                   -15                 -10
caa gtg tgc cgc cca gct acc ctg gac caa gct acc agg gct acc aca      340
Gln Val Cys Arg Pro Ala Thr Leu Asp Gln Ala Thr Arg Ala Thr Thr
            -5                  1               5
cca tgc cgc cta cgg g                                                356
Pro Cys Arg Leu Arg
    10
```

<210> 315
<211> 162
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..162

<221> sig_peptide
<222> 40..150
<223> Von Heijne matrix
score 5.59999990463257
seq VLMLSLPLPPTPQ/QA

<400> 315
```
tacatgtgca gaatgtgcag atttgtcaca taggtgtgt atg tgc cac agg cgt        54
                                           Met Cys His Arg Arg
                                                       -35
tgg ctg cac cta tca acc cgt cat cta ggt ttt aag ccc cgc atc cat      102
Trp Leu His Leu Ser Thr Arg His Leu Gly Phe Lys Pro Arg Ile His
        -30                 -25                 -20
tac gta ttt gtc tta atg ctg tcc ctc ccc ttg ccc ccc acc ccc caa      150
Tyr Val Phe Val Leu Met Leu Ser Leu Pro Leu Pro Pro Thr Pro Gln
    -15                 -10                 -5
cag gcc ctc ggg                                                      162
Gln Ala Leu Gly
1
```

<210> 316
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 297..404

<221> sig_peptide
<222> 297..353
<223> Von Heijne matrix
score 5.59999990463257
seq FVIFPAALLLCWG/GL

<400> 316
```
taagctgaaa aagaatataa aaattaaaga gaaattgaaa atctaagtct tgcagtgaga     60
atgaccagaa atcgtttccc tctctggggg gttcctgttt aatatgaaag tcctcttaac    120
aagcgtggac agaggaagtt ttaggtttga tttgaacttc atgtacatga catatttcat    180
ttttttttct tccctcacaa atttcaaccc aggccacttg tttgcagaga ctgccaaacc    240
ttccattgct gcttccaaga tactcctgga atctgagatt accttttatc ctcttg atg    299
                                                              Met
gac cat gtt gtt att ttt gtc att ttc cct gca gct ctt ctg ctt tgc      347
Asp His Val Val Ile Phe Val Ile Phe Pro Ala Ala Leu Leu Leu Cys
            -15                 -10                 -5
tgg gga gga ctc atc ccc cta tgc atc atc tac ccc ccg ata gct gac      395
Trp Gly Gly Leu Ile Pro Leu Cys Ile Ile Tyr Pro Pro Ile Ala Asp
        1               5                   10
aca gtt ggg                                                          404
Thr Val Gly
15
```

<210> 317
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 359..448

<221> sig_peptide
<222> 359..433
<223> Von Heijne matrix
score 5.59999990463257
seq LIIILXFDIYSLA/FI

<221> misc_feature
<222> 323,410
<223> n=a, g, c or t

<400> 317
```
tatgtctttt gaatttgtga tgtacatatt aacagtagat taagttgaaa taataaaatc     60
tgtattgttt atgatttatc agttatatga tgagtagaat atagtctatt gtggscmagt    120
gtgtatatat aacataaaca atacattaac ccaattttgt gtgaaaatta ttttgggacc    180
tagtagcttt cttggtcaca acctttcaaa caaacaaatt ttttttaaat taattttttc    240
ccttaataaa gaaaacaatt cctcaatgtg taatagcaaa taccttttaa caggtcatat    300
atcatcaatg ctttctttga aancgtactg atgcttacaa gatgctttac gagtaaag      358
atg ctt aca aat ctt ttc ttt caa gta gct cat cct ctg atc att att      406
Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile
-25                 -20                 -15                 -10
ctg ntg ttt gat atc tac tcc cta gca ttt atc cat gac gtg gg           450
```

```
Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val
                -5                   1               5
```

<210> 318
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 313..393

<221> sig_peptide
<222> 313..354
<223> Von Heijne matrix
score 5.59999990463257
seq LFGLRGMLPLTQQ/AP

<400> 318

```
aatcgaaaac agcaaatcac acaactgtta aaaatatttt vtgtttacaa agccaagcca    60
aaattttatg ttttcctccc caaactttga tataaacact aacatttttt agcatgtata   120
aacatcatta ttaaccagtg tcctattaaa actccttttc tatgatagaa tgtctgttrc   180
ttttaggtgg ataaggccta gatgattggc ctctaccagc atcctcatct ctgtccctga   240
tgcccagctt carcctcgct cctgyatgct ggaccgcttc agtghagctc tcagacttgc   300
tctgtgtctc ac atg cty ttt ggc tta cgt gga atg ctc cca ctc acc cag   351
              Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln
                              -10                 -5
caa gct ccc att cct cat tta aga tgt aaa ttg agt gtc acc tc          395
Gln Ala Pro Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr
    1               5                   10
```

<210> 319
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..256

<221> sig_peptide
<222> 20..82
<223> Von Heijne matrix
score 5.59999990463257
seq ACVYACVCASVSA/CV

<400> 319

```
catctgtgtg tgcgtgtgt atg cgt gtg tgt atg cgt ctg tgt gca tgt gtg    52
                     Met Arg Val Cys Met Arg Leu Cys Ala Cys Val
                         -20                 -15
tat gcg tgt gtg tgc gca tca gtg tct gca tgt gtg tat rtg tgt gta     100
Tyr Ala Cys Val Cys Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val
-10                 -5                  1               5
tgt atg tst gtg cgc gcg cat ctg tgt gtg tgc atg tgt gta tgt atg     148
Cys Met Xaa Val Arg Ala His Leu Cys Val Cys Met Cys Val Cys Met
            10                  15                  20
tgt gtg cat ctc tgt gtg tgc atg tgt gta tgt gtg tgt gca tct gtg     196
Cys Val His Leu Cys Val Cys Met Cys Val Cys Val Cys Ala Ser Val
        25                  30                  35
tgt gtg tgc atg tgt gca tgc gtg tgt atg tgt gtg tgc gtg cgt gca     244
Cys Val Cys Met Cys Ala Cys Val Cys Met Cys Val Cys Val Arg Ala
    40                  45                  50
tct gtg tgt gtg c                                                   257
```

```
Ser Val Cys Val
55

<210> 320
<211> 325
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 256..324

<221> sig_peptide
<222> 256..318
<223> Von Heijne matrix
      score 5.59999990463257
      seq LIANLVLFISIAA/LR

<400> 320
accacgcctc ctccaagtcc cagcgaaccc gcgtgcaacc tgtccctaaa aaagccaaag    60
cagtcactct ttacctccca ctttccctcc tcccagcctt tggcaaccac taatctactt   120
tccgtgtata tggatttacc tattcaggac atttcatatg tcctttggtg actggcttct   180
ttcactttgc acaatgtttt taaggttcat tcctgtcata gtgtgtgtca gtacgaaccc   240
ctccttaacc atcta atg gtt atc acc tct aat agt tat ctc ata gcc aat    291
                 Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn
                     -20                 -15                 -10
ctt gtt tta ttt ata tct atc gcc gcc ctc cgg g                       325
Leu Val Leu Phe Ile Ser Ile Ala Ala Leu Arg
            -5                   1

<210> 321
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..201

<221> sig_peptide
<222> 31..183
<223> Von Heijne matrix
      score 5.5
      seq LSLHASLVTKAFS/IN

<400> 321
catcacaaga acccagagtg gaattctggg atg gaa gag ctg gac aga aag tgg     54
                                 Met Glu Glu Leu Asp Arg Lys Trp
                                     -50                 -45
aga gag aag gtc ctc cca gcg gca aag cta att aaa agg aga aac ctg     102
Arg Glu Lys Val Leu Pro Ala Ala Lys Leu Ile Lys Arg Arg Asn Leu
            -40                 -35                 -30
ttt tcc aca tgc act cct caa tat ggy aca cat gct gct ttc ttg tca     150
Phe Ser Thr Cys Thr Pro Gln Tyr Gly Thr His Ala Ala Phe Leu Ser
        -25                 -20                 -15
tta cat gcc tca ctt gtc acc aaa gca ttt tca atc aat tcc tgg gag     198
Leu His Ala Ser Leu Val Thr Lys Ala Phe Ser Ile Asn Ser Trp Glu
    -10                 -5                   1               5
tgg                                                                 201
Trp

<210> 322
<211> 159
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..157

<221> sig_peptide
<222> 77..151
<223> Von Heijne matrix
      score 5.5
      seq PLLLCPLSSGSPC/PR

<400> 322
aacaaaggga cagaatggtc ccagggttcc ttcttcttcc ttccagttaa gagctcagag    60
tggaagtggg ctgggg atg gtg tcg ggg gcc caa gct ccc agc tcc caa agg   112
                  Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg
                  -25                 -20                 -15
ccc ctg ctt cta tgc cct ttg agc tca ggt agc ccc tgc ccc cgg gg      159
Pro Leu Leu Leu Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg
            -10                 -5                  1

<210> 323
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 325..420

<221> sig_peptide
<222> 325..405
<223> Von Heijne matrix
      score 5.5
      seq SFLPSLLSSFLLS/LP

<221> misc_feature
<222> 117
<223> n=a, g, c or t


<400> 323
catgcaggat agtaatacgt tagaatcaaa aataaggtta tacttagaaa atattgattt    60
gcctttttga ttttgcatgt gtataatctg gctctgaaat cagtgacacg aagtganctt   120
cgaaacaagc ctgagcaata gaagtagatg tggaaataac ttcggtttct caaggcaaat   180
actttgatag gaacaaacaa ccgtttagat atagaagatg tgatacattc ctttaaaaag   240
aatttgacct tatgtcattg taggcacacc tcatatttca attattcata tagtttttct   300
tgagcaattg ctggtttaag aata atg tca tgt ctt ttg cgt gct tat atc      351
                           Met Ser Cys Leu Leu Arg Ala Tyr Ile
                                   -25                 -20
att tgg ata ttt cct tcc ttc ctt cct tcc ctc ctt tct tcc ttc ctt     399
Ile Trp Ile Phe Pro Ser Phe Leu Pro Ser Leu Leu Ser Ser Phe Leu
            -15                 -10                 -5
ctt tcc ctc ccc cct tcc ggg                                         420
Leu Ser Leu Pro Pro Ser Gly
        1               5

<210> 324
<211> 210
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> 9..209

<221> sig_peptide
<222> 9..116
<223> Von Heijne matrix
score 5.5
seq LHFVYCFLCCAEA/FL

<400> 324
```
ctccttat atg ttt cag tta ctg atc ctt tgt cag atg aat agt ttg aaa      50
         Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys
             -35                 -30                 -25
ata ttt tct ccc att ctt gga tgg tct ctt cat ttt gtt tat tgt ttc       98
Ile Phe Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe
        -20                 -15                 -10
ctt tgc tgt gca gaa gcc ttt tta ctt gat atg atc cca ttt atg caa      146
Leu Cys Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln
    -5                  1               5                   10
ttt tac ttt ggt tac ctg tgc ttg tgg ggt att act tta aaa atc ttt      194
Phe Tyr Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe
                15                  20                  25
gcc cag tcc aat tgg g                                                210
Ala Gln Ser Asn Trp
            30
```

<210> 325
<211> 192
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..192

<221> sig_peptide
<222> 31..174
<223> Von Heijne matrix
score 5.5
seq VCLRLHVLSAVQT/ER

<400> 325
```
aggctgctgc agttggcgma tgaggcgacc atg gcc ttg ctg ggt aag cgc tgt      54
                                 Met Ala Leu Leu Gly Lys Arg Cys
                                             -45
gac gtc ccc acm aac ggc tgc gga ccc gac cgc wgg aam wac ggc gwy      102
Asp Val Pro Thr Asn Gly Cys Gly Pro Asp Arg Xaa Xaa Xaa Gly Xaa
-40                 -35                 -30                 -25
aac ccg caa ara cga gat cat cac cag cmt mgt gtc tgc ctt aga ctc      150
Asn Pro Gln Xaa Arg Asp His His Gln Xaa Xaa Val Cys Leu Arg Leu
                -20                 -15                 -10
cat gtg ctc agc gct gtc car act gaa cgc cga ggt gat ggg              192
His Val Leu Ser Ala Val Gln Thr Glu Arg Arg Gly Asp Gly
            -5                  1               5
```

<210> 326
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

```
<222> 71..181

<221> sig_peptide
<222> 71..166
<223> Von Heijne matrix
      score 5.5
      seq TLALLSSDSVATG/SV

<400> 326
aatttcgcgg cctagtgggg cgtacgggcc tcttttgaaa gcctgagtta cgatgtattg      60
agcgcgtcgt atg cgg cca gca cta agg tcc ttc tgg cac tcc tct ggt        109
           Met Arg Pro Ala Leu Arg Ser Phe Trp His Ser Ser Gly
                   -30                 -25                 -20
gga ccg ccc cca tcg gcc aca ctt gcc ctg ctc tcc agt gat tct gta       157
Gly Pro Pro Pro Ser Ala Thr Leu Ala Leu Leu Ser Ser Asp Ser Val
                -15                 -10                  -5
gct act ggc tcc gta gtc tcg cgg                                       181
Ala Thr Gly Ser Val Val Ser Arg
            1               5

<210> 327
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..185

<221> sig_peptide
<222> 39..116
<223> Von Heijne matrix
      score 5.5
      seq LFSGWLVWWGSRS/SQ

<221> misc_feature
<222> 143,145,175
<223> n=a, g, c or t


<400> 327
caaagacgca ctacttagta cagagaggtt ttgaatac atg ctc tgt gca tgc aag      56
                                          Met Leu Cys Ala Cys Lys
                                                  -25
gca cgt ggg gtg atg ctg ctg ctg ttc tca ggg tgg ttg gtt tgg tgg       104
Ala Arg Gly Val Met Leu Leu Leu Phe Ser Gly Trp Leu Val Trp Trp
-20                 -15                 -10                  -5
ggc agt agg tcc tca cag twc ctc aga atg cct gag agn tna gta agt       152
Gly Ser Arg Ser Ser Gln Xaa Leu Arg Met Pro Glu Xaa Xaa Val Ser
                    1               5                   10
ggg gag ggt cga agc gat cdv dng cca cat ggg                           185
Gly Glu Gly Arg Ser Asp Xaa Xaa Pro His Gly
        15                  20

<210> 328
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..209
```

```
<221> sig_peptide
<222> 57..182
<223> Von Heijne matrix
      score 5.5
      seq SLILPTSPSPAHS/GS

<400> 328
gacttaggts yaggcgactg cccagacaat gactggtccc gcataccgag cagagc atg      59
                                                              Met
atc agc agc agt ctg agt gga aga gtg cct gtg atc tta ggg aac ctg       107
Ile Ser Ser Ser Leu Ser Gly Arg Val Pro Val Ile Leu Gly Asn Leu
    -40                 -35                 -30
atg ggc gtt gga gca gcg gtt cga cgc atg ggt ttc tct tta atc ctt       155
Met Gly Val Gly Ala Ala Val Arg Arg Met Gly Phe Ser Leu Ile Leu
-25                 -20                 -15                 -10
ccg act tcc cca agc cca gcg cac tca ggt tcc gct cca agt gcg gga       203
Pro Thr Ser Pro Ser Pro Ala His Ser Gly Ser Ala Pro Ser Ala Gly
                -5                   1                   5
ccc cgc g                                                             210
Pro Arg

<210> 329
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..316

<221> sig_peptide
<222> 149..286
<223> Von Heijne matrix
      score 5.5
      seq ILLISTLFYSLLS/GS

<400> 329
acacttaacc catctgtttt ctctaatgca cgacagattc ctttcagaca ggacaactgt      60
gatatttcag ttcctgattg taaatacctc ctaagcctga agcttctgtt actagccatt     120
gtgrgcttca gtktcttcak yckgcaaa atg ggc ata ata car kct att ctt        172
                               Met Gly Ile Ile Gln Xaa Ile Leu
                                   -45                 -40
gcc aca tca agg gat tgt tat tcc ttt aaa aaa aaa cca ata cca aag       220
Ala Thr Ser Arg Asp Cys Tyr Ser Phe Lys Lys Lys Pro Ile Pro Lys
            -35                 -30                 -25
aag cct aca atg ttg gcc tta gcc aaa att ctg ttg att tca acg ttg       268
Lys Pro Thr Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu
        -20                 -15                 -10
ttt tat tca ctt cta tcg ggg agc cat gga aaa gra aat caa gac gtg       316
Phe Tyr Ser Leu Leu Ser Gly Ser His Gly Lys Xaa Asn Gln Asp Val
    -5                   1               5                   10
gg                                                                    318

<210> 330
<211> 223
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..221

<221> sig_peptide
```

```
<222> 135..203
<223> Von Heijne matrix
      score 5.5
      seq LPFVCLLLRNVYS/DL

<400> 330
aacagtgtgt gagagttccc tttcctccac atcctcgcca gcatctgtta ttgcctgtct     60
ttttgatacg agccttttta acaggggtaa gatgatatct cattgtagtt ttgatttgca    120
ttctctgatg atca atg atg ttg agc acc ttt tca tat gcc tgt ttg cca      170
                Met Met Leu Ser Thr Phe Ser Tyr Ala Cys Leu Pro
                            -20                 -15
ttt gta tgt ctt ctt ttg aga aat gtc tat tca gat ctt ttg ccc aat      218
Phe Val Cys Leu Leu Leu Arg Asn Val Tyr Ser Asp Leu Leu Pro Asn
    -10                 -5                  1               5
cgg gg                                                                223
Arg

<210> 331
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 272..361

<221> sig_peptide
<222> 272..343
<223> Von Heijne matrix
      score 5.5
      seq LIVVLVCISLVII/DD

<400> 331
aatggacacc taggttgctt ccatatctga gctattgtga ataatgctgc aatgaacatg     60
ggagtggaga catctcctaa gcatactgat ttcagttcct ttgggtatat acccagaagt    120
gggatcatgt ggtaatcttg tttttacttt tttgaggaac ctccatacca ttatccatga    180
tggctatagt aatttacatt cataccagca gtgcacaagg gtctcctttt ctgtatacac    240
ttgccaacac ttgttatctt tcattttttt g atg cta gcc att cta aca ggt       292
                                   Met Leu Ala Ile Leu Thr Gly
                                                       -20
ggg agg tgg tat ctc ata gtg gtt tta gtt tgc att tcc ttg gtg att      340
Gly Arg Trp Tyr Leu Ile Val Val Leu Val Cys Ile Ser Leu Val Ile
        -15                 -10                 -5
att gat gat gat gag cac ggg g                                         362
Ile Asp Asp Asp Glu His Gly
    1               5

<210> 332
<211> 89
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..87

<221> sig_peptide
<222> 34..75
<223> Von Heijne matrix
      score 5.5
      seq LLPLGLKVLGLQA/RG

<400> 332
```

```
cccagaccgg tcttgaactc ctggcctcaa ctg atg ctc ctg cct ctg ggt ctc      54
                                     Met Leu Leu Pro Leu Gly Leu
                                                     -10
aaa gtg ctg gga tta cag gcg aga ggc acc acg ct                       89
Lys Val Leu Gly Leu Gln Ala Arg Gly Thr Thr
     -5                   1
```

<210> 333
<211> 399
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 255..398

<221> sig_peptide
<222> 255..338
<223> Von Heijne matrix
score 5.5
seq PTLLVMWLSPQMA/SS

<400> 333

```
ttcactgcaa ggcggcggca ggagaggttg tggtgctagt ttctctaagc catccagtgc     60
catcctcgtc gctgcagcga cacacgctct cgccgccgcc atgactgagc agatgaccct    120
tcgtggcacc ctcaagggcc acaacggctg ggtaacccag atcgctacta ccccgcagtt    180
cccggacatg atcctctccg cctctcgagg tacggactaa gataagacca tcatcatgtg    240
gaaactgacc aggg atg aga cca act atg gaa ttc cac agc gtg ctc tgc      290
                Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys
                            -25                 -20
ggg gtc act ccc act ttg tta gtg atg tgg tta tct cct cag atg gcc      338
Gly Val Thr Pro Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala
    -15                 -10                  -5
agt tcg ccc tct cag gct cct ggg atg gaa ccc tgc gcc tct ggg atc      386
Ser Ser Pro Ser Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile
1               5                   10                  15
tca caa cgg gca a                                                    399
Ser Gln Arg Ala
            20
```

<210> 334
<211> 188
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 33..188

<221> sig_peptide
<222> 33..131
<223> Von Heijne matrix
score 5.5
seq SLCLLTVAVLVLT/FK

<400> 334

```
aatgaagggt actagaacac ctgcccatcc at atg gga aaa aaa aaa atc tgg       53
                                    Met Gly Lys Lys Lys Ile Trp
                                                    -30
acc cct agc tca tat ccc atg ccc agt cat aaa cat gta tcc cta tgt      101
Thr Pro Ser Ser Tyr Pro Met Pro Ser His Lys His Val Ser Leu Cys
    -25                 -20                 -15
ctt cta acg gtt gca gtt tta gtt ctt aca ttt aag tct tta att cat      149
```

```
Leu Leu Thr Val Ala Val Leu Val Leu Thr Phe Lys Ser Leu Ile His
-10                 -5                  1                   5
ttt gag tda att ttt gca tat gag ata ggg gtc cag ggg                   188
Phe Glu Xaa Ile Phe Ala Tyr Glu Ile Gly Val Gln Gly
            10                  15
```

<210> 335
<211> 115
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..115

<221> sig_peptide
<222> 23..94
<223> Von Heijne matrix
score 5.5
seq CPSLLSPISPSQA/CP

<400> 335

```
ccaatacaca tcactcagtg gc atg agc cct gtc ctc tgc ttc cat cgc tgc       52
                         Met Ser Pro Val Leu Cys Phe His Arg Cys
                                         -20                 -15
tcc tgt ccc tcc ctc ctc agc ccc atc tcc cca tcc cag gcc tgt cct       100
Ser Cys Pro Ser Leu Leu Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro
                -10                 -5                  1
gag ccc ctc ctt ggg                                                   115
Glu Pro Leu Leu Gly
        5
```

<210> 336
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 197..298

<221> sig_peptide
<222> 197..268
<223> Von Heijne matrix
score 5.5
seq IMFVCMCVCVCVC/VY

<400> 336

```
catgcttgtt gtaacgtgtc aaacaataca gaggtgtagg gaaaatacct agtgccaccc      60
tccactccaa aaccccatgt cgccagagat aaccatttat tcagacagtg agtatctatt     120
aagtatctat tgctaggctt tggagatagc ataatgaaca aaatggatgt gctctctgcc     180
cttgtgattt ggacag atg ctt cag tta tct ttt tct gtg ttt ata ttg att     232
                  Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile
                                  -20                 -15
atg ttt gta tgt atg tgc gtg tgt gtg tgt gtg tgt gtg tat cga ctg       280
Met Phe Val Cys Met Cys Val Cys Val Cys Val Cys Val Tyr Arg Leu
        -10                 -5                  1
ttt tct tcc tcc tcc ccg gg                                            300
Phe Ser Ser Ser Ser Pro
5                   10
```

<210> 337
<211> 307

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..307

<221> sig_peptide
<222> 5..277
<223> Von Heijne matrix
score 5.5
seq RVLLGAGIPPVSS/AP

<400> 337

```
caca atg aag tcg act gtt tcg tcg agg gaa gtg gcc acc gtt gat aaa       49
     Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys
         -90                 -85                 -80
atg aaa aga cgc cat gca gaa tac tgt gca cag ggt ctc cag aga ttt        97
Met Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe
    -75                 -70                 -65
aaa gcc caa ctt tct caa gat acc ctt ccc cav cat cca cat ctg gag       145
Lys Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu
-60                 -55                 -50                 -45
awa gag aag ggg ctt gaa ggc ttg gag gaa aat gtg cct cta aag gga       193
Xaa Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly
                -40                 -35                 -30
gag aaa cct gga gaa ggg ggt cca gag tct cct aag aag aga aga agg       241
Glu Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg
            -25                 -20                 -15
gtg ctt ctc gga gcg ggc atc cca cca gta agc tca gct ccc agg aga       289
Val Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg
        -10                  -5                   1
cag agc cag cag gca aca                                               307
Gln Ser Gln Gln Ala Thr
5                   10
```

<210> 338
<211> 123
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..123

<221> sig_peptide
<222> 16..75
<223> Von Heijne matrix
score 5.5
seq VHLFFFFFXETGS/RS

<400> 338

```
ttaattaaac tgtgg atg cac aac agt tgt aga cct gtg cac ctt ttt ttc        51
                 Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe
                 -20                 -15                 -10
ttt ttt ttt yct gag aca ggt tct cgt tct aat ycc tgg ctg gag tsc        99
Phe Phe Phe Xaa Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa
             -5                   1                   5
agt ggt gcg atc ata gct aac tcc                                       123
Ser Gly Ala Ile Ile Ala Asn Ser
    10                  15
```

<210> 339

<211> 451
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 318..449

<221> sig_peptide
<222> 318..443
<223> Von Heijne matrix
score 5.40000009536743
seq TFRLYLSLPVSQA/GP

<221> misc_feature
<222> 310..311,394
<223> n=a, g, c or t

```
<400> 339
gtcacaaaag gagcactaag agcctgcttt actttcttcc tcagttgagt cgtggggaca    60
gcttgaagga gccaacctca attgcagaga gcagccgtca ccccagctac cgctcagagc   120
ccagcttgga accagagagc ttccgttctc ctacctttgg caaaagtttt cacttcgatc   180
cactatccag tggctcacgc tcctccagcc tcaagtcagc ccagggcaca ggctttgagc   240
tgggccagtt gcaatccatt cgttcagagg gcaccacctc cacctcctaa taagagcctg   300
gccaaccagn nacgcaa atg gaa gcc tat ctt aat gac agc ttg ctc aca      350
                   Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr
                               -40                 -35
cct tca gac agc cct gat ttt gag tca gtg cag gca ggg cct gna gcc     398
Pro Ser Asp Ser Pro Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala
    -30                 -25                 -20
aga ccc acc ttt agg cta tac ctc tcc ctt cct gtc agc cag gct ggc     446
Arg Pro Thr Phe Arg Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly
-15                 -10                  -5                   1
cca gc                                                              451
Pro
```

<210> 340
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..303

<221> sig_peptide
<222> 94..135
<223> Von Heijne matrix
score 5.40000009536743
seq PALGPALLQGSLX/RV

<221> misc_feature
<222> 244..245
<223> n=a, g, c or t

```
<400> 340
gcgcagggga gaaacaaggc gccttggagt tcaggtgact cccacacggg tcatgctgtt    60
gtctcctgat ccagccggcc ctgccaggtg acc atg cct gct ctg ggc cca gct   114
                                     Met Pro Ala Leu Gly Pro Ala
                                                         -10
ctt ctc cag ggc tct ctg kgc cgv gtg ggt cct cac cct cca gcs cct     162
```

```
Leu Leu Gln Gly Ser Leu Xaa Arg Val Gly Pro His Pro Pro Ala Pro
     -5                      1               5
tcc acc aac tgc att cac tcc caa tgg cac gta tct gca gca csk ggc      210
Ser Thr Asn Cys Ile His Ser Gln Trp His Val Ser Ala Ala Xaa Gly
10                  15                  20                  25
aag gga ccc cac ctc agg cac cct ctr sct ggg nns tac caa ctt cct      258
Lys Gly Pro His Leu Arg His Pro Leu Xaa Gly Xaa Tyr Gln Leu Pro
                30                  35                  40
gtt cca gct gag ccc tgg gct gca gct gga ggc cac agt gtc cac c        304
Val Pro Ala Glu Pro Trp Ala Ala Ala Gly Gly His Ser Val His
            45                  50                  55
```

<210> 341
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 315..377

<221> sig_peptide
<222> 315..371
<223> Von Heijne matrix
score 5.40000009536743
seq LCCSGCVPSLCCS/SY

<400> 341

```
gtagccgccg ccgaaacttc cgccgccgcg tccgccgcct ccggaactaa acggggtgag     60
gtcacattcg gttatctcta acgttggaaa acgatggagc taacacccat tatggagatt    120
aamcvacttt tcatcaggtt tttaacttaa gtcgtgagga atacaacggt gaacacaaga    180
ttcattttat tttcatcacc atgggacgta tcctgttgtt gagttctctg ggtcagacct    240
ctgaagactt ctcagatgga tcctagtctc wrrgcttgcc ctgaaattac tcgctgctca    300
gggagagagt tgaa atg gtt ggc atc ctc cca ctc tgt tgc tcc ggc tgt      350
                Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys
                                -15                 -10
gtc ccc tcg ctc tgt tgt tcc agc tat gt                               379
Val Pro Ser Leu Cys Cys Ser Ser Tyr
     -5                      1
```

<210> 342
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..288

<221> sig_peptide
<222> 223..264
<223> Von Heijne matrix
score 5.40000009536743
seq AHSILLLASQAGC/LR

<400> 342

```
gggacccttt tagctatgaa atattttgga ttgcgtaggg tcttgcgcag cgcgaaaagt     60
agcgtgggcc aggacagcgg gaggtaagtc gccaagaaaa gggttgggaa ragctcagaa    120
tcggacggct aggaagaaat gaccaaaagg agcctgatag ccccctattc tgcacgctgt    180
tcctggaaac cgcctttgca aagacagtga gagaaatcta ac atg gct cac tcc       234
                                               Met Ala His Ser
atc ttg ctt cta gcc tcg cag gcc ggc tgt ctt cgc tca ttc ctg ggc      282
Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg Ser Phe Leu Gly
```

```
-10                 -5                  1               5
aat tgg g                                                            289
Asn Trp

<210> 343
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..167

<221> sig_peptide
<222> 78..137
<223> Von Heijne matrix
      score 5.40000009536743
      seq WVFLVAIFKGVHC/EG

<400> 343
agctctggga gaggagcccc cgccctggga ttcccaggtg ttttcatttg gtgatcagca     60
ctgaacacag aagagtc atg acg gag ttt ggg ctg agc tgg gtt ttc ctt      110
                   Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu
                   -20                 -15                 -10
gtt gct att ttt aaa ggt gtc cac tgt gaa ggt cma att ggt gga gtc      158
Val Ala Ile Phe Lys Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val
                -5                  1               5
ggg ggg gcg gg                                                       169
Gly Gly Ala
        10

<210> 344
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..110

<221> sig_peptide
<222> 63..104
<223> Von Heijne matrix
      score 5.40000009536743
      seq NTVFLLLFFGCFF/FE

<400> 344
tgtgttttct ctgtcccaaa ttaaatgcat tggggaagtt tataattaca ggaattccac     60
gc atg aac act gtt ttt ttg ttg ttg ttt ttt ggt tgt ttt ttt ttt      107
   Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe
                -10                 -5                  1
gag ac                                                               112
Glu

<210> 345
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..347
```

```
<221> sig_peptide
<222> 207..278
<223> Von Heijne matrix
      score 5.40000009536743
      seq SCCCLSSSSFIAG/RR

<400> 345
tcatcgtcta cgtggacggc agctggagcc cgtggagcaa gtggtcggcc tgtgggctgg     60
actgcaccca ctggcggacc gtgagtgctc tgacccagca ccccgcaacg gaggggagga    120
gtgccagggc actgacctgg acacccgcaa ctgtaccagt gacctctgtg tacacactgc    180
ttctggccct gaggacgtgg ccctct atg tgg gcc tca tcg ccg tgg ccg tct     233
                             Met Trp Ala Ser Ser Pro Trp Pro Ser
                                         -20
gcb tgg tcc tgc tgc tgc ttg tcc tca tcc tcg ttt att gcc gga aga      281
Ala Trp Ser Cys Cys Cys Leu Ser Ser Ser Ser Phe Ile Ala Gly Arg
-15                 -10                 -5                  1
agg agg ggc tgg act cag atg tgg ctg act cgt cca ttc tca cct cag      329
Arg Arg Gly Trp Thr Gln Met Trp Leu Thr Arg Pro Phe Ser Pro Gln
            5                   10                  15
gct tcc agc ccg tca gca tc                                           349
Ala Ser Ser Pro Ser Ala
        20

<210> 346
<211> 191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..191

<221> sig_peptide
<222> 45..143
<223> Von Heijne matrix
      score 5.40000009536743
      seq FMLIILSAILLNS/FI

<400> 346
ccttccatag gtggtgtacc gttttgcatt cccatcagca ctgt atg aca atg ccc      56
                                                 Met Thr Met Pro
                                                             -30
att tct tca tat tcc cag aat gtg ttg tca aac ttt cac gat ggc tat      104
Ile Ser Ser Tyr Ser Gln Asn Val Leu Ser Asn Phe His Asp Gly Tyr
                -25                 -20                 -15
ttt atg tta att ata ctt tct gcc att tta cta aat tct ttt att ggt      152
Phe Met Leu Ile Ile Leu Ser Ala Ile Leu Leu Asn Ser Phe Ile Gly
            -10                 -5                  1
tgt gtc agc ttt tat cat tgc ttt tct tgg ggt tca ggg                  191
Cys Val Ser Phe Tyr His Cys Phe Ser Trp Gly Ser Gly
    5                   10                  15

<210> 347
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..227

<221> sig_peptide
<222> 144..203
```

```
<223> Von Heijne matrix
      score 5.40000009536743
      seq LSLVIFLLTVKHC/FR

<400> 347
tttcatatag ccacctcctc ttggtagcca gaagaccctt cggatgatgc cccaggtgta      60
aaactctctg gggcccgccc cactcggaag gattactgaa atgagtcatt tccgggacgc     120
ctttttact gttgaatgaa agg atg cta aca cat ggg gct tcc ctg tct tta      173
                         Met Leu Thr His Gly Ala Ser Leu Ser Leu
                         -20                -15
gtc ata ttt ctg tta aca gtg aag cat tgc ttt aga tac aga gta tac       221
Val Ile Phe Leu Leu Thr Val Lys His Cys Phe Arg Tyr Arg Val Tyr
-10                 -5                  1               5
aag act tt                                                            229
Lys Thr

<210> 348
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..210

<221> sig_peptide
<222> 106..171
<223> Von Heijne matrix
      score 5.40000009536743
      seq FWTSIPILPLSSG/RQ

<400> 348
aaagaatcca gttgagccta tcgggacttt tgacctacag aactgtgaga taaaaaatgg      60
gtgtcgtttt agataaccca tggcagcatt ccctcctctg ctgga atg tcg tca gtg     117
                                                  Met Ser Ser Val
                                                          -20
gag act gac tgg gga ttc tgg act tcc atc ccc atc ctc cca ctc agc       165
Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile Leu Pro Leu Ser
        -15                 -10                 -5
agt ggt agg cag ctc ccc ctc ccc act aga gaa tgg gga atg tgg           210
Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp Gly Met Trp
        1               5                   10

<210> 349
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 184..429

<221> sig_peptide
<222> 184..282
<223> Von Heijne matrix
      score 5.40000009536743
      seq LSAILSMLSLSFS/TT

<221> misc_feature
<222> 214
<223> n=a, g, c or t
```

```
<400> 349
aggacatcct ctccaatcca ccacacacca ccttacccct ctgctggcaa gaggggacct     60
gattcatcct cacgctaaac actcattcta cccaactgat tgagacagaa cagaagataa    120
ctgaaacttc tctgccttcc cgctgcaaga agtgaatgag cgatccctct caactgactk    180
raa atg ttt gcc tca ccc agg aga tgg agc tct ncg aag gcc ttc tct      228
    Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser
                -30                 -25                 -20
ggc cag cgg aca ctc cta tct gcc atc ctc agc atg cta tca ctc agc      276
Gly Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser
            -15                 -10                 -5
ttc tcc aca aca tcc ctg ctc agc aac tac tgg ttt gtg ggc aca cag      324
Phe Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln
        1               5                   10
aag gtg ccc aag ccc ctg tgc gag aaa ggt ctg gca gcc aag tgc ttt      372
Lys Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe
15                  20                  25                  30
gac atg cca gtg tcc ctg gat gga gat acc aac aca tcc acc cag gag      420
Asp Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu
                35                  40                  45
gtg gta mma ta                                                       431
Val Val Xaa

<210> 350
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 197..385

<221> sig_peptide
<222> 197..244
<223> Von Heijne matrix
      score 5.40000009536743
      seq HSVFLCAPALVFP/RP

<400> 350
aaagtaaagc ggaggcagcg ggggaagatg gcggcggccg ttccacagcg ggcgtggacc     60
gtggagcagc tgcgcagtga gcagctgccc aagaaggaca ttatcaagtt tctgcaggaa    120
cacggttcag attcggtacc agaggcgtag ggcggccgg gctggtgcgg ctgagggacg    180
cctcaccccc ctggag atg ccc ata cat tcc gta ttc ctc tgt gcc ccc gcc    232
                  Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala
                      -15                 -10                 -5
ctc gtc ttc ccg cgg ccg gtg gcc tgg aag gcg gag agg ccc agc ttg      280
Leu Val Phe Pro Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu
                1               5                   10
tgc ttt ggt gcc tcg ctc ccg cct ctc ggg cgt tct cta ctg ggg cag      328
Cys Phe Gly Ala Ser Leu Pro Pro Leu Gly Arg Ser Leu Leu Gly Gln
        15                  20                  25
ggg agc agc ttt att tct tgg ggc aca cag gct gca att gta gag tta      376
Gly Ser Ser Phe Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu
    30                  35                  40
kaa cct cat t                                                        386
Xaa Pro His
45

<210> 351
<211> 307
<212> DNA
<213> Homo sapiens

<220>
```

<221> CDS
<222> 68..307

<221> sig_peptide
<222> 68..253
<223> Von Heijne matrix
score 5.30000019073486
seq LACVFFLSHPLFX/XP

<221> misc_feature
<222> 279
<223> n=a, g, c or t

<400> 351
```
ttttactctg taattgttac taattgattt ttgmataggg agcacattcc catggttcaa      60
aattcaa atg gta tac gat gaa aaa tct ctc tcc tgt tcc cat acc cca      109
        Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro
                -60                 -55                 -50
gcc acc cag ttc ctc tcc tgg gat gca tcc agt gtt tac agt ttc tta      157
Ala Thr Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu
            -45                 -40                 -35
tat atc ctc tca gca aga gtt aat gta gac gta dgc agm tac att cgt      205
Tyr Ile Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg
        -30                 -25                 -20
gtg tac ata ctt gcc tgt gtg ttt ttc ctc tca cac ccc ctt ttt aad      253
Val Tyr Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa
    -15                 -10                 -5
sra cca aat ggt agt gta tat tgt cnm cgt cat tct ccc cct tac ctt      301
Xaa Pro Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu
1               5                   10                  15
ttt tgc                                                              307
Phe Cys
```

<210> 352
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..169

<221> sig_peptide
<222> 56..163
<223> Von Heijne matrix
score 5.30000019073486
seq VCLLIISLVLISG/LG

<400> 352
```
gttctttggt gatacaaaca ctgtattttg agtaatcttt tccctatatt tcgaa atg      58
                                                             Met
ctg cct tta tca cct act aaa ttc cta aat gtg ttc ttg ggc ctg ttc      106
Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu Phe
-35                 -30                 -25                 -20
ctc tat tat ctt caa ttg gta tgt ctg ctt att att tct ttg gtt ttg      154
Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val Leu
                -15                 -10                 -5
ata tct ggg tta ggg g                                                170
Ile Ser Gly Leu Gly
            1
```

<210> 353

```
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..292

<221> sig_peptide
<222> 149..235
<223> Von Heijne matrix
      score 5.30000019073486
      seq LNQTLMLLREVLA/SH

<400> 353
tttctaatct sbtcaaattt tatcaccata caatcagtgg taktgttgga aatagtgcaa    60
ctgcattatt gactaccatt gaagaaatgc atttgctaag caaaaaaata ttcttcaatt   120
agcttgaagt cttcatgcaa gtaaatta atg gac aag gtt gaa ctc cca cca      172
                               Met Asp Lys Val Glu Leu Pro Pro
                                                   -25
cct gat ctt gga cca agt tct gca cta aat cag aca ctc atg ttg ctg     220
Pro Asp Leu Gly Pro Ser Ser Ala Leu Asn Gln Thr Leu Met Leu Leu
    -20                 -15                 -10
cgt gaa gtt tta gca tct cac gat tct tca gtk gta cca tta gat gct     268
Arg Glu Val Leu Ala Ser His Asp Ser Ser Val Val Pro Leu Asp Ala
-5                  1               5                   10
cgt caa gct gat ttt gtg cag ggg g                                   293
Arg Gln Ala Asp Phe Val Gln Gly
            15

<210> 354
<211> 331
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..330

<221> sig_peptide
<222> 148..243
<223> Von Heijne matrix
      score 5.30000019073486
      seq LVWLWFVVPQTIT/MI

<221> misc_feature
<222> 124
<223> n=a, g, c or t


<400> 354
catttctagc ttttgdktta aagtgacaga cttgccactc ttcttttccc ttgaacactt    60
acaggctgtg ggagggttat tagttggtct aatttcaata mtgttccttt cyccagggaa   120
ttgnraggcc caaggagagg gagagag atg ggg gga aca gct ggt tgg agc agt   174
                              Met Gly Gly Thr Ala Gly Trp Ser Ser
                                      -30                 -25
cag aac aca cac aac att kga gta cac cat ctt gtg tgg ctg tgg ttc     222
Gln Asn Thr His Asn Ile Xaa Val His His Leu Val Trp Leu Trp Phe
            -20                 -15                 -10
gtg gtc ccc caa aca att aca atg ata aca cca aag atc act gaa cac     270
Val Val Pro Gln Thr Ile Thr Met Ile Thr Pro Lys Ile Thr Glu His
        -5                  1               5
aga cca sta ata aca gat atr dtr ata atg aya aca ttt gaa awa ttg     318
```

```
Arg Pro Xaa Ile Thr Asp Xaa Xaa Ile Met Xaa Thr Phe Glu Xaa Leu
10                  15                  20                  25
gga gaa tta ccc a                                                   331
Gly Glu Leu Pro

<210> 355
<211> 93
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..91

<221> sig_peptide
<222> 2..55
<223> Von Heijne matrix
      score 5.30000019073486
      seq ALYLCVCVCVCLI/AR

<400> 355
t atg tgt ctv agt gta gct ttg tat tta tgt gtg tgt gtg tgt gta tgt    49
  Met Cys Leu Ser Val Ala Leu Tyr Leu Cys Val Cys Val Cys Val Cys
              -15                 -10                 -5
ctg att gca cgg gtg tac ttt tgt att tat gtg tgt gtg tgg tt           93
Leu Ile Ala Arg Val Tyr Phe Cys Ile Tyr Val Cys Val Trp
        1               5                   10

<210> 356
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 92..178

<221> sig_peptide
<222> 92..133
<223> Von Heijne matrix
      score 5.30000019073486
      seq LHLLFGLFPVLWM/FL

<400> 356
tgacccttgt ccagtctttt ccaggaaaaa catgccctca agatgttttt ctatcttgag    60
gaaatgatgg aaatgagata gttccaaggg t atg ctt cac ctt ctt ttt ggc      112
                                   Met Leu His Leu Leu Phe Gly
                                                   -10
tta ttt cct gtt ctt tgg atg ttt cta gtg tat ttc ttt ctt tct tct     160
Leu Phe Pro Val Leu Trp Met Phe Leu Val Tyr Phe Phe Leu Ser Ser
        -5                  1               5
ttt ttt ttt ttt ttt ttt                                             178
Phe Phe Phe Phe Phe Phe
10                  15

<210> 357
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..105
```

```
<221> sig_peptide
<222> 40..93
<223> Von Heijne matrix
      score 5.30000019073486
      seq CVYLFCACMCVCA/FF

<221> misc_feature
<222> 54
<223> n=a, g, c or t


<400> 357
tatatttata taaatatata taaatacaca catatatat atg tat gtg tgt atn        54
                                           Met Tyr Val Cys Xaa
                                                           -15
tgt gtg tat ctt ttt tgt gca tgt atg tgt gta tgt gct ttt ttt ttt      102
Cys Val Tyr Leu Phe Cys Ala Cys Met Cys Val Cys Ala Phe Phe Phe
            -10                 -5                  1
ttt tt                                                                107
Phe

<210> 358
<211> 209
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 44..208

<221> sig_peptide
<222> 44..151
<223> Von Heijne matrix
      score 5.30000019073486
      seq FLFTLIGASLLQS/AS

<400> 358
ggggggcgac gtaagggcgc tccgcgagcc cgtctctcct cga atg aaa sga aac        55
                                                Met Lys Xaa Asn
                                                    -35
aac ctc cgg cga cag agc ccc gct ctc agg cac tgc tgg aga mcc gag      103
Asn Leu Arg Arg Gln Ser Pro Ala Leu Arg His Cys Trp Arg Xaa Glu
        -30                 -25                 -20
acc gac ttc ttt ctc ttt acc ctc att ggc gct tct ctc ctg cag tcc      151
Thr Asp Phe Phe Leu Phe Thr Leu Ile Gly Ala Ser Leu Leu Gln Ser
    -15                 -10                 -5
gcc tct ggg ccc tgc cgc att tct tsa smc tta aag tgg cat tct aaa      199
Ala Ser Gly Pro Cys Arg Ile Ser Xaa Xaa Leu Lys Trp His Ser Lys
1               5                   10                  15
ggc act tta a                                                         209
Gly Thr Leu

<210> 359
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..296

<221> sig_peptide
```

```
<222> 135..194
<223> Von Heijne matrix
      score 5.30000019073486
      seq LGLGLPLLPPNHP/SV

<400> 359
agcatttgcm ttcggagggc cagargggca ggcagagctt aattccttgg gcaaggctgg     60
ggctgttgga atggggtctg gaggccagga gccaccctgt ctgggccaga aaggggcctk    120
ggtgcagggc aggc atg tgg ccc aag arg ggg cta ctg gga ttg ggg ctc      170
                Met Trp Pro Lys Xaa Gly Leu Leu Gly Leu Gly Leu
                -20                 -15                 -10
cca ctg ctg ccc cct aac cat ccc tcg gta gcc caa ggg aca ctc gtt      218
Pro Leu Leu Pro Pro Asn His Pro Ser Val Ala Gln Gly Thr Leu Val
            -5                  1               5
tcc tcc cac tct ggt tct ggc tct gag ggt agg gtg gcg ctc agg agt      266
Ser Ser His Ser Gly Ser Gly Ser Glu Gly Arg Val Ala Leu Arg Ser
    10                  15                  20
gat gtc cac agc ccc aag aca acc csc caa cg                           298
Asp Val His Ser Pro Lys Thr Thr Xaa Gln
25                  30

<210> 360
<211> 460
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..458

<221> sig_peptide
<222> 54..179
<223> Von Heijne matrix
      score 5.30000019073486
      seq AMAXLFLSAPPQA/EV

<221> misc_feature
<222> 150,285,328
<223> n=a, g, c or t


<400> 360
gaggttgggc tgccgtgctg ctcggcggcg ctgaggccaa atagttgcat cac atg        56
                                                           Met
tat cta atc cga gag tct cat gct tct ggt agc tcc tca gtg acc agc      104
Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr Ser
    -40                 -35                 -30
tcc tgc tca ctg mcc tca gra agc ccc aac cct cag gca atg gck ncc      152
Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala Xaa
-25                 -20                 -15                 -10
ttg ttc ctg tct gcc cca ccc cag gcc gag gtg acc ttc gag gac gtg      200
Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp Val
                -5                  1               5
gct gtg tac ctc tcc cgg gag gaa tgg ggc cgc ctg ggc cct gct cag      248
Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala Gln
        10                  15                  20
agg ggc bkc tac agg gac gtg atg ctg gag acc tac ngg aac bta gtc      296
Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa Val
    25                  30                  35
tca ctg gga gta gga cct gca ggc ccc aag cnt gga gtg atc tcg cag      344
Ser Leu Gly Val Gly Pro Ala Gly Pro Lys Xaa Gly Val Ile Ser Gln
40                  45                  50                  55
ttg gag cga ggg gat gag ccc tgg gtc ctg gat gtt cag ggc acc tct      392
```

```
Leu Glu Arg Gly Asp Glu Pro Trp Val Leu Asp Val Gln Gly Thr Ser
                60                  65                  70
ggg aaa gag cac ctg aag aag tca aca gcc cag ctc ttg gga cca gaa      440
Gly Lys Glu His Leu Lys Lys Ser Thr Ala Gln Leu Leu Gly Pro Glu
            75                  80                  85
ctg aag tac aag gag ttg ay                                           460
Leu Lys Tyr Lys Glu Leu
        90
```

<210> 361
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..317

<221> sig_peptide
<222> 153..263
<223> Von Heijne matrix
score 5.30000019073486
seq ALSSLCVSWGTSS/TV

<400> 361

```
ctcttttccg gttaacgcgg cgtgagaagc catgagcagc aaagtctctc gcgacaccct     60
gtacgaggcg gtgcgggaag tcctgcacgg gaaccagcgc aasgccgcaa gttcctggag    120
acggtggagt tgcaggatca gcttgaagaa ct atg atc ccc aga agg aca agc      173
                                    Met Ile Pro Arg Arg Thr Ser
                                                -35
gct tct cgg gca ccg tca gtc ccc caa aac gca ggc tta agt cca ctc      221
Ala Ser Arg Ala Pro Ser Val Pro Gln Asn Ala Gly Leu Ser Pro Leu
-30                 -25                 -20                 -15
ccc gcc cta agt tct ctg tgt gtg tcc tgg ggg acc agc agc act gtg      269
Pro Ala Leu Ser Ser Leu Cys Val Ser Trp Gly Thr Ser Ser Thr Val
                -10                  -5                   1
acg agg cta agg ccg tgg ata tcc ccc aca tgg aca tcg agg gcg cgg g    318
Thr Arg Leu Arg Pro Trp Ile Ser Pro Thr Trp Thr Ser Arg Ala Arg
        5                   10                  15
```

<210> 362
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 192..359

<221> sig_peptide
<222> 192..233
<223> Von Heijne matrix
score 5.30000019073486
seq VCIFCFLTSKAFP/NP

<221> misc_feature
<222> 277
<223> n=a, g, c or t

<400> 362

```
tattgggttg ttttcttatt atcaaattgt gaaagttctt tacatattct gggtagaact     60
cctttatcag atacatgttt tgcaaatgtt ttctaccatt ctctgtctdh tctttctctt    120
```

```
aatactttca cagtttttca tagcagaaat ttataaatta atgaagccca ctttatactt   180
ttatttcttt t atg gtt tgc atc ttt tgt ttc tta act tcg aaa gct ttt    230
             Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe
                             -10                 -5
cct aac cct aga tca cag gat ttt ctc tta gat ttc tct agg cat tnt      278
Pro Asn Pro Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa
    1               5                   10                  15
ata ggt tta ggt ttc aca ttt agg tcc gca atg cat ttt gaa aac ttc      326
Ile Gly Leu Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe
                20                  25                  30
cgt ctg waa ggt ttg ggt caa gat tcc ctt tgt c                        360
Arg Leu Xaa Gly Leu Gly Gln Asp Ser Leu Cys
            35                  40
```

<210> 363
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..212

<221> sig_peptide
<222> 138..197
<223> Von Heijne matrix
score 5.30000019073486
seq GFCSVTSSPLASA/GR

<221> misc_feature
<222> 152
<223> n=a, g, c or t

<400> 363

```
cacaaaatca aaaackkagt tgacgtatgc cactttccag ttactattga gatatatatg    60
cgtgtgtgta tatattacat atatatgtta tatatcatat tkatatattt akaaawttat   120
atmgavcata catatat atg taw atr tat ktn kkt ava ggg ttt tgc tct      170
                   Met Xaa Xaa Tyr Xaa Xaa Xaa Gly Phe Cys Ser
                   -20                 -15                 -10
gtc aca agc agt cct ctt gcc tca gca ggt agg act aca cgc              212
Val Thr Ser Ser Pro Leu Ala Ser Ala Gly Arg Thr Thr Arg
                -5                  1               5
```

<210> 364
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 127..240

<221> sig_peptide
<222> 127..195
<223> Von Heijne matrix
score 5.30000019073486
seq LVPCPLLISVALS/VK

<221> misc_feature
<222> 71,73
<223> n=a, g, c or t

```
<400> 364
actttaactt cctggagctc taatttctcc ttctcaggta gaagaatgcc attcactccc    60
aagtggtgag nmncaagcag ccagtggtag gaagggtcat caagtcagtt gtcagaaacc   120
tcactk atg tca ctg twt ahg cta tgt gac cct gac cta gtt cct tgc      168
       Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys
                   -20                 -15                 -10
cct ctc ttg atc tca gtt gct tta tct gta aaa ttt cac att tkt cag     216
Pro Leu Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln
                -5                  1                   5
caa gtc aac ctt cca tgt tcc tct ca                                  242
Gln Val Asn Leu Pro Cys Ser Ser
        10                  15

<210> 365
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..246

<221> sig_peptide
<222> 7..123
<223> Von Heijne matrix
      score 5.30000019073486
      seq LXPCLTSFSCXGA/SF

<400> 365
tgtaca atg atg atc ctt atc cta att ctt gag cat atc gtc acc kcc       48
       Met Met Ile Leu Ile Leu Ile Leu Glu His Ile Val Thr Xaa
                       -35                 -30
aaa aga aac ccc aaa cct gtt aca gtc cct gct ttt ctg csc cct tgc      96
Lys Arg Asn Pro Lys Pro Val Thr Val Pro Ala Phe Leu Xaa Pro Cys
-25                 -20                 -15                 -10
ttg act tct ttc tct tgt kct gga gca tct ttc tct ctk ttw ggt gdg     144
Leu Thr Ser Phe Ser Cys Xaa Gly Ala Ser Phe Ser Leu Xaa Gly Xaa
                -5                  1                   5
aga agg ggt tgg caa cat ggc agc tgc tgc tcc acc att ccc tta ttt     192
Arg Arg Gly Trp Gln His Gly Ser Cys Cys Ser Thr Ile Pro Leu Phe
        10                  15                  20
csa act cta aat tcc ctt ggg cag gga ctc att ggc cca gcc tac ata     240
Xaa Thr Leu Asn Ser Leu Gly Gln Gly Leu Ile Gly Pro Ala Tyr Ile
    25                  30                  35
ggt gcd gg                                                          248
Gly Ala
40

<210> 366
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 293..349

<221> sig_peptide
<222> 293..340
<223> Von Heijne matrix
      score 5.30000019073486
      seq HAISILLCIGASS/QG
```

```
<221> misc_feature
<222> 36
<223> n=a, g, c or t


<400> 366
aaaacatata tccacacaaa aacttgcaca catakntca tagcagcatt attcatccaa     60
aaagtagagg tactcaaatg actttcaact gataaacaca gatgaacaaa atgtatgtcc   120
aaacagtaga atattattca gctataaaaa agaacagagt acacttagca aactaagaat   180
agaaggaact tcctcaatct gataaaggac atccatgaaa aacccaccac taatgtcata   240
cttaatcatg aaaaaccgaa tgcttttctc ctaagatagg aaaaagacaa gt atg tct   298
                                                          Met Ser
                                                              -15
act cat gcc atc tct att cta ctt tgt att ggt gct tct agc cag ggc     346
Thr His Ala Ile Ser Ile Leu Leu Cys Ile Gly Ala Ser Ser Gln Gly
                -10                 -5                  1
agg gg                                                              351
Arg

<210> 367
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..207

<221> sig_peptide
<222> 7..99
<223> Von Heijne matrix
      score 5.19999980926514
      seq ATVNAASLPPCFG/VK

<400> 367
gtctcg atg gag gag caa gaa acg gaa gag gtc ggg ggg aga agc agc      48
       Met Glu Glu Gln Glu Thr Glu Glu Val Gly Gly Arg Ser Ser
           -30                 -25                 -20
cgg aaa aat gca gcc acc gtc aac gcc gcc tcc ctg cca ccg tgc ttc      96
Arg Lys Asn Ala Ala Thr Val Asn Ala Ala Ser Leu Pro Pro Cys Phe
        -15                 -10                 -5
ggg gta aaa agc tgc cgt tgc cgt cgg tgc agt tgc cgt cgc tgc ctc     144
Gly Val Lys Ser Cys Arg Cys Arg Arg Cys Ser Cys Arg Arg Cys Leu
    1               5                   10                  15
cta tac ttc tct tgg cct cgg gga agg att tcc cca ccg gtg gga caa     192
Leu Tyr Phe Ser Trp Pro Arg Gly Arg Ile Ser Pro Pro Val Gly Gln
                20                  25                  30
tgt gcg ggg agg gga t                                               208
Cys Ala Gly Arg Gly
            35

<210> 368
<211> 446
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..445

<221> sig_peptide
<222> 11..109
```

<223> Von Heijne matrix
score 5.19999980926514
seq CCCHAGASSGATA/WE

<400> 368
```
agaatccaag atg cgc ggg atc car gca aar ggg tct ccg ggc cag agt        49
           Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser
                       -30                      -25
tcg gcc gst gtt ctg wcg cct tgc tgc tgt cac gcg ggc gct tcg tcc       97
Ser Ala Xaa Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser
-20                 -15                 -10                 -5
ggg gcg acg gcg tgg gag gag acc ccg cgg tcg cgt tgc cac atc gcc      145
Gly Ala Thr Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala
                1               5                   10
gtt kcg agt aca aat aca gct tca agg ggc cgc acc tgg tgc aga gcg      193
Val Xaa Ser Thr Asn Thr Ala Ser Arg Gly Arg Thr Trp Cys Arg Ala
        15                  20                  25
acg gga ccg tgc cct tct ggg ccc acg cgg gga gta agc cgg agc aga      241
Thr Gly Pro Cys Pro Ser Gly Pro Thr Arg Gly Val Ser Arg Ser Arg
    30                  35                  40
ggg ctg ggg gcc ggg ttc ctc tcc ccc ttc tgc tgc ctc ttc gcc ttt      289
Gly Leu Gly Ala Gly Phe Leu Ser Pro Phe Cys Cys Leu Phe Ala Phe
45                  50                  55                  60
cat ccg cgg cta ccc tgg tgt gct gag gtt ccc gtt cca gca gct gca      337
His Pro Arg Leu Pro Trp Cys Ala Glu Val Pro Val Pro Ala Ala Ala
                65                  70                  75
cac cat atg cgc tgt gga ggg gac ctc ctg gca gcc cct ccg ccg ggt      385
His His Met Arg Cys Gly Gly Asp Leu Leu Ala Ala Pro Pro Pro Gly
            80                  85                  90
ccc tcc tgg ttc gca cgg ttc cct ccg ctt gtc ccc gag tct ttc cct      433
Pro Ser Trp Phe Ala Arg Phe Pro Pro Leu Val Pro Glu Ser Phe Pro
        95                  100                 105
cac cat tct gtt c                                                    446
His His Ser Val
    110
```

<210> 369
<211> 125
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..123

<221> sig_peptide
<222> 22..93
<223> Von Heijne matrix
score 5.19999980926514
seq LIWVFGLVSVLSX/FL

<400> 369
```
ctatcaagag gctttccccc t atg ttt tct tct agg agt ttt atg gtt tca       51
                        Met Phe Ser Ser Arg Ser Phe Met Val Ser
                                        -20                 -15
ggt ctt att tgg gtc ttt ggt ctt gta tct gtt ttg agt bga ttt ttg       99
Gly Leu Ile Trp Val Phe Gly Leu Val Ser Val Leu Ser Xaa Phe Leu
                -10                 -5                  1
tgt atg gtg tat gat cag ggt cag gg                                   125
Cys Met Val Tyr Asp Gln Gly Gln
        5                   10
```

<210> 370

```
<211> 132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..131

<221> sig_peptide
<222> 39..77
<223> Von Heijne matrix
      score 5.19999980926514
      seq MLLAVSLSLVSNC/NF

<400> 370
atcttagagg aaagtctttc agtttttccc cattcagt atg tta tta gct gtg agc      56
                                          Met Leu Leu Ala Val Ser
                                                          -10
ctg tcc ctt gtc tct aat tgt aac ttt gta ctc act gac caa ctt ttc       104
Leu Ser Leu Val Ser Asn Cys Asn Phe Val Leu Thr Asp Gln Leu Phe
        -5                  1               5
cct gcc cct gcs tcc ctc atc ccc gaa g                                 132
Pro Ala Pro Ala Ser Leu Ile Pro Glu
10                  15

<210> 371
<211> 127
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..126

<221> sig_peptide
<222> 4..90
<223> Von Heijne matrix
      score 5.19999980926514
      seq TGVFLFSIIGSFG/FP

<400> 371
tga atg aac caa gat ttc aac cca gaa att gag gct tca cca caa gtg        48
    Met Asn Gln Asp Phe Asn Pro Glu Ile Glu Ala Ser Pro Gln Val
                    -25                 -20                 -15
aag act ggg gtt ttc ttg ttt tca att att ggg agt ttt gga ttt cca        96
Lys Thr Gly Val Phe Leu Phe Ser Ile Ile Gly Ser Phe Gly Phe Pro
                -10                 -5                  1
gga atg tgc aat tgt aaa aac cca gcc cgg g                             127
Gly Met Cys Asn Cys Lys Asn Pro Ala Arg
        5                   10

<210> 372
<211> 196
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..196

<221> sig_peptide
<222> 125..184
<223> Von Heijne matrix
```

```
      score 5.19999980926514
      seq IVSSLFSWLLSLT/SV

<221> misc_feature
<222> 119
<223> n=a, g, c or t


<400> 372
taaaaatctt ttatgttcta cccactcctt cctcgttccc tctccccact cctccctccc    60
cccatcttaa gcccatggca acccctgatc tttttactgt ctccatcgtt ttgccttbnc   120
caga atg cca tgt agt tgg agt cat ata gta agt agc ctt ttc agt tgg    169
     Met Pro Cys Ser Trp Ser His Ile Val Ser Ser Leu Phe Ser Trp
     -20                 -15                 -10
ctt ctt tca ctt acc agt gtg ccc ggg                                 196
Leu Leu Ser Leu Thr Ser Val Pro Gly
-5                  1

<210> 373
<211> 148
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..148

<221> sig_peptide
<222> 56..139
<223> Von Heijne matrix
      score 5.19999980926514
      seq PVLSCCCLTAGRA/RL

<400> 373
actttcttca cacccaggac gcagggtgcc gctgccggcc acagaaaccc caaga atg     58
                                                             Met
ttt ttc ttt ggc tat tca gag gac atc tat tgt gtg tca ggc cct gtg     106
Phe Phe Phe Gly Tyr Ser Glu Asp Ile Tyr Cys Val Ser Gly Pro Val
        -25                 -20                 -15
ctg agc tgt tgt tgc ctg aca gca gga aga gcg cgg ctc tgg             148
Leu Ser Cys Cys Cys Leu Thr Ala Gly Arg Ala Arg Leu Trp
    -10                 -5                  1

<210> 374
<211> 200
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..199

<221> sig_peptide
<222> 26..73
<223> Von Heijne matrix
      score 5.19999980926514
      seq AALICPWSSQVPS/SP

<400> 374
ctagggagga ctcaatgctc tttgt atg cct tat gca gcg ctg atc tgt ccc      52
                            Met Pro Tyr Ala Ala Leu Ile Cys Pro
                                -15                 -10
tgg agt tcc cag gtt ccc agc tcc ccc cct gca agc ctt gaa gcc tcc     100
```

```
Trp Ser Ser Gln Val Pro Ser Ser Pro Pro Ala Ser Leu Glu Ala Ser
        -5                  1                   5
agc aac gtc tat ctc cag gag agc agg gca gcc tat gca agt gtt ccg      148
Ser Asn Val Tyr Leu Gln Glu Ser Arg Ala Ala Tyr Ala Ser Val Pro
10                  15                  20                  25
gca gga cca gaa gtg gcc act caa cac acg tcc tca cca gtc acc cct      196
Ala Gly Pro Glu Val Ala Thr Gln His Thr Ser Ser Pro Val Thr Pro
                30                  35                  40
atg g                                                                200
Met
```

<210> 375
<211> 112
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..111

<221> sig_peptide
<222> 52..105
<223> Von Heijne matrix
score 5.19999980926514
seq LTYSLAFLLFIKA/GT

<400> 375

```
aataaccctt tcacagcact tgcctgtttt taatgaatct aattattcac a atg caa      57
                                                         Met Gln
ctt tta tat tta aca tac tct tta gct ttc ctg cta ttt atc aag gct      105
Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile Lys Ala
    -15                 -10                 -5
ggc acc g                                                            112
Gly Thr
1
```

<210> 376
<211> 146
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 74..145

<221> sig_peptide
<222> 74..133
<223> Von Heijne matrix
score 5.19999980926514
seq AAAVTSSAAPSRA/RQ

<400> 376

```
ggctggagcg cgcgcctcct agcggascgg ggcaattgga aggccgcgcc tcaggaaaac      60
aggatggtag tga atg gca ccg agc cgc ccc agg gct gcc gcc gtc acc        109
               Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr
               -20                 -15                 -10
tcc tcg gcg gct ccg agt cgt gcg agg cag ggg gcc c                     146
Ser Ser Ala Ala Pro Ser Arg Ala Arg Gln Gly Ala
            -5                  1
```

<210> 377
<211> 389
<212> DNA

```
<213> Homo sapiens

<220>
<221> CDS
<222> 218..388

<221> sig_peptide
<222> 218..343
<223> Von Heijne matrix
      score 5.19999980926514
      seq QHLLSWAXQXGRX/QV

<221> misc_feature
<222> 139
<223> n=a, g, c or t


<400> 377
cattttgtcg gtagaggcag aaggwgaagg tcgggttgta gaagctgggg tggccggcag    60
ctcgctcatc ggtgttcgtg ggctttgtcg gtccgtgcct cgtctctccc tggaaaggga   120
gggaggcttc gacgtcgrnr aggragmmgc tgccgcgtta gttccgagct tgaagtcact   180
aggacttctc tcaaacttgt gtgctgagga gactcag atg ttg gcc tca gct cct    235
                                         Met Leu Ala Ser Ala Pro
                                                     -40
agg ctg aac tca gca gat cgg ccc atg aaa act tct gta ttg aga caa     283
Arg Leu Asn Ser Ala Asp Arg Pro Met Lys Thr Ser Val Leu Arg Gln
    -35                 -30                 -25
agg aag gga tct gtc aga aag caa cac ttg tta tct tgg gct tdg cag     331
Arg Lys Gly Ser Val Arg Lys Gln His Leu Leu Ser Trp Ala Xaa Gln
-20                 -15                 -10                 -5
yaa ggh aga kga cag gta gtg gag atc ctg caa tct gaa aag cag act     379
Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu Gln Ser Glu Lys Gln Thr
                1               5                   10
daa rgt gac g                                                       389
Xaa Xaa Asp
        15

<210> 378
<211> 143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..142

<221> sig_peptide
<222> 2..115
<223> Von Heijne matrix
      score 5.19999980926514
      seq LHGSLDAVSQAQG/RP

<400> 378
a atg tac ccc cta ggc agg gga gag cag ggc cct gct gca ccc aag tcc    49
  Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser
              -35                 -30                 -25
tgg ttg ctc ctc ccc acc aca ctg gcc ctc cat gga agc ctt gat gca     97
Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala
        -20                 -15                 -10
gtg agc cag gcc caa gga cgc ccc ggc cac cct gac gca ccc ccc a      143
Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro
    -5                  1                   5
```

```
<210> 379
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..260

<221> sig_peptide
<222> 198..245
<223> Von Heijne matrix
      score 5.19999980926514
      seq FIAALFTIAETWN/QP

<400> 379
cagatggtgg tgaggttgta gagaaaaagg aacgcttata cactgttggt gcgagtgtaa     60
attagtttaa ccattgtgga agatgatatg gcaattccac aaagacctaa agtcagraat    120
tmcmattcaa cccagtaatc ccattactgg gtatatactc aaaggaatat aaattgttgt    180
gttacaaaga cacatgc atg cgt gtg ttc att gca gca ctg ttc aca ata       230
                   Met Arg Val Phe Ile Ala Ala Leu Phe Thr Ile
                       -15                 -10
gca gag aca tgg aat caa ccc aaa tgc cca g                            261
Ala Glu Thr Trp Asn Gln Pro Lys Cys Pro
-5                  1               5

<210> 380
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..227

<221> sig_peptide
<222> 63..152
<223> Von Heijne matrix
      score 5.19999980926514
      seq LCFLSVHFRLRWG/DS

<400> 380
gggacgtggg aaaatgacta cgcgtcactc gtgatgtcgc gcatccgata ggccctttc      60
ag atg gca aaa ggc ctg agg gtg aat ctg ggc gag ctg gtt gag tcc       107
   Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser
   -30                 -25                 -20
atg cgt ttg tgc ttc ctc tca gtc cac ttt cgc tta cga tgg ggc gac      155
Met Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp
-15                 -10                 -5                  1
tct tgt cca tcg tca cct cac cgg gaa act ttt cct gcc ggg cca gtt      203
Ser Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val
            5                   10                  15
aat ggt ccc ctg tac cac ccc cgg g                                    228
Asn Gly Pro Leu Tyr His Pro Arg
        20                  25

<210> 381
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

<222> 39..299

<221> sig_peptide
<222> 39..89
<223> Von Heijne matrix
score 5.09999990463257
seq QLLVLFGSQTGTA/QD

<400> 381
```
agtttttagt ctcagaccag accaccgggc gcgccccg atg ccg agc ccg cag ctt      56
                                          Met Pro Ser Pro Gln Leu
                                                      -15
ctg gtg ctc ttc ggc agc cag aca ggc acg gct cag gat gtg tcg gag       104
Leu Val Leu Phe Gly Ser Gln Thr Gly Thr Ala Gln Asp Val Ser Glu
    -10                 -5                  1                5
aga ctg ggt cgc gag gcc cgg ggc cgg cgg ctt ggc tgc cgg gtg cag       152
Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg Leu Gly Cys Arg Val Gln
                10                  15                  20
gcc ctg gac tcc tac ccg gtg gtg aat ctg att aac gag ccc ctg gtg       200
Ala Leu Asp Ser Tyr Pro Val Val Asn Leu Ile Asn Glu Pro Leu Val
            25                  30                  35
ata ttt gtt tgt gca act ayw ggc caa gga gac ccc cct gac aac atg       248
Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly Asp Pro Pro Asp Asn Met
        40                  45                  50
aag aac ttc tgg agg ttt ata ttc cgg aag aac ctg ccc tcc acc gcc       296
Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys Asn Leu Pro Ser Thr Ala
    55                  60                  65
cgg g                                                                 300
Arg
70
```

<210> 382
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..151

<221> sig_peptide
<222> 8..130
<223> Von Heijne matrix
score 5.09999990463257
seq SFLFLACIFQGXS/XX

<400> 382
```
atacata atg tct tcc att ttg ggt gtc tca tcc tca tgg tgg tat tta        49
        Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu
            -40                 -35                 -30
tat tat ggc tat tgt ata ttt gtt aaa aag tgc tct ttt tgc agt ttc        97
Tyr Tyr Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe
        -25                 -20                 -15
ctg ttc ctt gcc tgt att ttt caa ggc tkt tck ckt kat wca aac aca       145
Leu Phe Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr
    -10                 -5                  1                   5
caa agc                                                               151
Gln Ser
```

<210> 383
<211> 255
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 101..253

<221> sig_peptide
<222> 101..184
<223> Von Heijne matrix
      score 5.09999990463257
      seq CLCGSAPCLLCRC/CP

<400> 383
gcgtccggaa gtgtctcgca gatagtaaat aatctcggaa aggcgagaaa gaagctgtct      60
ccatcttgtc tgtatccgct gcwcttgtga cgttgtggag atg ggg agc gtc ctg       115
                                            Met Gly Ser Val Leu
                                                        -25
ggg ctg tgc tcc atg gcg agc tgg ata cca tgt ttg tgt gga agt gcc       163
Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys Leu Cys Gly Ser Ala
            -20                 -15                 -10
ccg tgt ttg cta tgc cga tgc tgt cct agt gga aac aac tcc act gta       211
Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly Asn Asn Ser Thr Val
        -5                  1               5
act aga ttg atc tat gca ctt ttc ttg ctt gtt gga gta tgg gg            255
Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val Gly Val Trp
10                  15                  20

<210> 384
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 128..454

<221> sig_peptide
<222> 128..265
<223> Von Heijne matrix
      score 5.09999990463257
      seq IGSCSVMSSGALC/VP

<400> 384
tacaactttg aaaagccctt cctctggctt gctagacagc tcattggaga ccgtaacttg      60
gaatttgttg ccatgcctgc tcttgcctca ccagagattg tcatggaccc aaatttggca     120
gtgtagt atg agc wkr wtt agm agg ttg stt aga caa ctg ctc tcc cag       169
        Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln
            -45                 -40                 -35
rtg agg rwg atg acc tgt gag aat gaa gct gga gcc cag tgt car aag       217
Xaa Arg Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys
        -30                 -25                 -20
tct agt ttt ata ggc agc tgt tct gtg atg tca agt ggt gca ctg tgt       265
Ser Ser Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys
    -15                 -10                 -5
gtg cca ctt tat tat cta gct aag ggc aac atg tgc tcc atc tgt ggg       313
Val Pro Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly
1               5                   10                  15
atg ctg aag gag atg aat ggg ctt tgg agt gaa tgt gac agt tta aaa       361
Met Leu Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys
            20                  25                  30
aat acc ttc att gtt tgg rcc tgc ata ttt agc tgt ttg gga atg caa       409
Asn Thr Phe Ile Val Trp Xaa Cys Ile Phe Ser Cys Leu Gly Met Gln
        35                  40                  45
ttg awt tct tct kgr gtt tca aat gta aga ctg cta ctg tca cat ca        456
```

```
Leu Xaa Ser Ser Xaa Val Ser Asn Val Arg Leu Leu Leu Ser His
    50                  55                  60
```

<210> 385
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 1..192

<221> sig_peptide
<222> 1..78
<223> Von Heijne matrix
      score 5.09999990463257
      seq AFPFVCLTFCVGG/GP

<400> 385

```
atg cct cat cca ctg gct acc tct gcg ttt ctg cgt tcc gcc ttt cct       48
Met Pro His Pro Leu Ala Thr Ser Ala Phe Leu Arg Ser Ala Phe Pro
    -25                 -20                 -15
ttt gtt tgt ctc acg ttt tgc gtg gga ggc ggt ccc ggg att tca ggg       96
Phe Val Cys Leu Thr Phe Cys Val Gly Gly Gly Pro Gly Ile Ser Gly
-10                 -5                  1               5
gtc tac cgg ctc ctt atg gcg aat gca acc cga aga gag agt gag gta      144
Val Tyr Arg Leu Leu Met Ala Asn Ala Thr Arg Arg Glu Ser Glu Val
            10                  15                  20
agc ctc cgc ggg ttg ggc agg gac gga gag ggg gcc cgc gcg act cca g    193
Ser Leu Arg Gly Leu Gly Arg Asp Gly Glu Gly Ala Arg Ala Thr Pro
        25                  30                  35
```

<210> 386
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..279

<221> sig_peptide
<222> 199..267
<223> Von Heijne matrix
      score 5.09999990463257
      seq SLMVFLNLFFLNC/DP

<400> 386

```
tgtttatagg ttttaactct tatggttaga atggttgtga gtcatacgwg tgtcagacct     60
ctgctaattt cctcaggaca cattcccaga agtggaatta ccaagtcaaa gagcataaat    120
actttagaga tacatgataa attgtgccag ctacctttcc aaaagagttg tactagttga    180
ggtttctgcc agcagtat atg aca gtt ggg ctc cat att tta aga gat tca      231
                    Met Thr Val Gly Leu His Ile Leu Arg Asp Ser
                                -20                 -15
cta atg gtg ttt ctc aac ctt ttt ttt tta aac tgt gac cca cac agg      279
Leu Met Val Phe Leu Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg
        -10                 -5                  1
gg                                                                   281
```

<210> 387
<211> 111
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 5..109

<221> sig_peptide
<222> 5..67
<223> Von Heijne matrix
      score 5.09999990463257
      seq MFCVSLLLHHAYP/LP

<400> 387
cacc atg gta aga tgg gga cat ccc cct atg ttc tgt gtc tct ctc ctg      49
     Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu
         -20                 -15                 -10
ctc cac cat gct tat cct ttg cct tcc acc atg att gta agt ttc cca       97
Leu His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro
    -5                  1               5                   10
agg cct ccc ctg gg                                                   111
Arg Pro Pro Leu

<210> 388
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..374

<221> sig_peptide
<222> 96..173
<223> Von Heijne matrix
      score 5.09999990463257
      seq AMVCFGCPGGASS/RC

<221> misc_feature
<222> 344
<223> n=a, g, c or t


<400> 388
ttttggccgc catgttttcg tcgcagtaac tgccttggtg tcagtagtca ttgccagttt     60
cgggcgttct ggacaattgg gatgctgcag agttc atg gct ggg gct gct cgt       113
                                      Met Ala Gly Ala Ala Arg
                                          -25
tgg gtg gga caa kaa tcc tct gca atg gtt tgt ttt ggc tgc cca gga      161
Trp Val Gly Gln Xaa Ser Ser Ala Met Val Cys Phe Gly Cys Pro Gly
-20                 -15                 -10                 -5
ggt gcg tca agt cgc tgc cgc tcc cct cgt ggg cgt cag gcc tca aga      209
Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg Gly Arg Gln Ala Ser Arg
                1               5                   10
gtt ccc cgc cta gaa aat gga gct cag cga gtc gtg cgt acc atg gtg      257
Val Pro Arg Leu Glu Asn Gly Ala Gln Arg Val Val Arg Thr Met Val
        15                  20                  25
cac ctg gtt ttg cag cct aag cgg gtc act tta gtg cat cct cct cgc      305
His Leu Val Leu Gln Pro Lys Arg Val Thr Leu Val His Pro Pro Arg
    30                  35                  40
gga ttg gag cct gtt tgc acc cct ata gcm vga atg arn ccc aag tca      353
Gly Leu Glu Pro Val Cys Thr Pro Ile Ala Xaa Met Xaa Pro Lys Ser
45                  50                  55                  60
cac ggg ctc aga agt tct ttg                                          374
His Gly Leu Arg Ser Ser Leu
```

65

<210> 389
<211> 192
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..192

<221> sig_peptide
<222> 52..153
<223> Von Heijne matrix
score 5.09999990463257
seq PXLLSXLHGLLYG/SP

<400> 389
```
ggcagacttc aaccaggctg tgggaggaga gctcagtggg gcacagagaa g atg ggt      57
                                                         Met Gly
gtt gtc agt ggg ggt gtt ggt gac ttg acc aca aaa acc caa gag aat      105
Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln Glu Asn
        -30                 -25                 -20
ggg ctc tta cca gvc cty ctc tcc wkc ctk cac gga ctg ctc tat ggc      153
Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu Tyr Gly
    -15                 -10                 -5
agc cct gat gca gar ctc acg ggc ccg gat ccc tgg gat                  192
Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp
1               5                   10
```

<210> 390
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 321..371

<221> sig_peptide
<222> 321..365
<223> Von Heijne matrix
score 5.09999990463257
seq FLSXTCVLSCXRS/LS

<400> 390
```
tctgttcagg ttttgtattt gttcatagta taatcttggt ttgtaggttg tgtgtatctg      60
ggaagaaact ttacaatctc taacaggcct ggaaggtcta atctataaaa gtatttcatt     120
gaccttgaag aaggtcaatt atttatataa gaaaataaac tcaacatttt atccataaaa     180
aatgtaattc cggaatttat gttagtaaaa ttataacact gataacataa aaagtgctat     240
taatccttaa gaaagagtta ccttttcttt tctatcttca tcacagctag cccagtctta     300
gtctatttca ttagcttcct atg ggc ttc ctc tca ckt aca tgc gtg ctc tct     353
                      Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser
                      -15                 -10                 -5
tgc dtg cgc tcg ctc tct                                               371
Cys Xaa Arg Ser Leu Ser
            1
```

<210> 391
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 184..327

<221> sig_peptide
<222> 184..300
<223> Von Heijne matrix
      score 5
      seq LVCFFNSVSFLFG/VS

<400> 391
```
ccgttatgtg ttcagctcaa ttagattaat taccttcctc accaggagtc acaatgcttt      60
gcagtttatc tgcggtaact aaatgttagt tttgtaagta aaaggtactg ttattgacct     120
cgaaagggct atagttcctt tgaacttaca gagaagagtt ccaaacaact atttctaacc     180
aag atg gaa tat ggg tca gca aaa ttg tct tca ggt aga gtt ttc tac      228
    Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr
                    -35                 -30                 -25
ttg cca aga gac ttt ggc att gag agg aga gtt ctt gtt tgt ttt ttt      276
Leu Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe
                -20                 -15                 -10
aac tct gta tca ttt ctg ttt ggt gtc tct ara aaa aaa tcc gra caa      324
Asn Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln
            -5                   1                   5
tgg g                                                                328
Trp
```

<210> 392
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 252..302

<221> sig_peptide
<222> 252..290
<223> Von Heijne matrix
      score 5
      seq MLSGLVLNSWALA/YQ

<400> 392
```
tgaccttgta gcagttatct ttgttaaact ccttcatttc ttattttaaa taattaatta      60
attaatttag agacagggtc tcactatgtc acccaggctg tagtgcagtg gtgcaatcat     120
ggctcactgt agccttgacc tcccaggctc aagcaatctt cctacctcag cctctcaggc     180
agctgggact acagacccac agcactacgc ctgacttatg attttatttt ttgtggagac     240
agggtcttac t atg ttg tct ggg ctt gtc tta aac tct tgg gcc tta gcc     290
             Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala
                         -10                 -5
tac caa cta gct g                                                    303
Tyr Gln Leu Ala
1
```

<210> 393
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 298..366

<221> sig_peptide

```
<222> 298..345
<223> Von Heijne matrix
      score 5
      seq VFFXGXSIILVLG/ST

<221> misc_feature
<222> 265
<223> n=a, g, c or t


<400> 393
tttttccccg cccctgagac cctgcagcac catctgtcat ggcggctggg ctgtttggtt     60
tgagcgctcg ccgtcttttg gcggcagcgg cgacgcgagg gctcccggcc gcccgcgtcc    120
gctgggaatc tagcttctcc argamytgtg gtcgccccgt ccgctgtggc gggaaagcgg    180
tccccagaac cgaccacacc gtggcaagag gacccagaac ccgaggacga aaacttgtat    240
gagaagaasc cagactccca tggknatgac aaggaccccg ttttggacgt ctggaac       297
atg cga ctt gtc ttc ttc ktw ggc gks tcc atc atc ctg gtc ctt ggc      345
Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly
    -15                 -10                 -5
agc acc ttt gkg gcc tat ctg                                          366
Ser Thr Phe Xaa Ala Tyr Leu
1               5

<210> 394
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..125

<221> sig_peptide
<222> 21..68
<223> Von Heijne matrix
      score 5
      seq SDFFLLFVSLSLS/PF

<400> 394
agcttggcat ataggctcaa atg tta tca tca gat ttt ttt ctc ctc ttt gtc     53
                      Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val
                          -15                 -10
tct tta tct tta tct cca ttt cct ttt ttt ctt ttt cct ccc ctc ttt      101
Ser Leu Ser Leu Ser Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe
-5                  1               5                   10
tcc tgc ttt ctc tta ccc acc cgg g                                    126
Ser Cys Phe Leu Leu Pro Thr Arg
            15

<210> 395
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..327

<221> sig_peptide
<222> 154..195
<223> Von Heijne matrix
      score 5
      seq FIAALFTVAKIWN/QP
```

```
<400> 395
tgaaaatgta aattagtgca gttattatgg magtcagtat ggaacttcct caaaaaacta     60
acaataaaac tcccatatga tccagcaatc ctaccactgr atatttatcc aaaggaaagg    120
aagtcggtat atttaacagg catctgcacc ccc atg ttt att gca gca cta ttc     174
                                     Met Phe Ile Ala Ala Leu Phe
                                                         -10
aca gta gcc aag ata tgg aat caa cct aaa tgt cca tca acg gat gaa      222
Thr Val Ala Lys Ile Trp Asn Gln Pro Lys Cys Pro Ser Thr Asp Glu
        -5                  1               5
tgg ata aat aaa atg tgg tac ata tac aca atg gag tac tat cca gac      270
Trp Ile Asn Lys Met Trp Tyr Ile Tyr Thr Met Glu Tyr Tyr Pro Asp
10                  15                  20                  25
ata aaa aag aat gga att ctg aca ttt aag gca aca agg atg aac cgg      318
Ile Lys Lys Asn Gly Ile Leu Thr Phe Lys Ala Thr Arg Met Asn Arg
                30                  35                  40
aag aca tta tg                                                       329
Lys Thr Leu

<210> 396
<211> 99
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..97

<221> sig_peptide
<222> 5..49
<223> Von Heijne matrix
      score 5
      seq VCGCLCVWMCVCG/XV

<221> misc_feature
<222> 49
<223> n=a, g, c or t


<400> 396
gtat atg tgt gtg tgt ggg tgt tta tgt gtg tgg atg tgt gtg tgt ggn      49
     Met Cys Val Cys Gly Cys Leu Cys Val Trp Met Cys Val Cys Gly
     -15                 -10                 -5
wtt gtg tgt ata tac ata tgm gtg tat gtg tgt aca tgt gtg agg ggg       97
Xaa Val Cys Ile Tyr Ile Xaa Val Tyr Val Cys Thr Cys Val Arg Gly
1               5                   10                  15
ga                                                                    99

<210> 397
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..316

<221> sig_peptide
<222> 134..211
<223> Von Heijne matrix
      score 5
      seq LSLFVFFWLVGFS/FF
```

```
<221> misc_feature
<222> 284..285
<223> n=a, g, c or t


<400> 397
ttgtgaactc ttctattatt attaagtgtt gtcaattgtc agcatccata ttctattccg    60
atgatgaata gaagcattat atttcagcat caaaatgcag ttggggtcgt aatgagcatc   120
attagggacc tta atg gga gtc aga act gta tgt cat ttt att cag gtt      169
               Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val
                   -25                 -20                 -15
ttt cta agt tta ttt gtg ttt ttt tgg tta gtt ggt ttt tct ttt ttc     217
Phe Leu Ser Leu Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe
                -10                 -5                  1
ttt ttt tta cdb ttt tct acc aag cag gtg aga gtw gaa cag cat tgt     265
Phe Phe Leu Xaa Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys
        5                   10                  15
gat ttt aaa agt aca cca nnd gta gag tct tcc agt acc gtt ggc cat     313
Asp Phe Lys Ser Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His
    20                  25                  30
gcc                                                                 316
Ala
35

<210> 398
<211> 251
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..251

<221> sig_peptide
<222> 63..143
<223> Von Heijne matrix
      score 5
      seq LSCFYLLAIVSNA/VM

<400> 398
atgttgtagc ttctgtcata atttccttcc cttttaaggc tgaataattt tccattgtgt    60
at atg tac cat att ttg ttc atc cat tca ttc att gat aga tac ttg     107
   Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu
           -25                 -20                 -15
agt tgc ttc tac ctt ttg gca att gtg agt aat gct gtt atg aac atg     155
Ser Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met
        -10                 -5                  1
ggt gta caa atg tct gtt ttg agt cct tgt ttt gct ttc gtg cat tct     203
Gly Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser
5                   10                  15                  20
att aaa aat gtt aag gtt ctt tgc ttt tta ctt ttt ttt ctc ttt ggg     251
Ile Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly
                25                  30                  35

<210> 399
<211> 120
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..120
```

<221> sig_peptide
<222> 10..75
<223> Von Heijne matrix
score 5
seq VQWLLVYSPSCAA/TI

<400> 399
```
tcatttacc atg cag ttc acc gtt tta atg tgt cca gtt cag tgg ttg tta      51
          Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu
                  -20                 -15                 -10
gtg tat tca ccc agt tgt gca gcc acc atc aca gtc aat ttt aaa aca        99
Val Tyr Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr
            -5                  1               5
ttt tca tca ccc caa acc ggg                                            120
Phe Ser Ser Pro Gln Thr Gly
    10                  15
```

<210> 400
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 342..461

<221> sig_peptide
<222> 342..452
<223> Von Heijne matrix
score 5
seq VSCLSAGLRVCCS/QR

<221> misc_feature
<222> 246,260
<223> n=a, g, c or t

<400> 400
```
ctctgtcccc gcggctgggt ctcgtctgct ccggttcctg ggctcctaat tcttggtcca      60
gcttcttcca ggcacatcct cttctctgcc ctccgtccat tttggagccg gagatggtgg     120
gctkggggcc gccccagtag tgagacagtg gaagtaaacc ccatctgccg ttcccgtgcg     180
tagagaaaaa cgttgaccgc gaggctgggg aggagagttg cctctgagga agaagggcac     240
agaganccaa aattagtttn gaaagcatcc tgatttggtg cccgaggcct ggaaagaaat     300
ggcggctggg gtgcggcgga ggtaggggag gaaaacgttg g atg aga agg gcc tgg     356
                                              Met Arg Arg Ala Trp
                                                          -35
act cag gaa agg gaa ccg cgt ccg tgt gag ccc gct gag cgc gca gac       404
Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro Ala Glu Arg Ala Asp
        -30                 -25                 -20
cct gcc cct gtc tcc tgt ctg tct gca ggt ctg cgc gtc tgt tgt tcc       452
Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu Arg Val Cys Cys Ser
    -15                 -10                 -5
cag cgc tct gc                                                        463
Gln Arg Ser
1
```

<210> 401
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

```
<222> 94..204

<221> sig_peptide
<222> 94..168
<223> Von Heijne matrix
      score 4.90000009536743
      seq DFFICLLAICVSS/FE

<400> 401
tactgtttat tgattctttg attatggcca ttcttacagg agtaaggtgg tatcacactg    60
tggttttgat ttgcatttcc ctgatcatta gtg atg ttg cat ttg att tgc att    114
                                     Met Leu His Leu Ile Cys Ile
                                     -25                 -20
tcc ctg atc gtt aat gat ttt ttc ata tgt ttg ttg gcc att tgc gta    162
Ser Leu Ile Val Asn Asp Phe Phe Ile Cys Leu Leu Ala Ile Cys Val
            -15                 -10                 -5
tct tct ttt gag aat tgt cta ttt atg tcc tta gcc cac agt gg         206
Ser Ser Phe Glu Asn Cys Leu Phe Met Ser Leu Ala His Ser
        1               5                   10

<210> 402
<211> 330
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..329

<221> sig_peptide
<222> 42..230
<223> Von Heijne matrix
      score 4.90000009536743
      seq VTSLANLIPPVKA/XP

<400> 402
acagggctcc actgcagtta ggagccggtg agtccgggtg g atg agg tca gag cgc    56
                                              Met Arg Ser Glu Arg
                                                          -60
ccc atg gtg tgg tgc tgc ctc ttt gtc cgt tcg cag cga aaa cgg aaa    104
Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser Gln Arg Lys Arg Lys
            -55                 -50                 -45
cag agc acc caa gat gaa gat gct gtt agc ctt tgc agt ctc gac ata    152
Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu Cys Ser Leu Asp Ile
        -40                 -35                 -30
agt gag cct agt aat aaa cgg gtc aaa ccc ctt tcc cga gtc acg tcg    200
Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser
    -25                 -20                 -15
cta gca aac ctc atc ccg ccc gtg aag gcc ayg cca tta aag cgc ttc    248
Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa Pro Leu Lys Arg Phe
-10                 -5                  1               5
agt caa acc ctg cag cgc tcc att agc ttc cgc agt gag agt cgc cct    296
Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Arg Pro
            10                  15                  20
gac atc ctc gcc ccc cga ccc tgg tcc aga aat g                      330
Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn
        25                  30

<210> 403
<211> 311
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 168..311

<221> sig_peptide
<222> 168..227
<223> Von Heijne matrix
      score 4.90000009536743
      seq CILISTAFPSLLT/QI

<400> 403
tgagcagatg gtgccaggat ttaaacctat gtttatcaga tgcagatgac ccaaacagtg      60
gcttatctgt tggtaatttt tatttagatc aagttaaaca taaatgactt tgcattactc     120
tttggtcact ttttcctagt catttcaaat agtctgtctt atttctc atg gtt ttt       176
                                                    Met Val Phe
                                                    -20
tgg aca aaa ttt tgt att tta att agt aca gca ttt cct tct tta ttg       224
Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro Ser Leu Leu
        -15                 -10                 -5
aca cag att att ttc cct aaa tct att aca ttt gct ttc cag ttt ttc       272
Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe Gln Phe Phe
    1               5                   10                  15
tgg aac agg gaa aaa caa aaa aca aaa aca cca act ggg                   311
Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly
                20                  25

<210> 404
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..274

<221> sig_peptide
<222> 80..190
<223> Von Heijne matrix
      score 4.90000009536743
      seq MLIMLGIFFNVHS/AV

<400> 404
ccctgcgagg gcatcctggg ctttctccca ccgctttccg agcccgcttg cacctcggcg      60
atccccgact cccttcttt atg gcg tcg ctc ctg tgc tgt ggg ccg aag ctg      112
                     Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu
                                 -35                 -30
gcc gcc tgc ggc atc gtc ctc agc gcc tgg gga gtg atc atg ttg ata       160
Ala Ala Cys Gly Ile Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile
    -25                 -20                 -15
atg ctc gga ata ttt ttc aat gtc cat tcc gct gtg ttg att gag gac       208
Met Leu Gly Ile Phe Phe Asn Val His Ser Ala Val Leu Ile Glu Asp
-10                 -5                  1               5
gtt ccc ttc acg gag aaa gat ttt gag aat ggc ccc cag aac ata tac       256
Val Pro Phe Thr Glu Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr
            10                  15                  20
aac ctt tac gag cat ggg                                               274
Asn Leu Tyr Glu His Gly
        25

<210> 405
<211> 153
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 69..152

<221> sig_peptide
<222> 69..116
<223> Von Heijne matrix
      score 4.90000009536743
      seq SALLLEXLQXAIP/RX

<400> 405
tttcccctgc cctgtcctct cattcccctt cttctggagc atttcatcca cagacccctt      60
gcccaaga atg tct gtc tca gct ctg ctt cta gag mtc ctc caa gmt gcc      110
         Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala
                 -15                 -10                 -5
atc cct cgy mam acc tca ggc ttm caa gac ctg ccc aac tgg g             153
Ile Pro Arg Xaa Thr Ser Gly Xaa Gln Asp Leu Pro Asn Trp
        1               5                   10

<210> 406
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 57..206

<221> sig_peptide
<222> 57..173
<223> Von Heijne matrix
      score 4.90000009536743
      seq VIAIVSFTTLCSS/LY

<400> 406
aaataaaaaa tattaaaaaa taatctcatc tttgatttta gatttagggg gtgtgc atg      59
                                                              Met
cag gct tgt tat atg ggt atg tgg tat act gcc gag gct tgg ggt acg       107
Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly Thr
            -35                 -30                 -25
att gag tcc ctc acc cag gta gtg agc gta atc gca ata gtt agt ttt       155
Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser Phe
        -20                 -15                 -10
aca acc ctg tgc tcc tct ctg tat tcc ccc caa gta gtc ccc agt gtt       203
Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser Val
    -5                  1               5                   10
ggg                                                                   206
Gly

<210> 407
<211> 479
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 277..477

<221> sig_peptide
<222> 277..462
<223> Von Heijne matrix
      score 4.90000009536743
```

```
      seq PLAACPLLLPIFS/HA

<221> misc_feature
<222> 22
<223> n=a, g, c or t


<400> 407
aatggattga gatggggaag anaaaaagcc ccaaattcat gaaatgtagc tgckacagtc     60
cccacctcct tagctgtccc caaaacctaa gcaggtaatc ataacttcca ttctgtgctc    120
accttacctc tgctggcacc tttttggaca gggttctcta cttggcgagg tgacccaaat    180
cttcattcct gcagggtctg agtcctmrgc cgctgcgatc gtttgaacat tgtttgtccc    240
cacmraaact catcttgagg cttggtcccc actgta atg atg ttg aga ggt ggc      294
                                         Met Met Leu Arg Gly Gly
                                                 -60
ggg aca ttt aag grg tgt ttg agt cat gag gga tcc agc ttc acg aag      342
Gly Thr Phe Lys Xaa Cys Leu Ser His Glu Gly Ser Ser Phe Thr Lys
    -55                 -50                 -45
gga tta gcg cag gag tgc gtg agt rct tct tgt ggg act cga ttg att      390
Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser Cys Gly Thr Arg Leu Ile
-40                 -35                 -30                 -25
act gca gtw gcc agt kgt tac aaa gca agg ctg cct ctg gcc gcg tgc      438
Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg Leu Pro Leu Ala Ala Cys
                -20                 -15                 -10
ccd ctt ctg ctt cct att ttc tcc cat gct aga agc agc ac               479
Pro Leu Leu Leu Pro Ile Phe Ser His Ala Arg Ser Ser
            -5                  1               5

<210> 408
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..287

<221> sig_peptide
<222> 84..203
<223> Von Heijne matrix
      score 4.90000009536743
      seq SLKICGLVFGILA/LT

<400> 408
agccgactca cttgcaactc cacctcagca gtggtctctc agtcctctca aagcaaggaa     60
agagtactgt gtgctgagag acc atg gca aag aat cct cca gag aat tgt gaa    113
                          Met Ala Lys Asn Pro Pro Glu Asn Cys Glu
                          -40                 -35
gac tgt cac att cta aat gca gaa gct ttt aaa tcc aag aaa ata tgt      161
Asp Cys His Ile Leu Asn Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys
-30                 -25                 -20                 -15
aaa tca ctt aag att tgt gga ctg gtg ttt ggt atc ctg gcc cta act      209
Lys Ser Leu Lys Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr
                -10                 -5                  1
cta att gtc ctg ttt tgg ggg agc aag cac ttc tgg ccg gag gta ccc      257
Leu Ile Val Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro
        5                   10                  15
aaa aaa gcc tat gac atg gag cac act acg gg                           289
Lys Lys Ala Tyr Asp Met Glu His Thr Thr
    20                  25

<210> 409
<211> 341
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 94..339

<221> sig_peptide
<222> 94..216
<223> Von Heijne matrix
      score 4.90000009536743
      seq LSLVSHAPGEALA/RA

<400> 409
gtgttgcaga aatccggcaa tcgacctgag gacttgcgag ccgctcagct cccgggacgt     60
ttggagctgc tgctaaataa tttctgctca gcc atg tcg ccg gct cca gat gca     114
                                     Met Ser Pro Ala Pro Asp Ala
                                         -40                 -35
gcc ccg gct cct gcg tcg atc tcc ctg ttt gac ctc agc gcg gat gct     162
Ala Pro Ala Pro Ala Ser Ile Ser Leu Phe Asp Leu Ser Ala Asp Ala
                -30                 -25                 -20
ccg gtc ttt cag ggc ctg agc ctg gtg agc cac gcg cct ggg gag gct     210
Pro Val Phe Gln Gly Leu Ser Leu Val Ser His Ala Pro Gly Glu Ala
            -15                 -10                 -5
ctg gcc cgg gct ccg cgt act tcc tgt tca ggc tca ggg gag aga gaa     258
Leu Ala Arg Ala Pro Arg Thr Ser Cys Ser Gly Ser Gly Glu Arg Glu
        1               5                   10
agc cca gaa aga aag cta ctc cag ggt cct atg gat att tca gag aag     306
Ser Pro Glu Arg Lys Leu Leu Gln Gly Pro Met Asp Ile Ser Glu Lys
15                  20                  25                  30
tta ttt tgt tca act tgt gac cag acc ttc cag aa                      341
Leu Phe Cys Ser Thr Cys Asp Gln Thr Phe Gln
                35                  40

<210> 410
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..320

<221> sig_peptide
<222> 153..257
<223> Von Heijne matrix
      score 4.90000009536743
      seq LFIFIGSLQPVPT/RF

<400> 410
cacacacaaa ctctcaagtg gcctaattcc ctctcaccaa accaatcaca atacagataa     60
aagagaataa cttgtgttca tttttgtaca aacaaaaaag atataaattg tgaatgrtgc    120
atgrttttta awtwmccaag taaactgggc aa atg ctt ctg cat tat tta aag      173
                                    Met Leu Leu His Tyr Leu Lys
                                    -35                 -30
cta aaa ggt gat cag tgg aaa ctt tcc tct gtt agt act cta ata ctt     221
Leu Lys Gly Asp Gln Trp Lys Leu Ser Ser Val Ser Thr Leu Ile Leu
            -25                 -20                 -15
ttt ata ttt atc ggc tca cta caa cct gtg cct acc agg ttc aag cga     269
Phe Ile Phe Ile Gly Ser Leu Gln Pro Val Pro Thr Arg Phe Lys Arg
        -10                 -5                  1
ttc tcc tgt ctc gdc cac ctg agt agc cga gac cac agg caa gca cta     317
Phe Ser Cys Leu Xaa His Leu Ser Ser Arg Asp His Arg Gln Ala Leu
```

```
5                    10                   15                   20
cgg g                                                                  321
Arg

<210> 411
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..635

<221> sig_peptide
<222> 84..542
<223> Von Heijne matrix
      score 4.90000009536743
      seq MIVSLAAVAWVGQ/QV

<400> 411
gggttgtggt tggtgtgcgg gtttcggttg gaggactcgt tggggaggtg gcctgcgctt      60
gtagagactg catccccgag acg atg gcg gag gga gat aat cgc agc acc aac     113
                          Met Ala Glu Gly Asp Asn Arg Ser Thr Asn
                                          -150                -145
ctg ctg gct gca gag act gca agt ctg gaa gaa cag ctg caa gga tgg       161
Leu Leu Ala Ala Glu Thr Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp
            -140                -135                -130
gga gaa gtg atg ctg atg gct gat aaa gtc ctc cga tgg gaa aga gcc       209
Gly Glu Val Met Leu Met Ala Asp Lys Val Leu Arg Trp Glu Arg Ala
        -125                -120                -115
tgg ttt cca cct gcc atc atg ggt gtg gtt tct ttg gtg ttt ctg att       257
Trp Phe Pro Pro Ala Ile Met Gly Val Val Ser Leu Val Phe Leu Ile
    -110                -105                -100
atc tac tat cta gat cca tct gtt ctg tcc ggc gtt tcc tgt ttt gtt       305
Ile Tyr Tyr Leu Asp Pro Ser Val Leu Ser Gly Val Ser Cys Phe Val
-95                 -90                 -85                 -80
atg ttt ttg tgc ttg gct gac tac ctt gtt ccc att cta gcg cct aga       353
Met Phe Leu Cys Leu Ala Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg
                -75                 -70                 -65
att ttt ggc tcc aat aaa tgg acc act gaa caa cag caa aga ttc cat       401
Ile Phe Gly Ser Asn Lys Trp Thr Thr Glu Gln Gln Gln Arg Phe His
            -60                 -55                 -50
gaa att tgc agc aat cta gta aaa act cga cgc aga gct gtg ggt tgg       449
Glu Ile Cys Ser Asn Leu Val Lys Thr Arg Arg Arg Ala Val Gly Trp
        -45                 -40                 -35
tgg aaa cgc ctc ttc aca cta aag gaa gaa aaa cct aag atg tac ttc       497
Trp Lys Arg Leu Phe Thr Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe
    -30                 -25                 -20
atg acc atg atc gtt tcc ctt gct gcg gtt gct tgg gtg gga caa caa       545
Met Thr Met Ile Val Ser Leu Ala Ala Val Ala Trp Val Gly Gln Gln
-15                 -10                 -5                  1
gtc cac aac ctg ctt ctc acc tac ctg ata gtg act tcc tta cta ttg       593
Val His Asn Leu Leu Leu Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu
            5                   10                  15
ctt cct gga cta aac caa cat gga atc att ttg aag tac att               635
Leu Pro Gly Leu Asn Gln His Gly Ile Ile Leu Lys Tyr Ile
        20                  25                  30

<210> 412
<211> 335
<212> DNA
<213> Homo sapiens
```

<220>
<221> CDS
<222> 33..335

<221> sig_peptide
<222> 33..110
<223> Von Heijne matrix
score 4.90000009536743
seq LLRGLLAGPAATS/WS

<400> 412
```
aatggacgag aggtcagggt aggtttttga ag atg gcg gcc ctc aag gct ctg        53
                                    Met Ala Ala Leu Lys Ala Leu
                                            -25                 -20
gtg tcc ggc tgt ggg cgg ctt ctc cgt ggg cta cta gcg ggc ccg gca       101
Val Ser Gly Cys Gly Arg Leu Leu Arg Gly Leu Leu Ala Gly Pro Ala
                -15                 -10                 -5
gcg acc agc tgg tct cgg ctt cca gct cgc ggg ttc agg gaa gtg gtg       149
Ala Thr Ser Trp Ser Arg Leu Pro Ala Arg Gly Phe Arg Glu Val Val
            1               5                   10
gag acc caa gaa ggg aag aca act ata att gaa ggc cgt atc aca gcg       197
Glu Thr Gln Glu Gly Lys Thr Thr Ile Ile Glu Gly Arg Ile Thr Ala
    15                  20                  25
act ccc aag gag agt cca aat cct cct aac ccc tct ggc cag tgc ccc       245
Thr Pro Lys Glu Ser Pro Asn Pro Pro Asn Pro Ser Gly Gln Cys Pro
30                  35                  40                  45
atc tgc cgt tgg aac ctg aag cac aag tat aac tat gac gat gtt ctg       293
Ile Cys Arg Trp Asn Leu Lys His Lys Tyr Asn Tyr Asp Asp Val Leu
                50                  55                  60
ctg ctt agc cag ttc atc cgg cct cat gga ggc atg ctg ccc               335
Leu Leu Ser Gln Phe Ile Arg Pro His Gly Gly Met Leu Pro
            65                  70                  75
```

<210> 413
<211> 158
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..156

<221> sig_peptide
<222> 25..93
<223> Von Heijne matrix
score 4.90000009536743
seq LVGFKQVVAWTFA/SD

<221> misc_feature
<222> 17
<223> n=a, g, c or t

<400> 413
```
agaaactgac atttgbntgt ttta atg ggg tcc ctg ctg ttc atc agg cag          51
                          Met Gly Ser Leu Leu Phe Ile Arg Gln
                                          -20                 -15
aca ctt gtg ggc ttt aaa cag gtc gtt gct tgg acc ttt gct tct gat       99
Thr Leu Val Gly Phe Lys Gln Val Val Ala Trp Thr Phe Ala Ser Asp
                -10                 -5                  1
tca cat tgt gsa aaw gtg gww atg gtd wtc tws agt cag ttg arw aat      147
Ser His Cys Xaa Xaa Val Xaa Met Val Xaa Xaa Ser Gln Leu Xaa Asn
        5                   10                  15
```

```
ccc cca ctg gg                                                    158
Pro Pro Leu
    20

<210> 414
<211> 202
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..202

<221> sig_peptide
<222> 59..130
<223> Von Heijne matrix
      score 4.90000009536743
      seq LLLRGSLLASXRA/XX

<221> misc_feature
<222> 160
<223> n=a, g, c or t


<400> 414
ctgggagcga ccgctccgct cgtctcgttg gttccggagg tcgctgcggc ggtgggaa      58
atg ctg gcg cgc gcg gcg gag grc act ggg gcc ctt ttg ctg agg ggc     106
Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly
                -20                 -15                 -10
tct cta ctg gct tct grc cgc gck ycg sys vcg cct cct ctg gga ttg     154
Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu
            -5                  1               5
scc cgn aac acc gwt ggt act gtt cgt gcc gca gca gga ggc ctg ggt     202
Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly
    10                  15                  20

<210> 415
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..229

<221> sig_peptide
<222> 146..196
<223> Von Heijne matrix
      score 4.90000009536743
      seq LLSFCLCSDFISQ/DA

<400> 415
gtmaaactcc cgcagacttc tctgtagatc gctgagcgat actttcggca gcacctcctt      60
gattctcagt tttgctggag gccgcaacca ggccctactc aaccctcctt cccaggaggc     120
ccaggccccc aagctcagat caccc atg aat gcc tcc ctc ttg tct ttc tgc      172
                            Met Asn Ala Ser Leu Leu Ser Phe Cys
                                        -15                 -10
ctt tgt tca gat ttc atc tct caa gat gcc ctc ctt ctc act gtc ata     220
Leu Cys Ser Asp Phe Ile Ser Gln Asp Ala Leu Leu Leu Thr Val Ile
            -5                  1               5
ttt cct ccc                                                         229
Phe Pro Pro
    10
```

```
<210> 416
<211> 265
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..263

<221> sig_peptide
<222> 27..206
<223> Von Heijne matrix
      score 4.90000009536743
      seq LVGVIVHSGQAHA/GH

<400> 416
atgatgaaca aataaggttt ccctgg atg cta aac atg gag cct tac aca gtt      53
                             Met Leu Asn Met Glu Pro Tyr Thr Val
                             -60                 -55
tca gga atg gct cgc caa gat tct tct tct gaa gtt ggg gaa aat ggg      101
Ser Gly Met Ala Arg Gln Asp Ser Ser Ser Glu Val Gly Glu Asn Gly
    -50                 -45                 -40
cga agt gtg gat cag ggc ggt gga gga tcc cca cga aaa aag gtt gcc      149
Arg Ser Val Asp Gln Gly Gly Gly Gly Ser Pro Arg Lys Lys Val Ala
-35                 -30                 -25                 -20
ctc aca gaa aac tat gaa ctt gtc ggt gtc atc gta cac agt ggg cag      197
Leu Thr Glu Asn Tyr Glu Leu Val Gly Val Ile Val His Ser Gly Gln
                -15                 -10                 -5
gca cac gca ggc cac tac tat tcc ttc att aag gac agg cga ggg tgt      245
Ala His Ala Gly His Tyr Tyr Ser Phe Ile Lys Asp Arg Arg Gly Cys
            1               5                   10
gga aaa gga aag tgg ctg gg                                           265
Gly Lys Gly Lys Trp Leu
    15

<210> 417
<211> 228
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..228

<221> sig_peptide
<222> 160..219
<223> Von Heijne matrix
      score 4.90000009536743
      seq LHLXSSRXPPILA/SP

<221> misc_feature
<222> 166..167,190
<223> n=a, g, c or t


<400> 417
ttgtctgtct taggcctgga cactgttgtt gacttatttc cagattttaa tttctctttg     60
gttgaagact gccaactgtc tcatagagtg tttgatttat ttatttatty athtwgacat    120
gaggwykctc tctgcmaacc caggctggak tgcagtgac atg atv nng gct cac       174
                                           Met Xaa Xaa Ala His
                                           -20
ttc agc ctc cac ctc nkg agc tca agg art cck ccc atc tta gcc tcc      222
```

```
Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro Pro Ile Leu Ala Ser
-15                 -10                 -5                  1
cca gta                                                             228
Pro Val

<210> 418
<211> 225
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..223

<221> sig_peptide
<222> 125..175
<223> Von Heijne matrix
      score 4.90000009536743
      seq VCELSIFFTYVLA/IY

<400> 418
aaaagtttgt aataagttgc actttcatca agactgtatt agggagtcca gtctccccac    60
atccttgtca gcacgggatg acatcagtct tttaaatctt accaacttat tgggaaaaaa   120
aaaa atg ata cgt cct gtt tgt gaa ttg agc att ttt ttc acc tat gta    169
     Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val
             -15                 -10                 -5
cta gcc att tac ata tct cct tct gtg aat tgt ctg ttt ata tcc ttt     217
Leu Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe
        1               5                   10
cct gcg gg                                                          225
Pro Ala
15

<210> 419
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..293

<221> sig_peptide
<222> 42..128
<223> Von Heijne matrix
      score 4.80000019073486
      seq LLSARLLSQEKRA/AE

<400> 419
gtgctctatg gagctattgc ggccgtgggt ggtcgcgggc r atg cgg ggc tgc cag    56
                                              Met Arg Gly Cys Gln
                                                              -25
ctc ctc ggg ctt cgt agc tct tgg ccc ggg gac cta cta agt gct cgg     104
Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp Leu Leu Ser Ala Arg
                -20                 -15                 -10
ctc ttg tcc caa gag aag cgg gca gcg gaa acg cac ttt ggg ttt gag     152
Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr His Phe Gly Phe Glu
            -5                  1               5
act gtg tcg gaa gag gag aag agg ggg gac tta aca tca gtt gta agt     200
Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu Thr Ser Val Val Ser
    10                  15                  20
cta gag tac cct gaa gtg caa tta cag ggt caa agg gtc tat gcm ttc     248
Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln Arg Val Tyr Ala Phe
```

```
25                  30                  35                  40
ctg tca ccc att tgt acc tat ggc tct gag gga tgc agc ctc aag          293
Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly Cys Ser Leu Lys
                45                  50                  55

<210> 420
<211> 194
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..194

<221> sig_peptide
<222> 30..134
<223> Von Heijne matrix
      score 4.80000019073486
      seq PWVLDIFLTLVFA/LG

<400> 420
agttgctaga aagcaatgcg cctattcac atg gag aat ctt ccc ttt cct cta      53
                                Met Glu Asn Leu Pro Phe Pro Leu
                                -35                 -30
aaa tta ctt agt gcc tca tca cta aac acc ccc agc tcc aca cca tgg      101
Lys Leu Leu Ser Ala Ser Ser Leu Asn Thr Pro Ser Ser Thr Pro Trp
        -25                 -20                 -15
gtg ttg gat atc ttc ctc acc ttg gtg ttt gcc ctg ggg ttc ttc ttc      149
Val Leu Asp Ile Phe Leu Thr Leu Val Phe Ala Leu Gly Phe Phe Phe
    -10                 -5                  1                   5
cta tta ctc ccc tac ttc tct tac ctc cgt tgt gac aac cca cca          194
Leu Leu Leu Pro Tyr Phe Ser Tyr Leu Arg Cys Asp Asn Pro Pro
                10                  15                  20

<210> 421
<211> 90
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..88

<221> sig_peptide
<222> 29..67
<223> Von Heijne matrix
      score 4.80000019073486
      seq MCVCVFAIFGVRC/CV

<221> misc_feature
<222> 61
<223> n=a, g, c or t


<400> 421
tatttgggat ttgttgctct gtgtgtat atg tgc gtg tgt gtg ttt gct ata       52
                               Met Cys Val Cys Val Phe Ala Ile
                                              -10
ttt ggg gtn cgt tgc tgt gtg tgt gtc cgc tgt att tg                   90
Phe Gly Val Arg Cys Cys Val Cys Val Arg Cys Ile
-5                  1                   5

<210> 422
```

```
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..159

<221> sig_peptide
<222> 22..153
<223> Von Heijne matrix
      score 4.80000019073486
      seq XPCPLLFPGACFP/CP

<400> 422
tcatttgggt ttttatttaa t atg att tgc ata ttt tac tct aag att tcc        51
                        Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser
                                        -40                 -35
atc tct gtc ggc tgt ggg agg aca gca gcc gag caa gtt gga tgt aaa        99
Ile Ser Val Gly Cys Gly Arg Thr Ala Ala Glu Gln Val Gly Cys Lys
                -30                 -25                 -20
cag agg tca ttt cac ckc ccy tgc cct ctg ctg ttt cct ggt gcd tgc       147
Gln Arg Ser Phe His Xaa Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys
            -15                 -10                 -5
ttt ccc tgc cca ac                                                    161
Phe Pro Cys Pro
        1

<210> 423
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 333..419

<221> sig_peptide
<222> 333..380
<223> Von Heijne matrix
      score 4.80000019073486
      seq ICVSLMASDGASS/PV

<221> misc_feature
<222> 323..324,328
<223> n=a, g, c or t


<400> 423
ctgccgcygg acacgggttc ttccagcttt tggctattgt gaataacgct gctatggaca      60
tgaatgtaca aacatccctt cagatcctcc tttcagttct tgtgggtaca taccccgagt     120
ggaactgtgg catcatatgg taactctgtg tttaacattt tgaggaacca ccctactgct     180
tcccacagag gctgtaccag tttacttccc accaacagtg caaggattcc aatttctcca     240
catccgtgcc aacactattt tctttttgtc gctgttgtca ttgtttgtct ggaaaatagc     300
catgctgagg ggtgagaggt grnnghanrg tt atg aat ttg att tgc gtt tcc       353
                                    Met Asn Leu Ile Cys Val Ser
                                            -15                 -10
ctg atg gcc agt gat ggg gca tct tcc cct gtg ctt ggt ggc tct tca       401
Leu Met Ala Ser Asp Gly Ala Ser Ser Pro Val Leu Gly Gly Ser Ser
                -5                  1                   5
cac tct tcc tcc cwt rgg g                                             420
His Ser Ser Ser Xaa Xaa
        10
```

<210> 424
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 256..432

<221> sig_peptide
<222> 256..396
<223> Von Heijne matrix
      score 4.80000019073486
      seq LVSALPQASFSSS/SE

<400> 424
```
agtgaggagt carggaggtg tgtgtgagag agagagagaa aagagagaga cagagacggg     60
gagagagaga gggagagaga agagagggag gagggaagaa gaaaagacgg agggaggtga    120
ggaggaaggg agggggagag acagagacct agaggggctg aagacccaga cagagctggc    180
agagctactg agaagaggac tggagcgctc tgagagcctc tcaagatctt ttgggggagc    240
ccaataaatg tgaac atg gga tct gtc acr gga gct gtc ctc aag acg cta     291
                 Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu
                         -45                 -40
ctt ctg tta tct act caa aat tgg aac aga gtc gaa gct ggg aat tcc      339
Leu Leu Leu Ser Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser
-35                 -30                 -25                 -20
tat gac tgt gat gat cct ctt gtg tct gcc ttg cct cag gca tcc ttc      387
Tyr Asp Cys Asp Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe
                -15                 -10                  -5
agc agt tct tcc gag ctc tcc agc agt cat agt cct gga ttt gca          432
Ser Ser Ser Ser Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala
            1               5                   10
```

<210> 425
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 278..418

<221> sig_peptide
<222> 278..370
<223> Von Heijne matrix
      score 4.80000019073486
      seq FFLLFLFSSCDVP/VP

<400> 425
```
ccgaattatt ttagtgttac ttatctttga ataaaatgta tttttcttgg atcaattagt     60
tgcagcacgt tcttaggaat ggaatagaga agcatcctaa gccagaagga tttttttttt    120
tctagatcac agtgaagctt taatatggkk ggatatttgt cccagcccaa atcccatgct    180
gaattgaaac ccctagtgct ggaggtgggg cctggtggaa ggtgtttgga tcatgaggac    240
acatctctga tgaatggcct agctcatcct cttagtg atg atg agt gag tyc tca     295
                                         Met Met Ser Glu Xaa Ser
                                                 -30
caa gat ctg gtt gta aag tgt gcc cca cca csg cca ttc ttt ctc ttg      343
Gln Asp Leu Val Val Lys Cys Ala Pro Pro Xaa Pro Phe Phe Leu Leu
-25                 -20                 -15                 -10
ttc ctg ttt tct tca tgt gat gtg cct gtt ccc ctt cac ctt ctg caa      391
Phe Leu Phe Ser Ser Cys Asp Val Pro Val Pro Leu His Leu Leu Gln
                 -5                   1               5
```

```
tgg ctg caa agc ttc ctg agg cct agg g                                 419
Trp Leu Gln Ser Phe Leu Arg Pro Arg
        10                  15

<210> 426
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 54..230

<221> sig_peptide
<222> 54..134
<223> Von Heijne matrix
      score 4.80000019073486
      seq VLLTSGVKPQTFA/VS

<400> 426
gcagtgagtg ttacagttct taaagatggt gtgtccggag tttgttcctt cca atg        56
                                                           Met
ttc aga tgt gtc cgg ttt ctt cct tct ggc ggg ttc gtg gtc ttg ctg      104
Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu Leu
    -25                 -20                 -15
act tca gga gtg aag cca caa acc ttc gca gtg agt gtt aca gct ctt      152
Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala Leu
-10                 -5                  1               5
aaa ggt ggc atg ccc gga gtt gtt cat tcc tcc ggt ggg ttc gtg gtt      200
Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val Val
            10                  15                  20
ttg cta act tca gga gcg aas tgc aga cct tc                            232
Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro
        25                  30

<210> 427
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 226..381

<221> sig_peptide
<222> 226..315
<223> Von Heijne matrix
      score 4.80000019073486
      seq CLFLNARLAGTLC/QL

<400> 427
acagacatca gctcgggtca accgcgggcc tcgagcccga gtggctgagg gctgttacct     60
tcaaaccttt gaatcccacg ttttcccctt gacttcctgt caccgttaga gaaaagtgga    120
cagcgtctcg gtcacagagt tggagaaata gtgcagggac tcttcaggga gagcgttttc    180
ctcatcaaag caaactgcaa aatcgcttct gccggcgtgg acctg atg aga gtc ggt    237
                                                  Met Arg Val Gly
                                                  -30
cgt cgt gag gga cac cct ctg ttc cct aac gtc ccc cgc tgc tta ttt      285
Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro Arg Cys Leu Phe
    -25                 -20                 -15
tta aac gct cgg ttg gcg gga acc ctg tgc cag ctg aaa ctc ctt cag      333
Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu Lys Leu Leu Gln
-10                 -5                  1               5
```

ttt ggc cgc cta gga aac acc gag agt cac cta cat ggg ctg gct ggg 381
Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His Gly Leu Ala Gly
10 15 20
gg 383

<210> 428
<211> 132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..130

<221> sig_peptide
<222> 32..124
<223> Von Heijne matrix
score 4.80000019073486
seq LLCPLTCPHHSLS/TV

<400> 428
ttcaacaaat gagtcatagt gttttcgtat t atg tat ttt gat atc cag att 52
Met Tyr Phe Asp Ile Gln Ile
-30 -25
gtc tca gat gtg gtc agc ggg att ccc ttc aaa ctt ctg tgc cct tta 100
Val Ser Asp Val Val Ser Gly Ile Pro Phe Lys Leu Leu Cys Pro Leu
-20 -15 -10
aca tgt ccc cat cat tct ctg agc acc gtg gg 132
Thr Cys Pro His His Ser Leu Ser Thr Val
-5 1

<210> 429
<211> 165
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..165

<221> sig_peptide
<222> 25..117
<223> Von Heijne matrix
score 4.80000019073486
seq FSPFLPSLPLLEA/ER

<400> 429
caaactgttg aaaagttaac tctt atg tta ttt ata ttt tca gac ata gat 51
Met Leu Phe Ile Phe Ser Asp Ile Asp
-30 -25
tgg aag atg gac tta tgc ttt ttc tct ttc tct cct ttc ctt ccc tcc 99
Trp Lys Met Asp Leu Cys Phe Phe Ser Phe Ser Pro Phe Leu Pro Ser
-20 -15 -10
ctt cct ttg ttg gag gct gaa aga atg agg gtc agt gat caa ctt cag 147
Leu Pro Leu Leu Glu Ala Glu Arg Met Arg Val Ser Asp Gln Leu Gln
-5 1 5 10
tat acc act gga kac ggg 165
Tyr Thr Thr Gly Xaa Gly
15

<210> 430
<211> 236
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 52..234

<221> sig_peptide
<222> 52..159
<223> Von Heijne matrix
score 4.80000019073486
seq VLLAIGMFFTAWF/FV

<400> 430
gccgacgtgt tcttccggtg gcggasggcg gattagcctt cgcggggcaa a atg gag 57
Met Glu
-35
ctc gag gcc atg agc aga tat acc agc cca gtg aac cca gct gtc ttc 105
Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala Val Phe
-30 -25 -20
ccc cat ctg acc gtg gtg ctt ttg gcc att ggc atg ttc ttc acc gcc 153
Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe Thr Ala
-15 -10 -5
tgg ttc ttc gtt tac gag gtc acc tct acc aag tac act cgt gat atc 201
Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg Asp Ile
1 5 10
tat aaa gag ctc ctc atc tcc tta gtg gcc cga gg 236
Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
15 20 25

<210> 431
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 239..352

<221> sig_peptide
<222> 239..289
<223> Von Heijne matrix
score 4.80000019073486
seq LKLISTNFSLCQS/VQ

<221> misc_feature
<222> 345
<223> n=a, g, c or t

<400> 431
aggccttctg agtgcagctg gcaccatggg tgtgctccag agcaacttct gcttgctctg 60
agccccctgc cctgcctccc ctttcaccat gtttcctctg acaagatttt aagtacagca 120
attcaagaag atttctcctc ctaaacgaca tttatctgaa gtctattgcc tcttgattgc 180
tggaaaagad tcttaaaatc atttcaaaag taacttataa acaaacttat taaagtg 238
atg aaa gga gca ttg aaa tta att agc act aat ttt tca ctg tgc caa 286
Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
-15 -10 -5
agt gtg cag tgt cct tca gag gaa aca ata aca gat ctg gtg agt gtg 334
Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
1 5 10 15
cca tgc cag tng gga ctg gg 354
Pro Cys Gln Xaa Gly Leu
20

<210> 432
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..431

<221> sig_peptide
<222> 153..359
<223> Von Heijne matrix
score 4.80000019073486
seq MMVLSLGIILASA/SF

<400> 432

```
gtaaaaaaac actggaataa ggaagggctg atgactttca gaagatgaag gtaagtagaa     60
accgttgatg ggactgagaa accagagtta aaacctcttt ggagcttctg aggactcagc    120
tggaaccaac gggcacagtt ggcaacacca tc atg aca tca caa cct gtt ccc      173
                                    Met Thr Ser Gln Pro Val Pro
                                                    -65
aat gag acc atc ata gtg ctc cca tca aat gtc atc aac ttc tcc caa      221
Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln
        -60                 -55                 -50
gca gag aaa ccc gaa ccc acc aac cag ggg cag gat agc ctg aag aaa      269
Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys
    -45                 -40                 -35
cat cta cac gca gaa atc aaa gtt att ggg act atc cag atc ttg tgt      317
His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys
-30                 -25                 -20                 -15
ggc atg atg gta ttg agc ttg ggg atc att ttg gca tct gct tcc ttc      365
Gly Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe
                -10                 -5                  1
tct cca aat ttt acc caa gtg act tct aca ctg ttg aac tct gct tac      413
Ser Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr
        5                   10                  15
cca ttc ata gga ccc ggg                                              431
Pro Phe Ile Gly Pro Gly
    20
```

<210> 433
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..201

<221> sig_peptide
<222> 37..156
<223> Von Heijne matrix
score 4.80000019073486
seq IVSAACKCGSSQA/AI

<400> 433

```
aatatttatg aagcagtttg gaaccaaagg ggtagt atg gta gac gag tgt ctt       54
                                        Met Val Asp Glu Cys Leu
                                        -40                 -35
aca gag cct gtg tgg gga agc aaa agg caa ggg tgt agt tca cag gca      102
Thr Glu Pro Val Trp Gly Ser Lys Arg Gln Gly Cys Ser Ser Gln Ala
                -30                 -25                 -20
```

```
gaa gcg agc tgt gac att gtc agt gca gcg tgt aag tgt ggc tcc tca      150
Glu Ala Ser Cys Asp Ile Val Ser Ala Ala Cys Lys Cys Gly Ser Ser
            -15                 -10                 -5
cag gcg gcc att gat tgt gag acc tca tct tgc tct gaa gat ttc ccg      198
Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser Cys Ser Glu Asp Phe Pro
        1               5                   10
gtg                                                                  201
Val
15
```

<210> 434
<211> 334
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 242..334

<221> sig_peptide
<222> 242..283
<223> Von Heijne matrix
score 4.80000019073486
seq AWWFSGTFPLTHP/CS

<400> 434

```
aagctgtact ctttcagcac atttcctttc atctccccct tcttccctct tctgtgctct     60
caagactttc cccctcttgc tgccacagat gcagtgaagc ctgccatata taaggtacaa    120
tgtgtggcaa ctctgcaggt ggggtctatg caagctacag acccctctga gtgtggtcag    180
tgccttagcc tggcctggat gcctaccagg ccccaccaac acctagctgc tggatattat    240
a atg gca tgg tgg ttt tct gga acc ttc cca cta act cac ccc tgc agc    289
  Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
              -10                 -5                  1
gga tac ggc tct ctg atg gct cct tct agc cct acc cct tct ggg          334
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
        5                   10                  15
```

<210> 435
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..385

<221> sig_peptide
<222> 152..322
<223> Von Heijne matrix
score 4.80000019073486
seq VTSLANLIPPVKA/TP

<400> 435

```
agtcgagtcc tgcccggcta gaagccggct gtcggtctcc gtgtcgccgc cgccgcccgg     60
catcgtggag ctggggcccc cttttgcctg ggagttttgt agtcgcctag ggtcagcggt    120
gacatcccaa agggcaggcc cggcagccgc c atg gtg gcc aag gat tac ccc       172
                                   Met Val Ala Lys Asp Tyr Pro
                                               -55
ttc tac ctc acg gtc aag aga gcg aac tgc agc ctg gag cta cct ccg      220
Phe Tyr Leu Thr Val Lys Arg Ala Asn Cys Ser Leu Glu Leu Pro Pro
-50                 -45                 -40                 -35
gcc agc ggt ccg gcc aag gac gct gag gag cct agt aat aaa cgg gtc      268
Ala Ser Gly Pro Ala Lys Asp Ala Glu Glu Pro Ser Asn Lys Arg Val
```

```
                    -30                    -25                   -20
aaa ccc ctt tcc cga gtc acg tcg cta gca aac ctc atc ccg ccc gtg      316
Lys Pro Leu Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val
                -15                    -10                   -5
aag gcc acg cca tta aag cgc ttc agt caa acc ctg cag cgc tcc att      364
Lys Ala Thr Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile
        1                   5                   10
agc ttc cgc agt gag agc gcc t                                        386
Ser Phe Arg Ser Glu Ser Ala
15                  20
```

<210> 436
<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 191..472

<221> sig_peptide
<222> 191..274
<223> Von Heijne matrix
score 4.80000019073486
seq GVLLEPFVHQVGG/HS

<400> 436

```
tttttttggt gcgagagaaa caataggacg gaaacgccga ggaacccggc tgaggcggca     60
gcgagcatcc tggccagaac aagccaagga gccaagacga gagggacaca cggacaaaca    120
acagacagaa gacgtactgg ccgctggact ccgctgcctc cccatctcc ccgccatctg    180
cgcccggagg atg agc cca gcc ttc agg gcc atg gat gtg gag ccc cgc      229
           Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg
                           -25                   -20
gcc aaa ggc gtc ctt ctg gag ccc ttt gtc cac cag gtc ggg ggg cac      277
Ala Lys Gly Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His
-15                 -10                   -5                   1
tca tgc gtg ctc cgc ttc aat gag aca acc ctg tgc aag ccc ctg gtc      325
Ser Cys Val Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val
                5                   10                  15
cca agg gaa cat cag ttc tac gag acc ctc cct gct gag atg cgc aaa      373
Pro Arg Glu His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys
        20                  25                  30
ttc act ccc cag tac aaa gga caa agc caa agg ccc ctt gtt agc tgg      421
Phe Thr Pro Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp
    35                  40                  45
cca tcc ctg ccc cat ttt ttc ccc tgg tcc ttt ccc ctg tgg cca cag      469
Pro Ser Leu Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln
50                  55                  60                  65
gga                                                                  472
Gly
```

<210> 437
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 213..467

<221> sig_peptide
<222> 213..314
<223> Von Heijne matrix

```
      score 4.80000019073486
      seq ILAFLQSPRAILP/GN

<221> misc_feature
<222> 432..433
<223> n=a, g, c or t


<400> 437
ggattcccgc cccgaggttt ctaaatccag acattcccgt ttggctgagc actctaggcc    60
tacatccatg aagctaggag agcgacactc aaagactgca ctattgagag aagctaacgt   120
taaaggcagt gaatatattc gggagtccag ctccggaacc cgggagctct tttagtggga   180
ggggcggcgc tgatggcgct tctggcctcc ga atg cta ggg ggc gct gtg atc     233
                                    Met Leu Gly Gly Ala Val Ile
                                                    -30
gcc ggg cgg cct ctt ggg cgc tgg gag tcc acc gcg caa ssc atc ctg     281
Ala Gly Arg Pro Leu Gly Arg Trp Glu Ser Thr Ala Gln Xaa Ile Leu
        -25                 -20                 -15
gcc ttt ctt cag tcc cca cgt gcg atc ctt ccc ggc aac ttt ttc gag     329
Ala Phe Leu Gln Ser Pro Arg Ala Ile Leu Pro Gly Asn Phe Phe Glu
    -10                 -5                  1               5
aaa aat gcc caa att caa ggc ggc ccg tgg ggt ggg ggg tca gga aaa     377
Lys Asn Ala Gln Ile Gln Gly Gly Pro Trp Gly Gly Gly Ser Gly Lys
                10                  15                  20
aca tgc gcc cct ggc cga tsa gat cct ggc tgg gaa tgc ggt gcg ggc     425
Thr Cys Ala Pro Gly Arg Xaa Asp Pro Gly Trp Glu Cys Gly Ala Gly
            25                  30                  35
ggg ggt nng gga gaa gcg gcg ggg tcg cgg gam agg ara agc gg          469
Gly Gly Xaa Gly Glu Ala Ala Gly Ser Arg Xaa Arg Xaa Ser
        40                  45                  50

<210> 438
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..169

<221> sig_peptide
<222> 77..124
<223> Von Heijne matrix
      score 4.80000019073486
      seq ACFFHLFVSSLIS/FE

<400> 438
ttgataggaa tagcattgaa tctgtaaatt gctttgggca ctatggccat tttaataata    60
ttgattcttc ctatcc atg agc atg gca tgt ttt ttc cat ttg ttt gtg tca   112
                  Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser
                      -15                 -10                 -5
tct ctg att tcc ttt gag cag tgt ttt gka atg cta aga aaa ttg ctt     160
Ser Leu Ile Ser Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu
                1                   5                   10
aaa att ata                                                         169
Lys Ile Ile
        15

<210> 439
<211> 447
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 211..447

<221> sig_peptide
<222> 211..345
<223> Von Heijne matrix
      score 4.69999980926514
      seq PWLEVGLFFWLHA/AP

<400> 439
agaacaatgc tgcttggctc cctgaattca gcacccttcc tagggaatgt atgggtggat      60
cttttgcctt gcaggattct tttcatcttt tgcagggact tctggggccg gagtatgtaa     120
aactcctggg tctctgtgtg tgcctgagtg gctgctctac tgagactctg catacacagc     180
tctgtatatc ggacccawgg ccctggtggc atg ggc tca cga gga gat ccc ctg      234
                                 Met Gly Ser Arg Gly Asp Pro Leu
                                 -45                 -40
atc tgt ggg ttg caa aga tct gtg gga gaa gtg tgg ttt cct gga tgg       282
Ile Cys Gly Leu Gln Arg Ser Val Gly Glu Val Trp Phe Pro Gly Trp
        -35                 -30                 -25
ggt cac aca atc act cac tgc ttc cct tgg ctg gag gtg ggg ctt ttt       330
Gly His Thr Ile Thr His Cys Phe Pro Trp Leu Glu Val Gly Leu Phe
    -20                 -15                 -10
ttt tgg ctc cat gct gct cct ggg cgg gcg att gcc cta ccc cat ttt       378
Phe Trp Leu His Ala Ala Pro Gly Arg Ala Ile Ala Leu Pro His Phe
-5                  1               5                   10
tct tca ttc tct gtg ggt caa gdb gtt cac ttg gtc agt cca ttg tgr       426
Ser Ser Phe Ser Val Gly Gln Xaa Val His Leu Val Ser Pro Leu Xaa
            15                  20                  25
gam ctg gat att tca gtt gaa                                           447
Xaa Leu Asp Ile Ser Val Glu
        30

<210> 440
<211> 340
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 176..340

<221> sig_peptide
<222> 176..232
<223> Von Heijne matrix
      score 4.69999980926514
      seq ELLLLLPRGLCQV/CP

<221> misc_feature
<222> 20,279..281
<223> n=a, g, c or t


<400> 440
agaaaagcag ccgcagttgn gccgctccac cacgccgtcc gggtgggcct agcagtcgct      60
ccatttatcg cttgagatct ccagccttac cgcggctcga aatggacccc aactgctcct     120
gcaccactgg tgtctccwrc gcctgcaccg gctcctgcac gtgcaaagag tgcaa atg      178
                                                             Met
cac ctc ctg caa gaa gag ctg ctg ctc ctg ctg ccc cgt ggg ctg tgc       226
His Leu Leu Gln Glu Glu Leu Leu Leu Leu Leu Pro Arg Gly Leu Cys
            -15                 -10                 -5
caa gtg tgc cca cgg ctg tgt ctg caa agg gmc gtt gga gaa ctg cag       274
Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu Gln
```

```
                  1               5                   10
mtg cnn nky cct gat gtg gga aca gct ctt ctc cca gat gtt aat aga      322
Xaa Xaa Xaa Pro Asp Val Gly Thr Ala Leu Leu Pro Asp Val Asn Arg
15                  20                  25                  30
aca agc tgc aca acc tgg                                              340
Thr Ser Cys Thr Thr Trp
                35
```

<210> 441
<211> 409
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 292..408

<221> sig_peptide
<222> 292..375
<223> Von Heijne matrix
score 4.69999980926514
seq QLVTRLLLSPSQS/TQ

<400> 441

```
agaagatggg gaaagaggaa ggaaaggatg cccagataca gggagcttta gcgatgtagt     60
gaacggacag aagatcagga acaagttgag ttcattgtgt ggagatggca rraagatgga    120
gattggtgag ctgagtggag aagtgccata gagcggtgtt ttgccagagt gtctgcggat    180
tgctcatacc tgggaaggat tctttgtatg gttcccttag gctgagggag ggtatcagct    240
ttacagacct tgtgggatta caaaagggcc accacacact cttcaaccaa t atg tgt     297
                                                         Met Cys
cta tct tgc att caa ggc tca ttc ttt gtt gaa att ttg cag ttg gtc      345
Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln Leu Val
    -25                 -20                 -15
act agg cta ttg tta tct cca tct caa agt aca cag aca cac aca cac      393
Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His Thr His
-10                 -5                  1                   5
aca cac aca cac aca a                                                409
Thr His Thr His Thr
            10
```

<210> 442
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 203..319

<221> sig_peptide
<222> 203..298
<223> Von Heijne matrix
score 4.69999980926514
seq AILLLVXVSDKNE/QQ

<221> misc_feature
<222> 225..227,279
<223> n=a, g, c or t

<400> 442

```
cacactagaa tagactggaa caacttggat ttagtgattc cgatgcttat caggaaggtc     60
tctgttcttt tataggaaga aaaaacatag ttatttttct tttatgatac aaaggtatgc    120
```

```
tttctatgca agctggatac cagaccaaga ataataaatc acaatttcat aaggtttcta     180
agacttgata ttatatgggg at atg acc att ttg agg gaa atg tnn nca tca     232
                         Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser
                                 -30                 -25
ctt tat gta ctt gaa gct aag gat act gct atc tta ttg ctt gtt tna       280
Leu Tyr Val Leu Glu Ala Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa
        -20                 -15                 -10
gtg agc gat aag aat gaa cag cag ctt ggg agg ggc gtg g                 320
Val Ser Asp Lys Asn Glu Gln Gln Leu Gly Arg Gly Val
    -5                  1                   5
```

<210> 443
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 102..254

<221> sig_peptide
<222> 102..188
<223> Von Heijne matrix
      score 4.69999980926514
      seq ICCNLYFLLFCRS/SF

<400> 443

```
cttctttgta actcctgcat ataccttttgc atttatgtag cttctggagg gcacatggag     60
gtagctcacc atggttttaa tttgcatttc tctgataatg a atg aga ctt agt tct    116
                                              Met Arg Leu Ser Ser
                                                              -25
tcc tgt ggg ttg cct gtt aag act ttg cca ttt atc tgt tgc aat ctt      164
Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe Ile Cys Cys Asn Leu
                -20                 -15                 -10
tat ttc ttg ctg ttt tgt agg agt tct ttt tta tat ttt gga tat gat      212
Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu Tyr Phe Gly Tyr Asp
            -5                  1                   5
ccc att aat act tac atg tat tac aat gtt ttc tcc cac tcg gg            256
Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe Ser His Ser
    10                  15                  20
```

<210> 444
<211> 284
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 17..283

<221> sig_peptide
<222> 17..220
<223> Von Heijne matrix
      score 4.69999980926514
      seq GCLLXPLLVSCLG/SL

<400> 444

```
tagatggcga ctcccct atg tta ctg acg aga ccg gcg gtg agt gcg gga ggc     52
                   Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly
                               -65                 -60
gcg gas cgc ttc tct ccg ggc tct cgg ggc agg ggt tcg gac ttg gaa      100
Ala Xaa Arg Phe Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu
    -55                 -50                 -45
```

```
agg ggt ctg tgc ccc gcc cat ccc ggg gcc cct cct ttg ccc cgc ccc      148
Arg Gly Leu Cys Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro
-40                 -35                 -30                 -25
ccg gac cgc ctt ccc cat tca ttc tct cct acg ggg tgt ctc ctg hgc      196
Pro Asp Arg Leu Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa
                -20                 -15                 -10
ccc ctt ctg gtc tcg tgt ttg ggg tct ctg ctt ccg gtc acc caa acc      244
Pro Leu Leu Val Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr
            -5                  1               5
ctg ggg tcc ttc agt gct ggt ccc tgc ttc agg acc ctc a                284
Leu Gly Ser Phe Ser Ala Gly Pro Cys Phe Arg Thr Leu
    10                  15                  20
```

<210> 445
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..240

<221> sig_peptide
<222> 103..177
<223> Von Heijne matrix
score 4.69999980926514
seq ILXSLSSSVPSRA/GS

<400> 445

```
tcttttgtaa tgaagcatgg cagccaggcc tagcacactt ccctctgcac accatcctgc      60
tcaggcctct gtgcctcggc tgtgctgttc cttctgcttg ga atg cat tca ctg        114
                                               Met His Ser Leu
                                               -25
tgt cca ctt agc caa ttc cta cct att ctt tma agc ctc agt tcc agt      162
Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser Leu Ser Ser Ser
    -20                 -15                 -10
gtc ccc tcg agg gca ggc agt gct ttc cca tct gcc cta ggt cca ctc      210
Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala Leu Gly Pro Leu
-5                  1               5                   10
tac cag cct cta ctt ggg ccc cca gca tgg                              240
Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp
            15                  20
```

<210> 446
<211> 184
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..184

<221> sig_peptide
<222> 8..139
<223> Von Heijne matrix
score 4.69999980926514
seq LVFLSVXLLFLLF/LV

<400> 446

```
tcctttt atg cga aca caa gta tat gag ggg ttg tgt aaa aat tat ttt       49
        Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe
                    -40                 -35
tct ctt gct gta cta caa aga gat aga atc aaa ctg ctt ttt ttc gac       97
```

```
Ser Leu Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp
-30                 -25                 -20                 -15
ata ctg gtt ttt ctt tct gtt tww ctt ctc ttt ctt cta ttt ctt gtg      145
Ile Leu Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val
                -10                 -5                  1
gat atw atg gct aat adc aca aca agt tta ggg agg ccc                  184
Asp Ile Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
        5                   10                  15
```

<210> 447
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 34..360

<221> sig_peptide
<222> 34..168
<223> Von Heijne matrix
score 4.69999980926514
seq LLSLAQTTTKTTA/TT

<221> misc_feature
<222> 280
<223> n=a, g, c or t

<400> 447

```
aaaaactctt ttctttatcc tctttccaga aaa atg ggc caa ttc aca gct gca      54
                                     Met Gly Gln Phe Thr Ala Ala
                                     -45                 -40
atg gtt ggg aga att tcc tgt ctg gga gtc tgg aaa ctg cca aga gtg      102
Met Val Gly Arg Ile Ser Cys Leu Gly Val Trp Lys Leu Pro Arg Val
            -35                 -30                 -25
gaa agc tgc agc cag cca gcg agg cct ctg ttg tca ctg gcc caa aca      150
Glu Ser Cys Ser Gln Pro Ala Arg Pro Leu Leu Ser Leu Ala Gln Thr
        -20                 -15                 -10
aca aca aaa aca acc gca aca aca aca aca aca aca aaa cat gcc acg      198
Thr Thr Lys Thr Thr Ala Thr Thr Thr Thr Thr Thr Lys His Ala Thr
    -5                  1                   5                   10
tgt gca ctg gca tat aca aac acg ccc aca gaa cca vrc caa gcg gac      246
Cys Ala Leu Ala Tyr Thr Asn Thr Pro Thr Glu Pro Xaa Gln Ala Asp
                15                  20                  25
aag gct tca agg aga gct tct ggg ahv ctc rwv ncc gcg gcg agg cat      294
Lys Ala Ser Arg Arg Ala Ser Gly Xaa Leu Xaa Xaa Ala Ala Arg His
            30                  35                  40
atc cct tgg cat ggt gcc act gca gcc cag ctc cca gcc ccc ccg cca      342
Ile Pro Trp His Gly Ala Thr Ala Ala Gln Leu Pro Ala Pro Pro Pro
        45                  50                  55
tct gtc atc agc gct ctg                                              360
Ser Val Ile Ser Ala Leu
    60
```

<210> 448
<211> 123
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..122

<221> sig_peptide
<222> 39..92
<223> Von Heijne matrix
score 4.69999980926514
seq IAILFPNSGSCFA/FS

<400> 448
```
cttatctgat tcacagcccg tattcagatt tgccaatt atg ttg att ttc att att      56
                                          Met Leu Ile Phe Ile Ile
                                                          -15
gct att tta ttt ccc aat tca gga tca tgc ttt gca ttt agt tgt cat      104
Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys Phe Ala Phe Ser Cys His
        -10                 -5                   1
gtc tcc ttt ttt ttt ttt t                                            123
Val Ser Phe Phe Phe Phe
5                   10
```

<210> 449
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..191

<221> sig_peptide
<222> 18..62
<223> Von Heijne matrix
score 4.69999980926514
seq RCACFPFFPFAFC/HD

<400> 449
```
ctctctcctg ttcggtc atg gtg aga tgt gct tgc ttc ccc ttc ttc ccc        50
                   Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro
                   -15                 -10                 -5
ttc gcc ttc tgc cat gac tgt aag ttt ctt ggg gcc tcc cag tca tgc      98
Phe Ala Phe Cys His Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys
                1                   5                   10
ttc ttg tta agc cgg caa aac tgt gta agc aca gga kga cct tca tcc      146
Phe Leu Leu Ser Arg Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser
        15                  20                  25
aaa tct gat atc aac tca agg tct gga tct tgt tca ctg gca agg gg       193
Lys Ser Asp Ile Asn Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg
    30                  35                  40
```

<210> 450
<211> 302
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..301

<221> sig_peptide
<222> 8..88
<223> Von Heijne matrix
score 4.69999980926514
seq LAPLXLVFISLLP/AP

<221> misc_feature

```
<222> 292
<223> n=a, g, c or t


<400> 450
ccagcaa atg gtg agt ttg agg gta ggg gcc tct cca ttt cgg ttc cca        49
        Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro
                -25                 -20                 -15
ctg gcc ccc ctc tbt ttg gtt ttc atc tct ctt ctc cca gcc cca ttt        97
Leu Ala Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe
            -10                 -5                  1
ttt cct act ctt tcg ttt cct tgt tgc tgt gtg tcc tgg ctc ttt tct       145
Phe Pro Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser
    5                   10                  15
ctt tct gtg vtt gtc tct ctg cgt ctc agt ctt tbt gtg tcc tgt tta       193
Leu Ser Val Xaa Val Ser Leu Arg Leu Ser Leu Xaa Val Ser Cys Leu
20                  25                  30                  35
tct ctc tgg tgt ctc ttg gta ttg ttt ctc tct ccc act ctg tat gtc       241
Ser Leu Trp Cys Leu Leu Val Leu Phe Leu Ser Pro Thr Leu Tyr Val
                40                  45                  50
tct gac tca ttc tgc tca ttc tgt gtc ctc cct att gct ctc tgt ccc       289
Ser Asp Ser Phe Cys Ser Phe Cys Val Leu Pro Ile Ala Leu Cys Pro
            55                  60                  65
can gct cgt tct t                                                     302
Xaa Ala Arg Ser
        70

<210> 451
<211> 367
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 150..365

<221> sig_peptide
<222> 150..311
<223> Von Heijne matrix
      score 4.69999980926514
      seq PGLAFLAILTVLA/KP

<400> 451
aaaatgatcc atgcacacag cctctatagg aaagaaaaaa aatatccaat tgattttctt      60
ccctttctg cttctaaagt ataccaaatt tcactgtgat cttaatattc cccagaacag      120
acacctctga gcagagagca ggccttaga atg gcc cac ccc tgt tta gct cca      173
                                Met Ala His Pro Cys Leu Ala Pro
                                                -50
gca gaa cct tct act ctt tca caa acc kcc cat cca att caa aga acc      221
Ala Glu Pro Ser Thr Leu Ser Gln Thr Xaa His Pro Ile Gln Arg Thr
    -45                 -40                 -35
ctg aca act ttc cct cag gct tgg gtt cta acc agc agc ttt tcc ata      269
Leu Thr Thr Phe Pro Gln Ala Trp Val Leu Thr Ser Ser Phe Ser Ile
-30                 -25                 -20                 -15
cag cca ggc ctt gca ttc cta gcc att ctc acc gtg tta gcc aaa ccc      317
Gln Pro Gly Leu Ala Phe Leu Ala Ile Leu Thr Val Leu Ala Lys Pro
            -10                 -5                  1
ggs tcc tct amc tgg agt cct ggt cag ttc aca cca cac tcc ctg ctg      365
Gly Ser Ser Xaa Trp Ser Pro Gly Gln Phe Thr Pro His Ser Leu Leu
        5                   10                  15
gg                                                                    367

<210> 452
```

```
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 244..348

<221> sig_peptide
<222> 244..336
<223> Von Heijne matrix
      score 4.69999980926514
      seq HLYXSLFSSFLCS/TP

<400> 452
ttctttcark tcttactact catccttcat ttatctcctg gatcattgcc cagagaatga      60
aagaaattgc cagtcaagcc agccaggtag gttaaatcta tcctggcagt cctggagact     120
gctgcagact gactgcctga tgtccgtgcc cactggggtt tttccctttt cagaaaggat     180
ttctccctga tctctcccca caaactctgg ctttgctttt tcatttccta agagcaactc     240
aat atg cat ttc ccc atc caa gct acc ttc sac tat tcc cct act gat       288
    Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp
        -30                 -25                 -20
tct ctc tgt cat tta tat ttk tca ctc ttc tct tcc ttt ctc tgc tct       336
Ser Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser
    -15                 -10                 -5
acc cct gcc cgg g                                                     349
Thr Pro Ala Arg
1

<210> 453
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..269

<221> sig_peptide
<222> 87..194
<223> Von Heijne matrix
      score 4.69999980926514
      seq SCFVPSLVTGALQ/QS

<400> 453
agcagtccag agaagtgaaa tgacttgcct gaagccacag agcctgcaag tgcgagggct      60
gggattccaa tccaagctct gggcca atg gct ttg cat atc cta gaa tgc gag     113
                             Met Ala Leu His Ile Leu Glu Cys Glu
                                 -35                 -30
agg aac gtt tgt ttt gta gca gtt aga cag cct gct cat gaa agc tgc       161
Arg Asn Val Cys Phe Val Ala Val Arg Gln Pro Ala His Glu Ser Cys
        -25                 -20                 -15
ttt gtg ccc agc ctt gtg aca ggt gct tta caa caa tcc cag aca cag       209
Phe Val Pro Ser Leu Val Thr Gly Ala Leu Gln Gln Ser Gln Thr Gln
    -10                 -5                  1               5
cac cca cct tgg gtt tgc cct cag gta cag ggc tcc tat cca tcc tgg       257
His Pro Pro Trp Val Cys Pro Gln Val Gln Gly Ser Tyr Pro Ser Trp
                10                  15                  20
aag aac aga ggg a                                                     270
Lys Asn Arg Gly
            25

<210> 454
```

<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 317..490

<221> sig_peptide
<222> 317..412
<223> Von Heijne matrix
score 4.69999980926514
seq RVLXLCNSRVSFT/RX

<221> misc_feature
<222> 415..416
<223> n=a, g, c or t

<400> 454
taaggatatt acaaaacatt ttataaacac gtgggtctct tatgaagtac aatccaaagt 60
ttgcatacaa tttaaaacaa aagcaagaaa tgtcacgctt tgggaacact gtttktctca 120
cactaaaatg ttctatctga agcaagggga agtgtccaaa ttatagttca caaaatacct 180
ttatttctc acaacaaaat catccctagt cagcggccca acattactca tttctgtcat 240
caaaaacacc ctttctgtgg gttggtatga aatatccgca ggcatcacaa gtactataag 300
aaagggcttt ttcaaa atg tcc tgt act cac tcc tct tct aac ctg ggt aag 352
Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys
-30 -25
ttt tct gta cac aga gag tac cgt gtc ctc mta ctg tgt aac agt agg 400
Phe Ser Val His Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg
-20 -15 -10 -5
gtc tct ttc act cgn ntc cat gtg aag aga cca cca wac agg cta tgt 448
Val Ser Phe Thr Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys
1 5 10
gtg agc agc aaa ggc tgt tta ttt cac ctg ggt gca ggc agg ct 492
Val Ser Ser Lys Gly Cys Leu Phe His Leu Gly Ala Gly Arg
15 20 25

<210> 455
<211> 177
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..175

<221> sig_peptide
<222> 56..112
<223> Von Heijne matrix
score 4.69999980926514
seq AFPLLLVIILLFQ/KQ

<400> 455
cacattcata agtatgagct taggctgagg atatatatcc agtgggggat gaaac atg 58
Met
ctt aag aaa ttg agt gca ttt cct tta tta ttg gtt att att ttg cta 106
Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu Leu
-15 -10 -5
ttt caa aaa caa wtt gga ctt tta aaa aat tat amt tca cca cag aga 154
Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln Arg
1 5 10
cag gtg ttg ttt tgt aat cga ag 177

```
Gln Val Leu Phe Cys Asn Arg
15                  20

<210> 456
<211> 102
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 14..100

<221> sig_peptide
<222> 14..67
<223> Von Heijne matrix
      score 4.69999980926514
      seq CIFLAVLSKISWA/VN

<400> 456
ctaattgaaa agg atg tcc tat ttc cga tgt ata ttt ttg gca gtt ttg      49
               Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu
                           -15                 -10
tca aaa atc agt tgg gct gta aat atg tgc agt ctt att tct ggg tcc     97
Ser Lys Ile Ser Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser
    -5                  1               5                   10
tcg gg                                                              102
Ser

<210> 457
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..151

<221> sig_peptide
<222> 35..136
<223> Von Heijne matrix
      score 4.59999990463257
      seq LFLSISLITLYYS/SE

<400> 457
tgagttaaat tagacaactg taagagaaaa attt atg ctt tgt ata atg ttt ggt   55
                                      Met Leu Cys Ile Met Phe Gly
                                                      -30
att gaa act aat gaa att acc aag atg aca atg tct ttt ctt ttg ttt    103
Ile Glu Thr Asn Glu Ile Thr Lys Met Thr Met Ser Phe Leu Leu Phe
        -25                 -20                 -15
cta agt atc agt ttg ata act tta tat tat tcc tca gaa gca tgt ggg    151
Leu Ser Ile Ser Leu Ile Thr Leu Tyr Tyr Ser Ser Glu Ala Cys Gly
    -10                 -5                  1               5

<210> 458
<211> 285
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..285
```

<221> sig_peptide
<222> 16..132
<223> Von Heijne matrix
score 4.59999990463257
seq YVFXLLAPFLTRS/SP

<221> misc_feature
<222> 251
<223> n=a, g, c or t

<400> 458
```
agacctccag aaacc atg tgt caa gct cgg att gcc tta gac agg tgc aat      51
                 Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn
                                 -35                 -30
tta aga aca gct ttc atc ctc ttt kct ctc ata ttg tca cac tat gtg       99
Leu Arg Thr Ala Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val
        -25                 -20                 -15
ttc yga ctt ctg gct cct ttc ctc aca aga agc tca ccc agc tgg aac      147
Phe Xaa Leu Leu Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn
    -10                 -5                  1               5
tct tat ggg acc ttg gca cca gag acc aca aat tcc tct ttg aag ttt      195
Ser Tyr Gly Thr Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe
            10                  15                  20
tct aac agc aac aat ggt att tct gac ttg gct twc ttg tat ttc tcd      243
Ser Asn Ser Asn Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser
            25                  30                  35
cac gtt anc aaa att ggt tca gca tct acc atg ggc tac ggg              285
His Val Xaa Lys Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly
        40                  45                  50
```

<210> 459
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..311

<221> sig_peptide
<222> 15..86
<223> Von Heijne matrix
score 4.59999990463257
seq QGMLLAILEXCGA/IP

<400> 459
```
tcctcaagtt cttc atg gtc aag tcc gtc atc ttt ctt tcc ttc tgg caa       50
                Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln
                                -20                 -15
ggc atg ctc ctg gcc atc ctg gag rag tgt ggg gcc atc ccc aaa atc       98
Gly Met Leu Leu Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile
        -10                 -5                  1
cac tcg gcc cgc gtg tcg gtg ggc gag ggc acc gtg gct gcc ggc tac      146
His Ser Ala Arg Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr
5                   10                  15                  20
cag gac ttc atc atc tgt gtg gag atg ttc ttt gca gcc ctg gcc ctg      194
Gln Asp Phe Ile Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu
                25                  30                  35
cgg cac gcc ttc acc tac aag gtc tat gct gac aag agg ctg gac gca      242
Arg His Ala Phe Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala
            40                  45                  50
caa gtg cca aca tac ggc cct tac ggc cgc tgt gcc ccc atg aag agc      290
```

```
Gln Val Pro Thr Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser
        55                  60                  65
atc tcc agc agc ctc aag gag                                      311
Ile Ser Ser Ser Leu Lys Glu
    70                  75

<210> 460
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 161..424

<221> sig_peptide
<222> 161..418
<223> Von Heijne matrix
      score 4.59999990463257
      seq AAAALCILILLXA/MY

<400> 460
aggccgggct gatgcgcagg caatttatca tcttgatctc ccactgagtc agggagctct   60
cctgtcacca gtattgattt cagaggatgg actaaatttc ctaggatttc cattaagaat  120
taagaaaaaa gctctaagca cgcagggtag ccagacagac atg gat atg aga tgg    175
                                            Met Asp Met Arg Trp
                                                    -85
cac tgt gaa aac tcg cag acc aca gat gac atc ctt gtg gcc tca gca    223
His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile Leu Val Ala Ser Ala
    -80                 -75                 -70
gag tgt ccc agc gat gat gag gac att gac ccc tgt gag ccg agc tca    271
Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro Cys Glu Pro Ser Ser
-65                 -60                 -55                 -50
ggt ggg tta gcc aac cca acc cga gca ggc ggc aga gag ccg tat cca    319
Gly Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly Arg Glu Pro Tyr Pro
                -45                 -40                 -35
ggc tca gca gaa gtg atc cgg gag tcc agc agc acc acg ggt atg gtc    367
Gly Ser Ala Glu Val Ile Arg Glu Ser Ser Ser Thr Thr Gly Met Val
            -30                 -25                 -20
gtt ggg ata gta gcc gct gcc gcc ctg tgc atc ctt atc ctc ctc wat    415
Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile Leu Ile Leu Leu Xaa
        -15                 -10                 -5
gcc atg tac a                                                      425
Ala Met Tyr
    1

<210> 461
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 45..419

<221> sig_peptide
<222> 45..104
<223> Von Heijne matrix
      score 4.59999990463257
      seq PTLLTLCIGSVVS/SD

<400> 461
aaaaagctgt gggctcagaa gcagagttct ggggtgtctc cacc atg gcc tgg acy    56
```

```
                                                    Met Ala Trp Thr
                                                    -20
cct ctc tgg ccc act ctc ctc act ctt tgc ata ggt tct gtg gtt tct      104
Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly Ser Val Val Ser
    -15                 -10                 -5
tct gac ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag aga      152
Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln Arg
1               5                   10                  15
gtc agg atc aca tgc cag gga gac aac ctc gaa gag tat ttt gca agc      200
Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu Tyr Phe Ala Ser
            20                  25                  30
tgg tac cga cag agg ccc gga cag gcc cct gtc ctt gtc atc tat ggt      248
Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu Val Ile Tyr Gly
        35                  40                  45
aaa aac aac cgg ccc tca ggg att cca gsc cgr ktc tct ggc tcc aag      296
Lys Asn Asn Arg Pro Ser Gly Ile Pro Xaa Arg Xaa Ser Gly Ser Lys
    50                  55                  60
tca ggc aat aca gct tta ttg acc atc gyc ggg gct cag gcg gag gat      344
Ser Gly Asn Thr Ala Leu Leu Thr Ile Xaa Gly Ala Gln Ala Glu Asp
65                  70                  75                  80
gab gct gac tat tac tgt agt kat cgc gac cat act gat aat cgg tgg      392
Xaa Ala Asp Tyr Tyr Cys Ser Xaa Arg Asp His Thr Asp Asn Arg Trp
                85                  90                  95
gtg ttc ggc ggg ggg acc agg ctg aca g                                420
Val Phe Gly Gly Gly Thr Arg Leu Thr
            100                 105
```

<210> 462
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..255

<221> sig_peptide
<222> 46..105
<223> Von Heijne matrix
score 4.59999990463257
seq XILTCLIFRNSEG/FQ

<400> 462

```
tttttttttt tccccaagcg aaswtgaaca gttgctaagt ggaaa atg gag gct gaa     57
                                                  Met Glu Ala Glu
                                                  -20
ttt tac atg gkg att ctt acc tgc ttg atc ttc agg aac tca gaa ggg      105
Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg Asn Ser Glu Gly
    -15                 -10                 -5
ttt cag att gyc cat gtc cag aaa caa cag tgt ctt ttc aaa aat gag      153
Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu Phe Lys Asn Glu
1               5                   10                  15
aaa gtg gtc gtg ggc tca tgc aac agg acc atc cag aac cag cag tgg      201
Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln Asn Gln Gln Trp
            20                  25                  30
atg tgg act gag gat gaa aag ctc ctt cat gtt aaa tct gca ctg tgc      249
Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys Ser Ala Leu Cys
        35                  40                  45
ttg gcc at                                                           257
Leu Ala
    50
```

<210> 463

```
<211> 117
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 61..117

<221> sig_peptide
<222> 61..111
<223> Von Heijne matrix
      score 4.59999990463257
      seq ACALCVWLCVKSC/SI

<400> 463
aataggaaga caaaagacaa aaaaaaatcc accaccacca aaatatccct ttgtacatgt      60
atg tgc gtg tgc gcg tgt gct ttg tgt gtg tgg ttg tgt gtt aaa tca       108
Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
        -15                 -10                 -5
tgc agt att                                                           117
Cys Ser Ile
    1

<210> 464
<211> 142
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..140

<221> sig_peptide
<222> 39..101
<223> Von Heijne matrix
      score 4.59999990463257
      seq FIYLLAFCMPSLE/KC

<400> 464
cttattgtgg attgtggttt taattttgta tttccctg atg att agt gat gtt cag      56
                                          Met Ile Ser Asp Val Gln
                                              -20
cac ctt ttc ata tac ttg tta gcc ttt tgt atg cct tcc ttg gag aaa       104
His Leu Phe Ile Tyr Leu Leu Ala Phe Cys Met Pro Ser Leu Glu Lys
-15                 -10                 -5                   1
tgt cta tac ggg tct ttg gcc cac ttt ttt ttt ttt tt                    142
Cys Leu Tyr Gly Ser Leu Ala His Phe Phe Phe Phe
            5                   10

<210> 465
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 216..299

<221> sig_peptide
<222> 216..260
<223> Von Heijne matrix
      score 4.59999990463257
      seq LFRVLFSXTCALX/QD
```

<400> 465
agttacttct ttgctaggtt gaggaaaggg tggaagcgcc tcctgcagcc acgaatatcc 60
tccagtgcct gagagaaaac ggcctaatcg aaaacgtccg cggcatacat ccattcttaa 120
aacttgagtg gctgcttttc tgggtggaaa agagcggtat cagacagggt gagcagtcgg 180
ggaacggatg aacaaagact tgcaccgtgg ccctg atg cct ttg ttc cga gtt 233
Met Pro Leu Phe Arg Val
-15 -10
cta ttc agt tgw act tgt gcg ttg twa cag gac ttt aga atg cag ccc 281
Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln Asp Phe Arg Met Gln Pro
-5 1 5
tgc ccc cca acc ccc aag g 300
Cys Pro Pro Thr Pro Lys
10

<210> 466
<211> 235
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 146..235

<221> sig_peptide
<222> 146..217
<223> Von Heijne matrix
score 4.59999990463257
seq LLFYVLLFRNLYT/HT

<400> 466
tttatatctt taattgcaag gataaaagaa ggggtgcatc tcaaaggcca tgataaatat 60
aaaggataga aaagttacgt tgatggtgtg cccctcgata tctagaagat agcatagtcc 120
atgcattctc agaaagatcc tatcc atg tgg tat gta gag atg tgg gtt tct 172
Met Trp Tyr Val Glu Met Trp Val Ser
-20
ttt ttt cta ctt ttt tat gtg ctt ctt ttt aga aac tta tac aca cac 220
Phe Phe Leu Leu Phe Tyr Val Leu Leu Phe Arg Asn Leu Tyr Thr His
-15 -10 -5 1
aca cac cac act ggg 235
Thr His His Thr Gly
5

<210> 467
<211> 220
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 58..219

<221> sig_peptide
<222> 58..147
<223> Von Heijne matrix
score 4.59999990463257
seq VLVVSFVVGGLGC/NX

<221> misc_feature
<222> 218
<223> n=a, g, c or t

```
<400> 467
accacaactc ccagggtgct ccgcgtcctc gccgctgtcg ccgccgcgga gacaaag        57
atg gct gcg aga gtc ggc gcc ttc ctc aag aat gcc tgg gac aag gag       105
Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu
-30                 -25                 -20                 -15
cca gtg ctg gtc gtg tcc ttc gtc gtc ggg ggc ctc ggc tgt aat dct       153
Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa
                -10                 -5                  1
gcc ccc att gag ccc cta ctt caa gta ctc cgt cat gat caa caa ggc       201
Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly
        5                   10                  15
cac gcc cta caa cta cna c                                             220
His Ala Leu Gln Leu Xaa
    20

<210> 468
<211> 462
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 154..462

<221> sig_peptide
<222> 154..222
<223> Von Heijne matrix
      score 4.59999990463257
      seq WTCVAPVYPACSG/RR

<400> 468
gactgcagcc gcgagctcct ggaggcggcg ggatggaggc ggcggccgag cctggaaacc      60
tggccggcgt caggcacatc atcctggtcc tctcaggaaa ggggggcgtt gggaaaagca     120
ccatctccac ggagctggcc ctggcactgc gcc atg cag gca aga agg tgg gaa      174
                                     Met Gln Ala Arg Arg Trp Glu
                                                     -20
tcc tgg atg tgg acc tgt gtg gcc cca gta tac ccc gca tgc tcg ggg       222
Ser Trp Met Trp Thr Cys Val Ala Pro Val Tyr Pro Ala Cys Ser Gly
    -15                 -10                 -5
cgc agg gca rdr gct gtk sac cag tgs grr ccg cgg ctg ggc amc sgt       270
Arg Arg Ala Xaa Ala Val Xaa Gln Xaa Xaa Pro Arg Leu Gly Xaa Xaa
1               5                   10                  15
ctt cct gga ccg gga bca gag cat ctc gct cat gtc tgt ggg ctt cct       318
Leu Pro Gly Pro Gly Xaa Glu His Leu Ala His Val Cys Gly Leu Pro
            20                  25                  30
gct gga gaa gcc gga cga ggc cgt ggt gtg gag agg ccc caa gaa aaa       366
Ala Gly Glu Ala Gly Arg Gly Arg Gly Val Glu Arg Pro Gln Glu Lys
        35                  40                  45
cgc gct gat aaa gca gtw kgt gtc cga cgt ggc ctg ggg gga gct gga       414
Arg Ala Asp Lys Ala Val Xaa Val Arg Arg Gly Leu Gly Gly Ala Gly
    50                  55                  60
cta cct ggt ggt gac acg ccc cgg gga cct ccg atg agc aca tgg cca       462
Leu Pro Gly Gly Asp Thr Pro Arg Gly Pro Pro Met Ser Thr Trp Pro
65                  70                  75                  80

<210> 469
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 391..438
```

<221> sig_peptide
<222> 391..432
<223> Von Heijne matrix
      score 4.59999990463257
      seq FLFFFGNSPCCGA/TG

<400> 469
```
tatagtttca gttatgacat gagcacaaac atcatgattt ctgttctttt taatgcactc     60
agactggcta agaatatgtt ctgtgttggt gaatattcca tatgtatttg aaaataatat    120
atactctgct cttgttaggt tctagaaatg tcaattacct caaattctct gagagtgcag    180
ctcagttctt ctatatcctt actggtttct gcctacttgc tctgtcagtt actgagcaaa    240
aagtagcaaa gtctgcagct gtaatacatt tgtttatttc tctcattttt gttagtattt    300
gcttcatgta ctttgaagct rtgttgttag catgcataca cataggatga ttatggcttc    360
ttggaaaatt gacccctta gcattatgta atg ttc ctc ttt ttc ttt ggt aac     414
                                 Met Phe Leu Phe Phe Phe Gly Asn
                                                 -10
agt cca tgt tgt gga gcc aca ggg                                      438
Ser Pro Cys Cys Gly Ala Thr Gly
    -5                  1
```

<210> 470
<211> 131
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..130

<221> sig_peptide
<222> 11..85
<223> Von Heijne matrix
      score 4.59999990463257
      seq SLSLSLSASLIIS/PS

<400> 470
```
atcttttcac atg ggc ctc tcc cac cat cgg gtc tca gcc cca tct tct        49
           Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser
           -25                 -20                 -15
ctc tct ctc tct ctc tcg gcc tcc ctc att att tct ccc tct ccc tcc       97
Leu Ser Leu Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser
        -10                 -5                  1
gcc tct cca tct ctc ctt sct ccc cct bcc cgg g                       131
Ala Ser Pro Ser Leu Leu Xaa Pro Pro Xaa Arg
5                   10                  15
```

<210> 471
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..210

<221> sig_peptide
<222> 115..183
<223> Von Heijne matrix
      score 4.5
      seq LSMLLRLVSNSRP/PV

<400> 471

```
tggcgcgatc ttggctcacc gcaccttccg cctcccgggt tcgagcgctt ctcctgcctc      60
agcctcccga ttagcgggga tgacagggag tcaccccac gcctggcttg gctg atg        117
                                                           Met
ttt gtg ttt tta gta ggc acg ccg tgt ctc tcc atg ttg ctc agg ctg        165
Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg Leu
        -20                 -15                 -10
gtc tcc aac tcc cga cct cct gtg atg cgc cca cct cgg cct ggg g          211
Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
    -5                  1                   5
```

<210> 472
<211> 150
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..150

<221> sig_peptide
<222> 25..123
<223> Von Heijne matrix
score 4.5
seq VTITILFLIVSMA/LK

<400> 472

```
ctttattgag ggatacttta ctct atg aaa ttc act cat ttt aag tgt aca        51
                           Met Lys Phe Thr His Phe Lys Cys Thr
                                       -30                 -25
att cgg tta tta tta cta tat tta cag aat cct gta acc atc aca att        99
Ile Arg Leu Leu Leu Leu Tyr Leu Gln Asn Pro Val Thr Ile Thr Ile
            -20                 -15                 -10
tta ttt tta atc gtt tcc atg gcc ctg aaa ata aac cac ata ccc aag        147
Leu Phe Leu Ile Val Ser Met Ala Leu Lys Ile Asn His Ile Pro Lys
            -5                  1                   5
ggg                                                                    150
Gly
```

<210> 473
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 227..352

<221> sig_peptide
<222> 227..268
<223> Von Heijne matrix
score 4.5
seq SCMSLFPCCPAQS/KN

<400> 473

```
tatttgatta aaaaagactc ttcttgtttt ctgttttgtc tgagttttca ttatacccac      60
ttctcaacta ccccatccca mgggtagaag tttttaaaat ttgcatattt aamattcatt     120
ttcgamttat ctgaaattaa tcaatatctc tactgtagtc ttggataatg ccaagagttt     180
aaaatgctat aatccaaaca cctgtttgga ctcaatatgt catttt atg tct tgt        235
                                                   Met Ser Cys
atg tca ctt ttc ccc tgt tgc cct gct cag agt aag aat tat atg tta        283
Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn Tyr Met Leu
    -10                 -5                  1                   5
tta tta ttc att att tta ctt cca act caa ttt tta tat tca aaa tta        331
```

```
Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr Ser Lys Leu
                10                  15                  20
gtt aca att tgc tgt tgt ttt                                         352
Val Thr Ile Cys Cys Cys Phe
            25

<210> 474
<211> 141
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..141

<221> sig_peptide
<222> 64..105
<223> Von Heijne matrix
      score 4.5
      seq LVCCTINSSFALG/IS

<221> misc_feature
<222> 38
<223> n=a, g, c or t


<400> 474
tactttaagt tctagggtac gtctgcacaa cgtsrggntt tgatacatag gtatatatgt    60
gcc atg ttg gtt tgc tgc acc atc aac tca tca ttt gca tta ggt att     108
    Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile
                    -10                 -5                  1
tct cgt aat gct atc cct ctg cca gcc cct ggg                         141
Ser Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
            5                   10

<210> 475
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 92..298

<221> sig_peptide
<222> 92..250
<223> Von Heijne matrix
      score 4.5
      seq ALYVICQFILIRS/GV

<400> 475
cagattaaga gatggagaaa ggtgtagggm tgattctttt tttggtgaga cctcgcataa    60
ctatcataaa tttgacagtg agtatgagag a atg gga cgt ggt cct ggc ccc      112
                                   Met Gly Arg Gly Pro Gly Pro
                                                   -50
tta caa gag aga tct ctc ttt gag ama aag aga ggc gct cct cca agt     160
Leu Gln Glu Arg Ser Leu Phe Glu Xaa Lys Arg Gly Ala Pro Pro Ser
    -45                 -40                 -35
agc aat att gaa gac ttc cat gga ctc tta ccg aag gtt atc ccc atc     208
Ser Asn Ile Glu Asp Phe His Gly Leu Leu Pro Lys Val Ile Pro Ile
-30                 -25                 -20                 -15
tgt gct cta tat gtg att tgc cag ttc att cta ata agg agt gga gtc     256
Cys Ala Leu Tyr Val Ile Cys Gln Phe Ile Leu Ile Arg Ser Gly Val
```

```
                -10                -5                1
aac ata tca atg gag caa gtc aca gtc gtc gat gcc agt ctg gg           300
Asn Ile Ser Met Glu Gln Val Thr Val Val Asp Ala Ser Leu
        5                   10                  15
```

<210> 476
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 112..231

<221> sig_peptide
<222> 112..150
<223> Von Heijne matrix
score 4.5
seq MLYCVVVVHSVCC/AV

<400> 476

```
ttttaggggg gtttggttcg tttttgaact gtatacagat gaaattatac agaatgcttt     60
ttttttggta tatggccttt ttcactctgt agtgtatttg tgagattcat c atg ttg     117
                                                         Met Leu
tat tgt gta gtt gtg gtt cat tct gtt tgc tgt gca gta tac tat ttt      165
Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr Tyr Phe
    -10                 -5                  1                   5
gtg att att cat aca ata gaa cat att aca tat tta tgt atc cat tct      213
Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile His Ser
                10                  15                  20
acc att cta ctg tgt gtg g                                            232
Thr Ile Leu Leu Cys Val
            25
```

<210> 477
<211> 236
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..234

<221> sig_peptide
<222> 124..201
<223> Von Heijne matrix
score 4.5
seq VFXSLFLIQLLIS/FS

<221> misc_feature
<222> 171
<223> n=a, g, c or t

<400> 477

```
aagtggcagc btcagcaccc agggctgtgg taggtcacag tctctgggyk ggtctcagtg     60
tccaacactg tagctggtgc ctgccaggtt cccagtggtt ggggtcacca ggtctgaaga    120
gag atg tgc tgg ytg cgg gya tgg ggc cag atc ctc ctg cca gtt ttc      168
    Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe
        -25                 -20                 -15
cbn tcc ctc ttt ctc atc caa ttg ctt atc agc ttc tca gag aat ggt      216
Xaa Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly
    -10                 -5                  1                   5
```

```
ttt atc cac agc ccc atg gg                                         236
Phe Ile His Ser Pro Met
                10

<210> 478
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..200

<221> sig_peptide
<222> 138..179
<223> Von Heijne matrix
      score 4.5
      seq CGLXILCGPWLHA/AP

<400> 478
tctacatcac aggtkkatca gtgaaatatg tggtaagatg tacaaataag atgtgcccca    60
ccaccagaat gatcagttct gtgaggacac gtccgtgact gtaccctctt tcagaagtgc   120
tatcrattaa tgtggtt atg tgt ggc ctg akk atc ctc tgt ggg cct tgg      170
                   Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp
                               -10                 -5
ctc cat gca gca cct cca tcc ccg ccg cgg g                           201
Leu His Ala Ala Pro Pro Ser Pro Pro Arg
            1               5

<210> 479
<211> 151
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..150

<221> sig_peptide
<222> 25..123
<223> Von Heijne matrix
      score 4.5
      seq SISLLLMLXXYWS/CW

<400> 479
acatagcatt ttatgkacta gaaa atg ttc cat gga agg gtt atg gcc atg       51
                           Met Phe His Gly Arg Val Met Ala Met
                                       -30                 -25
ggt kat tta acc aaa cat tta aat cta aac att tct atc tca ctg ttg      99
Gly Xaa Leu Thr Lys His Leu Asn Leu Asn Ile Ser Ile Ser Leu Leu
                -20                 -15                 -10
ctt atg ctg wwd gwa tat tgg tct tgt tgg ata aaa tca ccc ccg scc     147
Leu Met Leu Xaa Xaa Tyr Trp Ser Cys Trp Ile Lys Ser Pro Pro Xaa
            -5                  1               5
atg g                                                               151
Met

<210> 480
<211> 511
<212> DNA
<213> Homo sapiens

<220>
```

<221> CDS
<222> 116..511

<221> sig_peptide
<222> 116..499
<223> Von Heijne matrix
score 4.5
seq LALHHLSSGHSSG/WT

<221> misc_feature
<222> 150
<223> n=a, g, c or t

<400> 480
```
gctcgcatca tggcggctga gtgggcttct cgtttctggc tttgggctac gctgctgatt      60
cctgcggccg cggtctacga agaccaagtg ggcaagtttg attggagaca gcaat atg      118
                                                             Met
ttg gga agg tca agt ttg ctc cst tgg aaa tnt tcc cct gga tcc aag      166
Leu Gly Arg Ser Ser Leu Leu Xaa Trp Lys Xaa Ser Pro Gly Ser Lys
        -125                -120                -115
aag ttg gtt gta gcc aca gag aag aat gtg att gca gca tta aat tcc      214
Lys Leu Val Val Ala Thr Glu Lys Asn Val Ile Ala Ala Leu Asn Ser
    -110                -105                -100
cga act ggg gag atc ttg tgg cgc cat gtt gac aag ggc acg gca gaa      262
Arg Thr Gly Glu Ile Leu Trp Arg His Val Asp Lys Gly Thr Ala Glu
-95                 -90                 -85                 -80
ggg gct gtg gat gcc atg ctg ctg cac gga cag gat gtg atc act gtg      310
Gly Ala Val Asp Ala Met Leu Leu His Gly Gln Asp Val Ile Thr Val
                -75                 -70                 -65
tcc aat gga ggc cga atc atg cgt tcc tgg gag act aac atc ggg ggc      358
Ser Asn Gly Gly Arg Ile Met Arg Ser Trp Glu Thr Asn Ile Gly Gly
            -60                 -55                 -50
ctg aac tgg gag ata acc ctg gac agt ggc agt ttc cag gca ctt ggg      406
Leu Asn Trp Glu Ile Thr Leu Asp Ser Gly Ser Phe Gln Ala Leu Gly
        -45                 -40                 -35
ctg gtt ggc ctg cag gag tct gta agg tac atc gca gtc ctg aag aag      454
Leu Val Gly Leu Gln Glu Ser Val Arg Tyr Ile Ala Val Leu Lys Lys
    -30                 -25                 -20
act aca ctt gcc ctc cat cac ctc tcc agt ggg cac tca agt ggg tgg      502
Thr Thr Leu Ala Leu His His Leu Ser Ser Gly His Ser Ser Gly Trp
-15                 -10                 -5                  1
aca tct cca                                                           511
Thr Ser Pro
```

<210> 481
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..427

<221> sig_peptide
<222> 212..382
<223> Von Heijne matrix
score 4.5
seq IWVRFNFLASSQA/CS

<400> 481
```
aggagaggga atttgtttta aaagagagaa agacattgag actgtgtaaa ggggatgttg      60
caacctttta aaatctgtga tctcagacca aattatacaa tataatctca gtaggtgcca     120
```

```
gtagtaggga aaagtgtcag ccctcgtgtc tggcactaag taccacccac cccaacccca    180
gtgatgggag cctctaaatg actgagattt a atg tct act acc tat ttg aat       232
                                   Met Ser Thr Thr Tyr Leu Asn
                                               -55
gag gac ttg aag aag aaa ttc agt gca gtk ata gag cag gtg ctt ttt      280
Glu Asp Leu Lys Lys Lys Phe Ser Ala Val Ile Glu Gln Val Leu Phe
-50                 -45                 -40                 -35
gca cac tta tcc cca cta cat gtg tgg ctc cag ctc agg tct ctc tgt      328
Ala His Leu Ser Pro Leu His Val Trp Leu Gln Leu Arg Ser Leu Cys
                -30                 -25                 -20
gag trt ttg acc tgc atc tgg gtt aga ttc aat ttt tta gcc tca agc      376
Glu Xaa Leu Thr Cys Ile Trp Val Arg Phe Asn Phe Leu Ala Ser Ser
            -15                 -10                 -5
caa gca tgc tcc aaa tgc aac tcc tcg ttt ctc atc atg tca tcc tct      424
Gln Ala Cys Ser Lys Cys Asn Ser Ser Phe Leu Ile Met Ser Ser Ser
        1               5                   10
tca cc                                                               429
Ser
15

<210> 482
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 145..384

<221> sig_peptide
<222> 145..261
<223> Von Heijne matrix
      score 4.5
      seq LIILDLLVPVIGL/IT

<400> 482
tacacgtaca gctcagcctt tctgttagct gcaacttcag tgttggtgaa ttattatgct     60
tctttgcaca ttgacttcta tggtgcctac aacacgtcag cttgtggaat tgagctgctt    120
cctcgaaaag gtccctcgct gtgg atg gca ctt atc gtt cta cag cta aca       171
                           Met Ala Leu Ile Val Leu Gln Leu Thr
                                               -35
ttt gga att gga tac gtt aca cta ctc cag att cat tcc atc tat tca      219
Phe Gly Ile Gly Tyr Val Thr Leu Leu Gln Ile His Ser Ile Tyr Ser
-30                 -25                 -20                 -15
caa tta att att ttg gat ctc ttg gtt cct gta ata ggc tta atc aca      267
Gln Leu Ile Ile Leu Asp Leu Leu Val Pro Val Ile Gly Leu Ile Thr
                -10                 -5                  1
gag cta cca tta cac atc aga gag act tta ctg ttt act tct tcc ttg      315
Glu Leu Pro Leu His Ile Arg Glu Thr Leu Leu Phe Thr Ser Ser Leu
        5                   10                  15
att ctc aca tta aat aca gtg ttt gtc ctg gca gtg aaa ctg aar tgg      363
Ile Leu Thr Leu Asn Thr Val Phe Val Leu Ala Val Lys Leu Lys Trp
    20                  25                  30
ttt tat tat tcc aca cga tat g                                        385
Phe Tyr Tyr Ser Thr Arg Tyr
35                  40

<210> 483
<211> 202
<212> DNA
<213> Homo sapiens

<220>
```

```
<221> CDS
<222> 39..200

<221> sig_peptide
<222> 39..110
<223> Von Heijne matrix
      score 4.5
      seq XVAXFLLTFYVIS/QV

<400> 483
catattaatg aaaagtgcca taaactgaaa aaccaaac atg agg gta gca ggt gct      56
                                          Met Arg Val Ala Gly Ala
                                                          -20
gca aar ttg gtg gta rct gtg gca rtg ttt tta ctg aca ttt tat gtt       104
Ala Lys Leu Val Val Xaa Val Ala Xaa Phe Leu Leu Thr Phe Tyr Val
            -15                 -10                 -5
att tct caa gta ttt gaa ata aaa atg gat gca agt tta gga aat cta       152
Ile Ser Gln Val Phe Glu Ile Lys Met Asp Ala Ser Leu Gly Asn Leu
        1               5                   10
ttt gca aga tca gca ttg gac aca gct gca cgt tct aca aag cct ccg       200
Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala Arg Ser Thr Lys Pro Pro
15                  20                  25                  30
gg                                                                    202

<210> 484
<211> 310
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 148..309

<221> sig_peptide
<222> 148..192
<223> Von Heijne matrix
      score 4.5
      seq TLVFLSTRQVLQC/QP

<400> 484
gcggggctgg aggcggtggc tgcggttgcg ggaccggcac tatgctgggc cttcctacca      60
cttatgtgtg gcttggtagt ggcctagggt ctctcctccc tgctgaagtc cctctcctgc     120
aggtggccgt ctgcccggcc cagcacc atg cac acg ctt gtg ttc ttg agc aca     174
                              Met His Thr Leu Val Phe Leu Ser Thr
                              -15                 -10
cgg cag gtg ctg cag tgc cag cca gct gcc tgc cag gcc ctg ccc ctg       222
Arg Gln Val Leu Gln Cys Gln Pro Ala Ala Cys Gln Ala Leu Pro Leu
    -5                  1               5                   10
ctg cca cgc gaa ctc ttc ccc ctg ctg ttc aag gtg gcc ttc atg ghc       270
Leu Pro Arg Glu Leu Phe Pro Leu Leu Phe Lys Val Ala Phe Met Xaa
                15                  20                  25
aag aag aca gtg gta ctg cgc gak ttg gta cac acg cgg g                 310
Lys Lys Thr Val Val Leu Arg Xaa Leu Val His Thr Arg
            30                  35

<210> 485
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 372..419
```

```
<221> sig_peptide
<222> 372..413
<223> Von Heijne matrix
      score 4.5
      seq TVVISCLVGECGS/WK

<400> 485
agccggtggc agcacagcca ggacagccat ttcctcagca gccttcggta aaggcaacag     60
attctgacgg taactgtgta tcagttggaa ttactgcact aactttgagg gccatactca    120
aggactccaa taataaccaa gtcaatggcc ttagtggaaa tacaacaatt ccgtttagca    180
gctgttgggc caactacaca gaccttactc cccttagaac aggaaaaaat tataagattg    240
aatttatact ggataatgtt gttggggtag aatccagaac tttcagcctg ctggcagagt    300
ctgtctctag cagtggcagc agcagcagca gcmacagcaa agcatcaact gtgggtacat    360
atgcccagat a atg act gtm gta att agc tgt ctg gtt gga gaa tgt ggc     410
             Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly
                             -10                 -5
tct tgg aaa t                                                         420
Ser Trp Lys
    1

<210> 486
<211> 226
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..225

<221> sig_peptide
<222> 10..150
<223> Von Heijne matrix
      score 4.5
      seq PIFGLLVPSQIFS/SL

<400> 486
caaccatac atg tgc aca ctc aca gac aca cac act cac gtc caa gtg cac     51
          Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His
                  -45                 -40                 -35
aag tca aaa cct tgc cag ctc ctc tcc cct cct cca cca rsc cat ggt       99
Lys Ser Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Pro Xaa His Gly
            -30                 -25                 -20
cct ctt ctt ctc cct atc ttt ggc ctt ctt gtg ccc tct cag att ttc      147
Pro Leu Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe
        -15                 -10                 -5
agc tct ctt ctc aat tct cta cat ctg ggc ctg cct tcc ttc cca aag      195
Ser Ser Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys
    1               5                   10                  15
atg cca ctc atg att ttc ctc ccc cgc tgg g                            226
Met Pro Leu Met Ile Phe Leu Pro Arg Trp
                20                  25

<210> 487
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..454

<221> sig_peptide
```

```
<222> 221..409
<223> Von Heijne matrix
      score 4.5
      seq QILXSTLAMKIHS/QQ

<400> 487
agaaaatgga ggcgaatctg tatttccagt taactgctca gaagagagat gctgaagagt      60
tgtagtcgtg catccttctc accctccgtt agaaagcctc ctctcatcct cagaagacta     120
ctgtcagagg atgtaggvat ggacatcccc tttgaagagg gcgtgctgag tcccagtgct     180
gcagacatga ggcctgaacc tcctaattct ctggatctta atg aca ctc atc ctc      235
                                            Met Thr Leu Ile Leu
                                                        -60
gga gaa tca agc tca cag ccc caa ata tca atc ttt ctc tgg acc aaa      283
Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile Phe Leu Trp Thr Lys
            -55                 -50                 -45
gtg aag gat cta ttc tct ctg atg ata act tgg aca gtc cag atg aaa      331
Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp Thr Val Gln Met Lys
        -40                 -35                 -30
ttg aca tca atg tgg atg aac ttg ata ccc ccg atg aag cag att ctt      379
Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro Met Lys Gln Ile Leu
    -25                 -20                 -15
tdg agt aca ctg gcc atg aag atc cac agc caa caa aga ttc tgg cca      427
Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln Gln Arg Phe Trp Pro
-10                 -5                  1               5
aga gtc aga gtc tat tcc aga ata tac                                  454
Arg Val Arg Val Tyr Ser Arg Ile Tyr
            10                  15

<210> 488
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 253..327

<221> sig_peptide
<222> 253..309
<223> Von Heijne matrix
      score 4.5
      seq VLFLLNLFQKIEE/EE

<400> 488
cggctaatgt gatgcctcca gctttgttct ttttgcttag gattgctttg gctatttggg      60
ctcctttttg ggtccatatt aattttaaaa cagtttttc tggttttgtg aaggatgtca     120
ttggtagttt ataggaatag cahtgaatct gtagattgct ttgggcagta tggccatttt     180
aacaatatta attcttccta tctatgaata tggaatgttt ttccatgtgt ttgtgtcatc     240
tctttatacc tg atg tat aaa gaa aag ctg gta tta ttc cta ctc aat ctg     291
              Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu
                          -15                 -10
ttc caa aaa att gag gag gag gaa ctc ttc cct aat ga                   329
Phe Gln Lys Ile Glu Glu Glu Glu Leu Phe Pro Asn
    -5                  1               5

<210> 489
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..412
```

<221> sig_peptide
<222> 149..292
<223> Von Heijne matrix
      score 4.5
      seq LELVATLPDDVQP/GP

<221> misc_feature
<222> 396
<223> n=a, g, c or t

<400> 489
```
gaaagtgcag gcagctgtgg aaggcgaagt tcaatcccag agtccgcccc ctgaattggg     60
gcctttccgg aggaggaagc tctgaaaaac agggggggccc agtgccattc cgcagggaat   120
tgtcgcttgc gttcagctgt tctacaca atg gac tca gta cct gcc act gtg       172
                               Met Asp Ser Val Pro Ala Thr Val
                                                   -45
cct tct atc gcc gct acc ccg ggg gac ccg gaa ctt gtg gga ccc ttg      220
Pro Ser Ile Ala Ala Thr Pro Gly Asp Pro Glu Leu Val Gly Pro Leu
-40                 -35                 -30                 -25
tct gtg ctc tac gca gcc ttc ata gcc aag ctg ctg gag cta gtt gct      268
Ser Val Leu Tyr Ala Ala Phe Ile Ala Lys Leu Leu Glu Leu Val Ala
                -20                 -15                 -10
aca ttg cct gat gat gtt cag cct ggg cct gat ttt tat ggr stg sca      316
Thr Leu Pro Asp Asp Val Gln Pro Gly Pro Asp Phe Tyr Gly Xaa Xaa
            -5                  1               5
tgg aaa ctg tat tta tca ctg cct tct tgg gaa tkg ttc gtt tgc cat      364
Trp Lys Leu Tyr Leu Ser Leu Pro Ser Trp Glu Xaa Phe Val Cys His
    10                  15                  20
ttt ctt atg gag act gtc ctt gtt gtg aag gnt aga gta tat cwa gtc      412
Phe Leu Met Glu Thr Val Leu Val Val Lys Xaa Arg Val Tyr Xaa Val
25                  30                  35                  40
ac                                                                   414
```

<210> 490
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..185

<221> sig_peptide
<222> 69..122
<223> Von Heijne matrix
      score 4.5
      seq AVWASVASPASIC/CG

<400> 490
```
agttccggcc tccaaggggc gggcagaagt tggaaacatg cggctgtcgg tcgctgcagc     60
gatctccc atg gcc gcg tat ttc gcc gta tgg gcc tcg gtc gcg agt ccc     110
         Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro
                     -15                 -10                 -5
gca tcc atc tgt tgc ggr amy tgg ctc aca ggg ctg gtg cgg cac gaa      158
Ala Ser Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu
                1                   5                   10
cgc atc gag gca cca tgg gcg cgt ggg                                  185
Arg Ile Glu Ala Pro Trp Ala Arg Gly
        15                  20
```

<210> 491

```
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 247..348

<221> sig_peptide
<222> 247..333
<223> Von Heijne matrix
      score 4.5
      seq ILLILQLLKXSLK/KC

<221> misc_feature
<222> 323..324
<223> n=a, g, c or t


<400> 491
ttatgtttaa aaggtcacaa gtctagaata actgaattgg gaattggaaa taccttaatt      60
ctataatttg tatctaaaat taggttttcc cttttaagtt gttaattttc tatggkttgt     120
gctgcatgct ttcactttta ttagtactta cagccaaaga gatgggcaaa tgtctagaaa     180
aattaatgtt ttgattcagg aatttgtgcc tagtgatggc ctccaataga gaattttcca     240
gagaga atg aag act cag ttt cta agt tgg ggc aaa ttt agt ttt tgt        288
       Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys
                       -25                 -20
ttt ggt att ctt ctt ata tta cag cta tta aaa bnn tct ctt aaa aaa       336
Phe Gly Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys
-15                 -10                 -5                  1
tgc cgg cac ggg                                                       348
Cys Arg His Gly
            5

<210> 492
<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..124

<221> sig_peptide
<222> 5..79
<223> Von Heijne matrix
      score 4.5
      seq LRFILPSSWDCRC/AP

<400> 492
ctac atg ctt cct gct gtg gct gtc tcg gaa ccc gtg gtc ctc cgc ttc       49
     Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe
     -25                 -20                 -15
att ctg ccg agt tcc tgg gat tgc agg tgc gcg ccg cca ctc ctg act        97
Ile Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr
-10                 -5                  1               5
ggt ttt tgt att ttt tgg ktg gag acg gg                                126
Gly Phe Cys Ile Phe Trp Xaa Glu Thr
            10                  15

<210> 493
<211> 300
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 119..298

<221> sig_peptide
<222> 119..217
<223> Von Heijne matrix
score 4.40000009536743
seq WLLMVAPRLPAGA/RD

<400> 493
```
acactgcctg cctggtgcag cccatgtgac gggtcgagct ccgggccctg ctgtccctgg    60
ccgggctatc ccagtggctt caggcacctt ctccagacct acccagaaag atgcccgg     118
atg gat cct gca gct ccg tgg ctt ttc tgg gaa gca gcg gcc cct gct     166
Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
            -30                 -25                 -20
ctc aag aga ccc tgg ctc ctg atg gtg gcc cca agg ttg cca gct ggt     214
Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
        -15                 -10                 -5
gct agg gac tca gga cag ttt ccc aga aaa ggc caa gcg ggc agc ccc     262
Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
    1               5                   10                  15
tcc agg ggc cgg gtg agg aag ctg ggg ggt gcg gtg gg                  300
Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
                20                  25
```

<210> 494
<211> 295
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 182..295

<221> sig_peptide
<222> 182..274
<223> Von Heijne matrix
score 4.40000009536743
seq SRLXALLSPYAFT/LX

<400> 494
```
tttatacaca cacacacaca cacactcata ttcattacat gtgtgtactt tctggttgct    60
tcagtaggac ttttctaggc ttctttggac tatgtgtgat attttacttc agggactgaa   120
tttcacaact gcctactatg caactttgtg attttcttga aagcacaakt actatatata   180
a atg aaa atg tcc acc ccc tcc ccg ctt tct aaa aaa gtg ctc aga aac   229
  Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
      -30                 -25                 -20
cag gtc tca aga ttg rtt gcg ttg ctt tcc cca tac gct ttc act ctg     277
Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
-15                 -10                 -5                  1
sct cgt ctt gcc tca ggg                                             295
Xaa Arg Leu Ala Ser Gly
            5
```

<210> 495
<211> 244
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> 70..243

<221> sig_peptide
<222> 70..114
<223> Von Heijne matrix
      score 4.40000009536743
      seq RFLLLYATQQGQA/KA

<400> 495
ggaagtcgcg ttgtgcaggt tcgtgcccgg ctggcgcggc gtggtttcac tgttacatgc      60
cttgaagtg atg agg agg ttt ctg tta cta tat gct aca cag cag gga cag     111
          Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln
          -15                 -10                 -5
gca aag gcc atc gca gaa gaa atg tgt rag caa gct gtg gta cat gga      159
Ala Lys Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly
    1               5                   10                  15
ttt tct gca gat ctt cac tgt att agt gaa tcc gat aag gtc tcg gtg      207
Phe Ser Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val
                20                  25                  30
att cag aat aca cct act ttt gca acg ggg ggg cgg g                     244
Ile Gln Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg
            35                  40

<210> 496
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..213

<221> sig_peptide
<222> 91..171
<223> Von Heijne matrix
      score 4.40000009536743
      seq FVNLNLCFAYTFA/LY

<400> 496
atttaagtcc agagagcaag gtgattgcag tttctttgtt cggtttgctt atttttttact      60
gcttatttct gtgtgcataa attcagcgac atg cta ata gac ata tgg tca atg     114
                                 Met Leu Ile Asp Ile Trp Ser Met
                                             -25                 -20
gtg ctt aga gaa aat ctg ttt gta aac ctg aat ctc tgt ttt gcc tac      162
Val Leu Arg Glu Asn Leu Phe Val Asn Leu Asn Leu Cys Phe Ala Tyr
                -15                 -10                 -5
aca ttt gca ttg tat tcc tgc cct gct cca act cgt tgt cct aga cca      210
Thr Phe Ala Leu Tyr Ser Cys Pro Ala Pro Thr Arg Cys Pro Arg Pro
            1               5                   10
tcc ag                                                                215
Ser

<210> 497
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..254

<221> sig_peptide
```

```
<222> 36..89
<223> Von Heijne matrix
      score 4.40000009536743
      seq WFPLSCSPSLPLS/IP

<400> 497
cttttggggt tcgctgtttc ttccctctct gctgg atg ctg tct tgc ccc tgg         53
                                       Met Leu Ser Cys Pro Trp
                                                       -15
ttt ccc cta tcc tgt tct ccc tcc ttg cct ctg agc atc cca gac tgc       101
Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro Leu Ser Ile Pro Asp Cys
        -10                 -5                  1
ctg cct gcc ttc ctc tgg ccg ctg ggg ata ccc tgg cct gat gga gag       149
Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile Pro Trp Pro Asp Gly Glu
5                   10                  15                  20
ggt cta aga cct tcc cgt ctt ctc cgg aca cgg gaa aac att acc cct       197
Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr Arg Glu Asn Ile Thr Pro
                25                  30                  35
ctc tct tta ttc gct atg ctg agt ggc agg gag ggt gcc ccg ctc ctg       245
Leu Ser Leu Phe Ala Met Leu Ser Gly Arg Glu Gly Ala Pro Leu Leu
            40                  45                  50
gtc ccc ctg g                                                         255
Val Pro Leu
        55

<210> 498
<211> 82
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..82

<221> sig_peptide
<222> 23..61
<223> Von Heijne matrix
      score 4.40000009536743
      seq MVVVSFLASSSLP/AE

<400> 498
ctttttcgtc tgggctgcca ac atg gta gtt gtt tcg ttt ctt gcc tcc tct       52
                         Met Val Val Val Ser Phe Leu Ala Ser Ser
                                     -10                 -5
tcc ttg ccg gcg gag acc cct aag caa ggg                                82
Ser Leu Pro Ala Glu Thr Pro Lys Gln Gly
            1               5

<210> 499
<211> 474
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..473

<221> sig_peptide
<222> 39..359
<223> Von Heijne matrix
      score 4.40000009536743
      seq IIILFVVITSRRG/SP
```

```
<400> 499
ttcctggacc gcgctggaag ccctggcggc ggcggccc atg ggg csc ttg gcg ctg    56
                                          Met Gly Xaa Leu Ala Leu
                                                  -105
cyc gcc tgg ctg cag ccc agg tat agg aag aat gcg tat ctt ttc atc     104
Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys Asn Ala Tyr Leu Phe Ile
    -100                -95                 -90
tat tac tta atc cag ttc tgt ggc cas tct tgg ata ttt gca aat atg     152
Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser Trp Ile Phe Ala Asn Met
-85                 -80                 -75                 -70
aca gtc aga ttc ttt tca ttt gga aaa gat tca atg gtt gac act ttt     200
Thr Val Arg Phe Phe Ser Phe Gly Lys Asp Ser Met Val Asp Thr Phe
                -65                 -60                 -55
tat gct att gga ctt gtg atg cga ctt tgc caa tcc gta tct ctc ctg     248
Tyr Ala Ile Gly Leu Val Met Arg Leu Cys Gln Ser Val Ser Leu Leu
            -50                 -45                 -40
gaa ctg ctg cac ata tat gtt ggc att gag tca aac cat ctt ctc cca     296
Glu Leu Leu His Ile Tyr Val Gly Ile Glu Ser Asn His Leu Leu Pro
        -35                 -30                 -25
agg ttt ttg cag ctc aca gaa aga ata atc atc ctt ttt gtg gtg atc     344
Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile Ile Leu Phe Val Val Ile
    -20                 -15                 -10
acc agt cga aga gga agt cca acg aga aat atg tgg tgt gtg tgt tat     392
Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn Met Trp Cys Val Cys Tyr
-5                  1               5                   10
tcg tct ttg gat cta tgg ata tgg tta rgt aca ctt ata gca tgk tda     440
Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa Thr Leu Ile Ala Xaa Xaa
            15                  20                  25
tca gtc ata gga ata tcc tat gct gtc ttg aca t                       474
Ser Val Ile Gly Ile Ser Tyr Ala Val Leu Thr
        30                  35

<210> 500
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 177..239

<221> sig_peptide
<222> 177..230
<223> Von Heijne matrix
      score 4.40000009536743
      seq SLTLTALLVPSRV/QP

<400> 500
cttcactcat ggggagagca tttctacctg acaccctccc atttctgttt tccttaccca     60
gatctacctt ctgagatatc atccttcttc agggagataa ggaaaaaaag ccacagggtc    120
ccggagagcc aggggaatgg tgagtgtttc ctgtctccat tactggctgt aacagg atg    179
                                                              Met
gac aca ttc cct tct ctt acc ctg act gcc tta ttg gtg cct agt aga     227
Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser Arg
        -15                 -10                 -5
gtt cag ccc cag gg                                                  241
Val Gln Pro Gln
    1

<210> 501
<211> 430
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 178..429

<221> sig_peptide
<222> 178..237
<223> Von Heijne matrix
      score 4.4000000953674
      seq LRYVASAVFGVIG/SQ

<221> misc_feature
<222> 17
<223> n=a, g, c or t


<400> 501
gaggtgagtc ctggrrntgc gtggttgggg cggagagcat tatctgcggc tccgattttg    60
cagattctgg ctgaggcgtt cgtgatgtca gcagcagccg agacgggcgt gttaaaggcc   120
ggttgctagg gctgggggaa ctcagattgc ttcacctgtg gtatcagaca tcacaac      177
atg ggg ctc acc aag cag tac cta cgc tat gtt gct agt gcg gtc ttt     225
Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
-20                 -15                 -10                 -5
ggc gtt atc ggc agc caa aaa ggt aat att gtc ttt gtg aca ctt cgt     273
Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
                1               5                   10
ggt gag aaa gga cgt tat gtg gca gta cca gct tgt gaa cac gtt ttc     321
Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
        15                  20                  25
atc wgg gac tta agg aaa gga gag aag att ctt atc ctt cag ggg ctt     369
Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
    30                  35                  40
aaa caa gaa gtt act tgc tta tgc ccc tcc cca gat ggg cta cac tta     417
Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
45                  50                  55                  60
gct gtt ggg tat g                                                   430
Ala Val Gly Tyr

<210> 502
<211> 413
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 333..413

<221> sig_peptide
<222> 333..404
<223> Von Heijne matrix
      score 4.4000000953674
      seq VFFSVLYVQQGLS/SQ

<221> misc_feature
<222> 7,359
<223> n=a, g, c or t


<400> 502
agggasnggc agtgatcacg caagccggag cggcgggctg acgttggacg agctgccagg    60
tagctgaaag caggcagcca ggcagccgag acacttccca gcgattccag cctgggctcc   120
gcagaagcct cgctgaatcc cagccagctg gttctaacct tccagaatcg caatcccttc   180
tccccacagc cagccctcgc cgagcaagca gcaggatgtt tgcagtgtcg cgcccagggc   240
```

```
tctgagactg agcctgccat ccactcgcac gcctttcttt cagggctttt cggctgttgg    300
ctacactgat gtgaccccc tcccttttg ga atg atg ggg atc ttt ttg gtg       353
                                  Met Met Gly Ile Phe Leu Val
                                                  -20
tat gtn gga ttt gtt ttc ttt tcc gtt tta tat gta caa caa ggg ctt    401
Tyr Val Gly Phe Val Phe Phe Ser Val Leu Tyr Val Gln Gln Gly Leu
        -15                 -10                 -5
tct tct caa gca                                                    413
Ser Ser Gln Ala
    1
```

<210> 503
<211> 167
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 26..166

<221> sig_peptide
<222> 26..91
<223> Von Heijne matrix
score 4.40000009536743
seq WVLDPALLLTCLT/FP

<400> 503

```
gaatcggaca acttaaagtc tcgat atg agc ctc gga ttg cat tcg aac tcc     52
                            Met Ser Leu Gly Leu His Ser Asn Ser
                                    -20                 -15
tgg gtt cta gac cca gct ctg cta cta act tgt ctg acc ttc ccc att    100
Trp Val Leu Asp Pro Ala Leu Leu Leu Thr Cys Leu Thr Phe Pro Ile
            -10                 -5                  1
tat aaa ctg ttg tgg gtg aga ggt ggg acw agg wga act ctr wgr gcv    148
Tyr Lys Leu Leu Trp Val Arg Gly Gly Thr Arg Xaa Thr Leu Xaa Ala
    5                   10                  15
ctg cac tcg gcg cgg acg g                                          167
Leu His Ser Ala Arg Thr
20                  25
```

<210> 504
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 217..420

<221> sig_peptide
<222> 217..396
<223> Von Heijne matrix
score 4.40000009536743
seq MWVXCXFCFVLFC/FE

<221> misc_feature
<222> 47..48,368..369,373
<223> n=a, g, c or t

<400> 504

```
ggktccgctc cctggggcgc acgtcagtca ggaggcggaa gcgcagnnga ggcgggaagg     60
ttgtagtgcc gcgagttgag ctcctcttgc ctaagtggtc gcgccccctt taagagcagc    120
```

```
gattgtaagg agaggcggtc ccggtgtcct cgggtcccag gtgattgtga agtgctgacc    180
aattgccact ggacatactt gaaacaaaat aggaaa atg gca gca aac tct tca      234
                                        Met Ala Ala Asn Ser Ser
                                        -60                 -55
gga caa ggt ttt caa aac aaa aat aga gtt gca atc ttg gca gaa ctg      282
Gly Gln Gly Phe Gln Asn Lys Asn Arg Val Ala Ile Leu Ala Glu Leu
                -50                 -45                 -40
aca aag aga aaa gaa aac tac tta tgc aga acc agt ctt caa caa atc      330
Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg Thr Ser Leu Gln Gln Ile
            -35                 -30                 -25
atc ctg gar cta ggt att gac act ata atg tgg gtt tnn tgt ntg ttt      378
Ile Leu Glu Leu Gly Ile Asp Thr Ile Met Trp Val Xaa Cys Xaa Phe
        -20                 -15                 -10
tgt ttt gtt ttg ttt tgt ttt gag acg gag tct cgc cct gtc              420
Cys Phe Val Leu Phe Cys Phe Glu Thr Glu Ser Arg Pro Val
    -5                      1               5
```

<210> 505
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 43..456

<221> sig_peptide
<222> 43..147
<223> Von Heijne matrix
score 4.40000009536743
seq PAPLLFLPPAAPG/GE

<221> misc_feature
<222> 416..417
<223> n=a, g, c or t

<400> 505

```
gtagtcggat agttggcggg tggttgagtg gaagcggtcg cc atg tcc gcg ggg         54
                                               Met Ser Ala Gly
                                               -35
agc gcg aca cat cct gga gct ggc ggg cgc cgc agc aaa tgg gac caa      102
Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser Lys Trp Asp Gln
    -30                 -25                 -20
cca gct cca gcc cca ctt ctc ttc ctc ccg cca gcg gcc cca ggt ggg      150
Pro Ala Pro Ala Pro Leu Leu Phe Leu Pro Pro Ala Ala Pro Gly Gly
-15                 -10                 -5                  1
gag gtc acc agc agt ggg gga agt cct ggg gsc acc aca gct gct cct      198
Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr Thr Ala Ala Pro
            5                   10                  15
tca gga gcc ttg gat gct gct gct gct gtg gct gcc aag att aat gcc      246
Ser Gly Ala Leu Asp Ala Ala Ala Ala Val Ala Ala Lys Ile Asn Ala
        20                  25                  30
atg ctc atg gca aaa ggg aag ctg aaa cca act cag rat gct tct gag      294
Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln Xaa Ala Ser Glu
    35                  40                  45
aag ctt cag gct cct ggc aaa ggc cta act agc aat aaa agc aag gat      342
Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn Lys Ser Lys Asp
50                  55                  60                  65
gac ctg gtg gta gct gaa gta gaa att aat gat gtg cct ctc aca tgt      390
Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val Pro Leu Thr Cys
                70                  75                  80
agg aac ttg ctg act cga gga cag ann caa gac gag atc agc cga ctt      438
```

```
Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu Ile Ser Arg Leu
            85                  90                  95
agt ggg gct gca gta tca a                                          457
Ser Gly Ala Ala Val Ser
        100

<210> 506
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 141..314

<221> sig_peptide
<222> 141..203
<223> Von Heijne matrix
      score 4.40000009536743
      seq IRAVCLSGGSCWG/GV

<400> 506
ctctttctgt cttgattttt ctgtgtgtct ctctgcgtct tgtctatttg ttttctctct    60
ttcttctctg tggccctccc ctttgtctct tcctttctgt tttctcctgt agttcctcct   120
cttctctccc ctgattgctc atg agt ccc ctt gat cag gct gta ata cgt gct   173
                      Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala
                          -20                 -15
gtg tgt ctc agt gga ggt tcc tgc tgg gga gga gtc cgt tgt ctt gtg     221
Val Cys Leu Ser Gly Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val
-10                 -5                  1               5
cgt ggg ggc ccg aac ata ggc cct gca gcc cag ctg ctt ggg ggc att     269
Arg Gly Gly Pro Asn Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile
            10                  15                  20
cca ctc tgc tgg cca cca gct gtg act gca ggt gaa gtg aaa ctg c       315
Pro Leu Cys Trp Pro Pro Ala Val Thr Ala Gly Glu Val Lys Leu
        25                  30                  35

<210> 507
<211> 208
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..208

<221> sig_peptide
<222> 152..196
<223> Von Heijne matrix
      score 4.40000009536743
      seq SFHFIXFLPFPWA/EX

<221> misc_feature
<222> 201..202
<223> n=a, g, c or t


<400> 507
agaatcgcgc aggcgcaatt gtgccctggt tcgccaagat gtcgttccca aagtataagc    60
cgtcgagcct gcgcactctg cctgagaccc tcgacccagc ccggctcctg tcctcctgta   120
ttcctgcagt ccttttaagg aagaaaagtg a atg aac tca ttt cat ttt att     172
                                   Met Asn Ser Phe His Phe Ile
                                   -15                 -10
```

```
tss ttc ctc cct ttc ccc tgg gct gaa wnn gcg cag                    208
Xaa Phe Leu Pro Phe Pro Trp Ala Glu Xaa Ala Gln
            -5                  1

<210> 508
<211> 169
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 65..169

<221> sig_peptide
<222> 65..151
<223> Von Heijne matrix
      score 4.40000009536743
      seq LLSTHTWTDTALA/FS

<400> 508
atacagacac ccagrsagga ccctgaacac acagacaggc acagggaccc ctgtgcccac     60
aggg atg ggc tgg cac tca cat agt tcc caa ggc gtg caw gca atg cct     109
     Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro
                     -25                 -20                 -15
ctg ctg ctg tcc aca cac acc tgg aca gac aca gcc ctg gca ttc agc      157
Leu Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser
                -10                 -5                  1
aca cac aca cac                                                      169
Thr His Thr His
        5

<210> 509
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..116

<221> sig_peptide
<222> 12..77
<223> Von Heijne matrix
      score 4.40000009536743
      seq WFLRSWTWPQTAG/RV

<400> 509
caattcaagt c atg crg gct gtg aga aac gcg ggg tcg tgg ttc ctg cgg      50
             Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg
                     -20                 -15                 -10
tcc tgg act tgg ccc cag aca gcc ggc agg gtc gtg gcc aga rsg ccg      98
Ser Trp Thr Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro
                -5                  1                   5
gcc ggg acc atc tgc aca gg                                           118
Ala Gly Thr Ile Cys Thr
        10

<210> 510
<211> 402
<212> DNA
<213> Homo sapiens

<220>
```

```
<221> CDS
<222> 334..402

<221> sig_peptide
<222> 334..378
<223> Von Heijne matrix
      score 4.40000009536743
      seq ALFILVSISLFYA/LF

<400> 510
cctcctcagc ctcctcagta ccattctgtt accaccattg gtcctgcatt ctgagtttgc    60
cacctggcac gtgcccttca aatgtctcca ctgcgtcttt gcctttccct tttctgttgc   120
gtgccatcat tccgattccg attttaacag caacctgctg atttcctgcc atagtttcct   180
actttccatt ctgagcccct ttaatccact tatacaatat aactactccc tgaattattt   240
ggtcatacca cttgtatctg ccgaacccct attcctcccc tggggtacgt tttccactaa   300
acacacacag ggaaatgcca cccaaatagc tct atg tgt gcc ttg ttc att ctt    354
                                     Met Cys Ala Leu Phe Ile Leu
                                     -15                 -10
gtt tcc att tct ttg ttt tat gca ctt ttt atc tct cca tcc ata caa     402
Val Ser Ile Ser Leu Phe Tyr Ala Leu Phe Ile Ser Pro Ser Ile Gln
            -5                   1               5

<210> 511
<211> 343
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..341

<221> sig_peptide
<222> 159..317
<223> Von Heijne matrix
      score 4.40000009536743
      seq NLVLYFLVHLLFS/LS

<400> 511
cagaggcttt tatttgcata aatgtcggac cgtcttagct ctcttgtgaa aggaactttt    60
tgccatatta tagtggctca ccttacctcc tggaatgcat tctggcctca agtctgtacc   120
tagcattgat agaggaagcc cagcctggtg tgcacagc atg tac ctg gtg tgc aca   176
                                          Met Tyr Leu Val Cys Thr
                                                      -50
aca tgc acc tgg tgt gta ttt tct gaa atg ttt gtt cat gga tta aac     224
Thr Cys Thr Trp Cys Val Phe Ser Glu Met Phe Val His Gly Leu Asn
        -45                 -40                 -35
atc act cag ctc gtg ctg agc cag ctg gat tac ttt ttc cat tcc aat     272
Ile Thr Gln Leu Val Leu Ser Gln Leu Asp Tyr Phe Phe His Ser Asn
    -30                 -25                 -20
ctg aca aac ttg gtc ttg tat ttc tta gtc cat tta ctt ttt tcc ctt     320
Leu Thr Asn Leu Val Leu Tyr Phe Leu Val His Leu Leu Phe Ser Leu
-15                 -10                 -5                   1
agc ctg ttt atg ccg ctg acg gg                                      343
Ser Leu Phe Met Pro Leu Thr
            5

<210> 512
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

```
<222> 7..420

<221> sig_peptide
<222> 7..240
<223> Von Heijne matrix
      score 4.40000009536743
      seq FWWWLGSLXVTWL/IH

<221> misc_feature
<222> 93,100,137..138
<223> n=a, g, c or t


<400> 512
taagtg atg aag ctg aaa tta tac cta tgt ata tta ggt ccc tgg ggc       48
       Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly
                   -75                 -70                 -65
tgc aak rkc aaa gta cca cta att ggg ttt ctt aaa aga ata aan hta      96
Cys Xaa Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa
                -60                 -55                 -50
tat nwt ctc aca gtt ctg aaa cct agd agt ctg ara tca ann tca gca     144
Tyr Xaa Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala
            -45                 -40                 -35
ggg ttg gtt cct tct gag gac tct aaa aaa gaa tct gtt tca tgc ctc     192
Gly Leu Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu
        -30                 -25                 -20
tct cct agg ttc tgg tgg tgg ctg gga agc ctg akt gtt act tgg ctt     240
Ser Pro Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu
    -15                 -10                 -5
ata cat gca tca ctc cag tct ctg tct cct ttt tct cat gcc att ttc     288
Ile His Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe
1               5                   10                  15
tca tgt gtc tct gtg ttt tcc ttt gct tat aag gat acc agt cat att     336
Ser Cys Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile
            20                  25                  30
gaa tta ggg cct gct cta ata acc tca tct caa tta cct ctg caa gga     384
Glu Leu Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly
        35                  40                  45
acc aat ttc caa ata atg tca cac tca cat gta gca                     420
Thr Asn Phe Gln Ile Met Ser His Ser His Val Ala
    50                  55                  60

<210> 513
<211> 324
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 219..323

<221> sig_peptide
<222> 219..317
<223> Von Heijne matrix
      score 4.40000009536743
      seq LKLLFLILILIAG/YR

<400> 513
aaaacattct gaatagttta tttgtcttga cggaaagtaa aaagaacaaa cttgttttat     60
acaaaatcag atgctccaaa tggtcagttg atgatgatac caatcaaaga aaactaagga    120
ggaagaaaaa gaaaacagga aagagaggag gcaacaggaa aatcggcctt cgtccttcag    180
tctacgcttg aaattgccag ggatggataa atctgaag atg aat gaa aaa aag aaa    236
                                          Met Asn Glu Lys Lys Lys
```

```
                                                              -30
cta ctg gga acg gaa cag aaa caa aaa aaa agg atg gga aat ctg aag      284
Leu Leu Gly Thr Glu Gln Lys Gln Lys Lys Arg Met Gly Asn Leu Lys
        -25                 -20                 -15
ctg cta ttt ctt att ctg atc tta ata gca gga tac agg g                324
Leu Leu Phe Leu Ile Leu Ile Leu Ile Ala Gly Tyr Arg
    -10                 -5                  1
```

<210> 514
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 212..301

<221> sig_peptide
<222> 212..292
<223> Von Heijne matrix
score 4.40000009536743
seq SALMLPLGCAVRT/RM

<400> 514

```
tttccctcac tctctgcctc ccccatcgca ccccacagga gggtttccct cactctctgc     60
ctccccccatc gcaacccaca ggagggtttc cctcactctg cctcctccaw cgcaccccca   120
kggaggtgtt ttccctcact ggttctgttg gtggcggtgg cagcaatccg agtcacatgg    180
caccagagta tgtcacgggt ggcggatctg a atg ggg ctg cag agc ctc aca       232
                                  Met Gly Leu Gln Ser Leu Thr
                                              -25
ctt cca gtg tct tgc agc cct tct gcc ctg atg ctt ccc ttg gga tgt      280
Leu Pro Val Ser Cys Ser Pro Ser Ala Leu Met Leu Pro Leu Gly Cys
-20                 -15                 -10                 -5
gct gtc cgc acg cgc atg ctt ga                                       303
Ala Val Arg Thr Arg Met Leu
                1
```

<210> 515
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 342..455

<221> sig_peptide
<222> 342..434
<223> Von Heijne matrix
score 4.40000009536743
seq LTTLESLAGSVXS/EQ

<400> 515

```
tcatatctgg waatggcaaa cagggatgaa aatcgattat gttttggaga ctcctttttgg    60
acatgtatca gtgtgttgat ttgcacaaac caataaaagc cctacatttt ttggaaatgg    120
atccctagat ttcaagcatg tataatcact caaagtggat atgatcacag gcattcttct    180
cttgagctca gcaaaactat gcctaccaac accgaagaga agtcaaagat tttatgaaa     240
aaaaattgca gatgatgttg gtgagataat aggatatgag caatgaaccc ttgggtgggg    300
ttccagggca cttaaattgc ctcgtgtctt gagtccttaa g atg gac tca aac aaa    356
                                             Met Asp Ser Asn Lys
                                                     -30
aaa tta gta tta tca ata aca ggt aat act gtg tgg att cta aca aca      404
Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val Trp Ile Leu Thr Thr
```

```
 -25                 -20                 -15
tta gaa tca tta gct ggc agt gtc aam tct gaa caa gat ttg tca gct     452
Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu Gln Asp Leu Ser Ala
-10                 -5                  1               5
tat                                                                 455
Tyr
```

<210> 516
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 196..360

<221> sig_peptide
<222> 196..336
<223> Von Heijne matrix
score 4.40000009536743
seq SFXXCLFLXLXXS/EM

<221> misc_feature
<222> 330..332
<223> n=a, g, c or t

<400> 516

```
aagagcgttg ggcagatata gtctgtagat atttttgaaa cgtctttggg tttgtcccat    60
ttggggtttg ctcagcttct tgaatctgta ggttttgggg atcccccamc ctgcaaattt   120
ggtgatattt ttgctcttat ttctkcaagt gaacttgaaa tcccaccctg ttggttttct   180
ccttctaaga ctctg atg acg tgt atg tta gcc tgt agg tgt agt ctc amg    231
                 Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa
                         -45                 -40
ggt ccc caa gat ttt cgt ttc tgc tct gtc ttt tct ctg ttg ctc aag     279
Gly Pro Gln Asp Phe Arg Phe Cys Ser Val Phe Ser Leu Leu Leu Lys
-35                 -30                 -25                 -20
ttg ggt aat ttc tat ttt tct ttt wct dtc tgt ctw ttt ctw dta ctd     327
Leu Gly Asn Phe Tyr Phe Ser Phe Xaa Xaa Cys Leu Phe Leu Xaa Leu
                -15                 -10                 -5
wyn nnt tct gag atg gag tcm cac tct ttc agc                         360
Xaa Xaa Ser Glu Met Glu Ser His Ser Phe Ser
            1               5
```

<210> 517
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 113..451

<221> sig_peptide
<222> 113..307
<223> Von Heijne matrix
score 4.40000009536743
seq FIEAALLIHGSAC/VY

<400> 517

```
atttcctgg gcgggaacag caaaatggcg ccagaactag tggcgggctg aggacgccgt     60
acccctcgga aggcagccct gcggtccctt tgccgcccgt tccctcccgg ac atg gag   118
                                                          Met Glu
```

```
                                                              -65
gac gtg gag gcg cgc ttc gcc cac ctc ttg cag ccc atc cgc gac ctc        166
Asp Val Glu Ala Arg Phe Ala His Leu Leu Gln Pro Ile Arg Asp Leu
                -60                 -55                 -50
acc aag aac tgg gag gtg gac gtg gcg gcc cag ctg ggc gag tat ctg        214
Thr Lys Asn Trp Glu Val Asp Val Ala Ala Gln Leu Gly Glu Tyr Leu
            -45                 -40                 -35
gag gag ctg gat cag atc tgc att tct ttt gac gaa ggc aag acc aca        262
Glu Glu Leu Asp Gln Ile Cys Ile Ser Phe Asp Glu Gly Lys Thr Thr
        -30                 -25                 -20
atg aac ttc att gag gca gcg ttg ttg atc cat ggc tct gcc tgc gtc        310
Met Asn Phe Ile Glu Ala Ala Leu Leu Ile His Gly Ser Ala Cys Val
-15                 -10                 -5                  1
tac agt aag aag gtg gaa tac ctc tac tca ctc gtc tac cag gcc ctt        358
Tyr Ser Lys Lys Val Glu Tyr Leu Tyr Ser Leu Val Tyr Gln Ala Leu
            5                   10                  15
gat ttc atc tct gga aag agg cgg gcc aag cag ctc tct tcg gtg cag        406
Asp Phe Ile Ser Gly Lys Arg Arg Ala Lys Gln Leu Ser Ser Val Gln
        20                  25                  30
gag gac agg gcc aat ggg gtt gca gct ccg ggg tcc cca gga ggc ag         453
Glu Asp Arg Ala Asn Gly Val Ala Ala Pro Gly Ser Pro Gly Gly
    35                  40                  45
```

<210> 518
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 185..244

<221> sig_peptide
<222> 185..229
<223> Von Heijne matrix
      score 4.40000009536743
      seq VSYLILTLLHVQT/AV

<400> 518

```
agtttcttc agaacagagg ctgagctcga agcgccgggc agtacagtga gggagagccg    60
agggaaccag cgcggtgcct agcggaactc cagggctgga atcccgagac acaagtgcat   120
ctgctagctg ttagcacttg gcagacggag ttctcctcta gggtagttct aactttgggt   180
aata atg ttt gtc agc tac ctg ata tta aca ttg ctc cac gtt caa aca    229
     Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr
     -15                 -10                 -5
gca gtg tta gca aga c                                               245
Ala Val Leu Ala Arg
1               5
```

<210> 519
<211> 275
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 96..275

<221> sig_peptide
<222> 96..170
<223> Von Heijne matrix
      score 4.40000009536743
      seq IFLLYFKFWGTCA/ER

<400> 519
```
ttgtttttta gaaaaatgaa taatttcttt ttatattatt ctgttacatt ttttccccac      60
ttaatagaac gtccagaaaa tctttgcatc tcaga atg cct gaa gct gcc ttg       113
                                       Met Pro Glu Ala Ala Leu
                                       -25             -20
ttc ttg ttt ttt tta ttc att ttt tta tta tac ttt aag ttc tgg ggt      161
Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu Tyr Phe Lys Phe Trp Gly
                -15                 -10                 -5
aca tgt gca gaa cgt gca ggt ttg tta cat agg tat act cgt gcc atg      209
Thr Cys Ala Glu Arg Ala Gly Leu Leu His Arg Tyr Thr Arg Ala Met
            1               5                   10
gag gtt tgc tgc acc cat caa cca tca tct aca tta ggt att tct cct      257
Glu Val Cys Cys Thr His Gln Pro Ser Ser Thr Leu Gly Ile Ser Pro
    15                  20                  25
aat gct ctc ctt ccc cta                                              275
Asn Ala Leu Leu Pro Leu
30                  35
```

<210> 520
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..180

<221> sig_peptide
<222> 91..159
<223> Von Heijne matrix
score 4.40000009536743
seq LCMHLSIHPXXCA/CI

<400> 520
```
gtctgagcgg cacagacgag atctcgatcg aaggcgagat ggcggacgtg ctagatcttc      60
acgaggctgg gggcgaagat ttcgccatgg atg agg atg ggg acg aga gca tcc     114
                                 Met Arg Met Gly Thr Arg Ala Ser
                                                 -20
ccg cct ctg tgc atg cat ctg tcc atc cat ccc cky mtc tgt gca tgc      162
Pro Pro Leu Cys Met His Leu Ser Ile His Pro Xaa Xaa Cys Ala Cys
-15                 -10                 -5                  1
atc tgt cca tcc atc cag gg                                           182
Ile Cys Pro Ser Ile Gln
            5
```

<210> 521
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 104..217

<221> sig_peptide
<222> 104..211
<223> Von Heijne matrix
score 4.40000009536743
seq XVCVCVCVCVCVC/VC

<221> misc_feature
<222> 145,151,174

```
<223> n=a, g, c or t


<400> 521
atttatgtag gcaggtggat gccaactgcc agtgcagggt ggcataagtt agcgttccaa      60
agttaagcta tggtgcattc caaatccatt cacacttagg aga atg tac cca aga       115
                                                Met Tyr Pro Arg
                                                    -35
gtg tgg gga tgt ttt caa tta ctg cat ttn ctt can bga aca aga acs       163
Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa Xaa Thr Arg Thr
        -30                 -25                 -20
aca ggt aag tnw gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt gtg tgt       211
Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys Val Cys Val Cys
    -15                 -10                 -5
gtg tgt g                                                             218
Val Cys
1

<210> 522
<211> 313
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..311

<221> sig_peptide
<222> 12..53
<223> Von Heijne matrix
      score 4.40000009536743
      seq AAVVLAATRLLRG/SG

<400> 522
ggagacgcaa g atg gcg gct gtg gtg ctg gcg gcg acg cgg ttg ctg cgg       50
             Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg
                             -10                 -5
ggc tcg ggt tct tgg ggc tgt tcg cgg ctg agg ttt gga cct cct gcg       98
Gly Ser Gly Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala
    1               5                   10                  15
tac aga cgg ttt agt agt ggt ggt gcc tat ccc aac atc ccc ctc tct       146
Tyr Arg Arg Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser
                20                  25                  30
tct ccc tta cct gga gta ccc aag cct gtt ttt gct aca gtt gat gga       194
Ser Pro Leu Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly
            35                  40                  45
cag gaa aag ttt gaa acc aaa gta acc aca ttg gat aat ggg ctt cgc       242
Gln Glu Lys Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg
        50                  55                  60
gtg gca tct cag aat aag ttt gga cag ttt tgt aca gta gga att ctt       290
Val Ala Ser Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu
    65                  70                  75
atc aat tca gga tcg aga tat ga                                        313
Ile Asn Ser Gly Ser Arg Tyr
80                  85

<210> 523
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

```
<222> 324..500

<221> sig_peptide
<222> 324..398
<223> Von Heijne matrix
      score 4.30000019073486
      seq ALYLSLNLYFANS/LY

<221> misc_feature
<222> 284,469..470,472
<223> n=a, g, c or t


<400> 523
gtctaggctc ttcaagttag gattcatatc tatgacatgt gctgtacagt gcttctactg    60
tgaggtagtc tcccagacag aaaccacatg ggccttcagg catagatggt cagtaaataa   120
ttactttaca gtggtgtcat ttcttaggag acmcagagtr agaccttaag tgagatctta   180
cctacctcct cccatccaat ctatccatac aaggttggac ctaaagcagc cttgagctta   240
ataatgatgt gtgttagaac aaggatactg agattagact aagntggttc tttaagtcag   300
ccgtctctga caaagggcac aca atg tac tgt ctg arg tgt gtg gag aaa ata   353
                          Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile
                          -25                 -20
gca aaa gct ctt tat ctc agc ctt aat tta tat ttt gca aat tca ctt     401
Ala Lys Ala Leu Tyr Leu Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu
-15                 -10                 -5                  1
tat tat atg tgt gtg tgt tca tac ata tac ttt tat tta tkt att tat     449
Tyr Tyr Met Cys Val Cys Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr
            5                   10                  15
ktk tat kkt tta ata aaa ann dng tct tat tat gtt gcc cag act ggt     497
Xaa Tyr Xaa Leu Ile Lys Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly
        20                  25                  30
ctc aa                                                              502
Leu

<210> 524
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 11..118

<221> sig_peptide
<222> 11..97
<223> Von Heijne matrix
      score 4.30000019073486
      seq SAVFLTAVFSSHS/WL

<400> 524
atctttgttg atg tgt cag ctc cgc agg ggt ttg ggg aaa cgg ccg ctg       49
           Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu
                           -25                 -20
agt gag gcg tcg gct gtg ttt ctc acc gcg gtc ttt tcc tcc cac tct      97
Ser Glu Ala Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser
    -15                 -10                 -5
tgg ctg gtt gga ccc cgc tat                                         118
Trp Leu Val Gly Pro Arg Tyr
1               5

<210> 525
<211> 276
<212> DNA
```

```
<213> Homo sapiens

<220>
<221> CDS
<222> 176..274

<221> sig_peptide
<222> 176..268
<223> Von Heijne matrix
      score 4.30000019073486
      seq LTFCLIDLSNVDS/GX

<400> 525
cctgagttct agtttgattg cactgtggtc tgagagacag tttgttataa tttctgttct     60
tttacgtttg ctgaggagag ctttacttcc aactatgtgg tcgattttgg aataggtgtg    120
gtgcggtgct gaaaaaaatg tatattctgt tgatttgggg tggagagttc tgtag atg     178
                                                             Met
tct gtt agg tcc act tgg tgc aga gct cag ttc aat tcc tgg gta tcc      226
Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val Ser
-30                 -25                 -20                 -15
ttg tta act ttc tgc ctc att gat ctg tct aat gtt gac agt ggg amg      274
Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly Xaa
                -10                  -5                   1
gg                                                                   276

<210> 526
<211> 366
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..366

<221> sig_peptide
<222> 103..261
<223> Von Heijne matrix
      score 4.30000019073486
      seq LRLTWLVAAGLEG/RV

<400> 526
tcactacttc tcccccggac tccttggtag tctgttagtg ggagatcctt gttgccgtcc     60
cttcgcctcc ttcaccgccg cagacccctt caagttctag tc atg gtg agt ggg       114
                                               Met Val Ser Gly
                                                           -50
gtt ccc tcg ggg ctg ggg aag agt gcg cgt ccc agg gga cgg cgg gcc      162
Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg Gly Arg Arg Ala
                -45                 -40                 -35
cgg aaa cta ctg cct gca cct cgg gcc gcg ccc agg aca gct cca gac      210
Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg Thr Ala Pro Asp
            -30                 -25                 -20
tac ccc ggg ccc ctc cgg tta acc tgg ctt gtg gcg gcc ggg ctg gaa      258
Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala Ala Gly Leu Glu
        -15                 -10                  -5
ggt cga gtt cac ttg gca gac acc agt tcg ggc cgg aaa acc tgg ccc      306
Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg Lys Thr Trp Pro
    1               5                  10                  15
ggg tgc ggc cat cag tgg aaa tgg aaa gcc ctc ttg atc cta gtg agg      354
Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu Ile Leu Val Arg
                20                  25                  30
gct ttc ccc gca                                                      366
Ala Phe Pro Ala
            35
```

```
<210> 527
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 316..426

<221> sig_peptide
<222> 316..408
<223> Von Heijne matrix
      score 4.30000019073486
      seq VCSSLRSXRPCWC/DG

<400> 527
catttcctaa tctctgcatt ttccagcaag taagtggtgg tgacttgttg ctttcaagta     60
tgttttgtct aaaattcata gatgctgaac tgtgtatatt tgttgtcaag tttgaaaggt    120
acttgggttt ttgggggtgt taggaggtag ggtggatgtt actattaaat acatttagac    180
tttttaaaat aagtgtaact gatcatttcc aacaaatatt tactatgtcc atacttgtgc    240
tccaaaagac aattctgtct tcctcttgag atacatgtct cggggcccct gtaggtctgg    300
tctgagaggg tcccc atg ggt ggc tgt gtc wgc tgg cgc ttt ctt gga cac     351
                 Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His
                     -30                 -25                 -20
tcc tct gct ctc agg act gtg tgt agc agt ctg cgc tca gya agg cca      399
Ser Ser Ala Leu Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro
                -15                 -10                  -5
tgt tgg tgt gat ggg ctt cgg ctc aga tg                               428
Cys Trp Cys Asp Gly Leu Arg Leu Arg
             1               5

<210> 528
<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..400

<221> sig_peptide
<222> 83..235
<223> Von Heijne matrix
      score 4.30000019073486
      seq STCLLRALSSELC/AP

<400> 528
gacacggaag tagctccgaa caggaagagg acgaaaaaaa taaccgtccg cgacgccgag     60
acaaaccgga cccgcaacca cc atg aac agc aaa ggt caa tat cca aca cag     112
                         Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln
                             -50                 -45
cca acc tac cct gtg cag cct cct ggg aat tcc agt ata ccc tca gac      160
Pro Thr Tyr Pro Val Gln Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp
    -40                 -35                 -30
ctt gca tct tcc tca ggc tcc acc cta tac cga tgc tcc acc tgc cta      208
Leu Ala Ser Ser Ser Gly Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu
-25                 -20                 -15                 -10
ctc aga gct cta tcg tcc gag ctt tgt gca ccc agg ggc tgc cac agt      256
Leu Arg Ala Leu Ser Ser Glu Leu Cys Ala Pro Arg Gly Cys His Ser
                -5                   1               5
ccc cac cat gtc agc cgc att tcc tgg acc ctc tct gta tct tcc cat      304
Pro His His Val Ser Arg Ile Ser Trp Thr Leu Ser Val Ser Ser His
```

```
        10                  15                  20
ggc cca gtc tgt ggc tgt tgg gcc ttt agg ttc cac aat ccc cat ggc      352
Gly Pro Val Cys Gly Cys Trp Ala Phe Arg Phe His Asn Pro His Gly
    25                  30                  35
tta tta tcc agt cgg tcc cat cta tcc amc tgg ctc cac agt gct ggt      400
Leu Leu Ser Ser Arg Ser His Leu Ser Xaa Trp Leu His Ser Ala Gly
40                  45                  50                  55
```

<210> 529
<211> 244
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 68..244

<221> sig_peptide
<222> 68..133
<223> Von Heijne matrix
score 4.30000019073486
seq LFFETGSPSVAQS/GV

<400> 529
```
cttacagagt taataagcat caaagaactt actgaaggac tttataaatt aaataccatt     60
atgtaga atg gtg gtg gtt agt gcc ttt att tat tta ttt ttt gag aca      109
        Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr
                -20                 -15                 -10
ggg tct ccc tct gtc gcc cag tct gga gtg cag tgg tgt gat ctc ggc      157
Gly Ser Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly
                -5                  1                   5
tta ctg cag cct ccg cct cct gga ttc aag cga ttc tct tgc ctc agc      205
Leu Leu Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser
    10                  15                  20
ctc cta ggt agb drg gat tgc aga cgt gcg cca ccc ggg                  244
Leu Leu Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro Gly
25                  30                  35
```

<210> 530
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..432

<221> sig_peptide
<222> 124..195
<223> Von Heijne matrix
score 4.30000019073486
seq LXFLGMFLSGMVA/QI

<400> 530
```
ggsctttgga ttggawagag gagctgggca ggaggcaggg caaggagaaa gctgttcggg     60
ggtcttgtct ggattttggt tgcctcctcc aatgttcctc tacctctact acaaggatgg    120
gtc atg ttt gtg tct gka aca rcg ttt ttc ttt kcg ctc ckc ttt ctg      168
    Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu
                    -20                 -15                 -10
ggc atg ttc ctc tct ggc atg gtg gct caa att gat gct aac tgg aac      216
Gly Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn
                -5                  1                   5
ttc ctg gat ttt gcc tac cat ttt aca gta ttt gtc ttc tat ttt gga      264
```

```
Phe Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly
        10                  15                  20
gcc ttt tta ttg gaa gca gca gcc aca tcc ctg cat gat ttg cat tgc      312
Ala Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys
    25                  30                  35
aat aca acc ata acc rgg cag cca ctc ctg agt gat aac cag tat aac      360
Asn Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn
40                  45                  50                  55
ata aac gta gca gcc tca att ttt gcc ttt atg acg aca gct tgt tat      408
Ile Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr
                60                  65                  70
ggt tgc agt ttg ggt ctg gct tta cg                                   434
Gly Cys Ser Leu Gly Leu Ala Leu
            75
```

<210> 531
<211> 406
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 284..406

<221> sig_peptide
<222> 284..361
<223> Von Heijne matrix
score 4.30000019073486
seq AXYLLVGLFPLKC/HX

<221> misc_feature
<222> 384
<223> n=a, g, c or t

<400> 531

```
taatatatgt magaatagca gggaccatgt cttctgttca atatkgtatc ctgagcacct     60
agtatttaag taggtatttc agtaaataat gtaacatata taataaataa tattaatatt    120
tgttgactaa atgaatttag gtctggacct tgatggctta atgtctttct aaaaatctac    180
ttccatatct aagcctttct tgactacttt cgccttttc tgtgaactta aaagtcttta     240
ttcattgttt gccggatgct aaacatttac aaaagtaatc ctt atg tca tct gaa      295
                                                Met Ser Ser Glu
                                                        -25
att ttc taw ktt dtk cak att gck tat gct tda tat ttg cta gtt ggt      343
Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr Leu Leu Val Gly
        -20                 -15                 -10
ctt ttc cct cta aaa tgc cac wag agt hat ttt tct aag tna caa atc      391
Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser Lys Xaa Gln Ile
    -5                  1               5                   10
tca tca ttt gtg gaa                                                  406
Ser Ser Phe Val Glu
                15
```

<210> 532
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..211

<221> sig_peptide

<222> 23..76
<223> Von Heijne matrix
score 4.30000019073486
seq LTVTLGRLASACS/HS

<400> 532
```
gtttccggcc gaggctgcgg cc atg gca gca tct tcc ctg acg gtc acc tta      52
                         Met Ala Ala Ser Ser Leu Thr Val Thr Leu
                                     -15                 -10
ggg cgg ctg gcg tcc gcg tgc agc cac agc atc ctg aga cct tcg ggg      100
Gly Arg Leu Ala Ser Ala Cys Ser His Ser Ile Leu Arg Pro Ser Gly
            -5                  1               5
ccc gga gca gcc tcc ctt tgg tct gct tct cga agg ttc aat tca cag      148
Pro Gly Ala Ala Ser Leu Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln
    10                  15                  20
agc act tca tat cta cca gga tat gtt cvt aaa aca tcc ctg agt tca      196
Ser Thr Ser Tyr Leu Pro Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser
25                  30                  35                  40
cca cct tgg ccg agg g                                                212
Pro Pro Trp Pro Arg
                45
```

<210> 533
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..147

<221> sig_peptide
<222> 76..129
<223> Von Heijne matrix
score 4.30000019073486
seq CICSCLFFSQYLX/XS

<400> 533
```
tataggtgat tataatcaag tgtaggcttc ctgaattttg acatcctttt agaacttggg      60
tctggaattc cagaa atg tta att gct gct tgt att tgt tct tgt ttg ttt      111
                 Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe
                             -15                 -10
ttt agc cag tat ttg gsy ytt tct aat cca gcc gcg gg                   149
Phe Ser Gln Tyr Leu Xaa Xaa Ser Asn Pro Ala Ala
    -5                  1               5
```

<210> 534
<211> 145
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..145

<221> sig_peptide
<222> 56..103
<223> Von Heijne matrix
score 4.30000019073486
seq WVLSYMWQSASLG/FS

<400> 534
```
tgggctactc atggywagat aagacttaca cttctgaaag aggccttaga gtttc atg      58
```

```
                                                           Met
aag tgc tgg gtt ctc agc tac atg tgg cag agt gca tct ctg ggt ttt      106
Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly Phe
-15                 -10                 -5                   1
agt aac agg att aaa tct mac ttg aga cct cca gca ggc                  145
Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly
            5                   10
```

<210> 535
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 81..383

<221> sig_peptide
<222> 81..287
<223> Von Heijne matrix
score 4.30000019073486
seq GIRLSCVLSHLQA/WD

<400> 535

```
aaatcctcag cagatttttg ttcaagagct gcttccagat tggcttctag ctgccagtgt     60
gaccttgggc agaaccttca atg tct gtg ggg ctg tgt ttt ctt atc tgg caa   113
                      Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln
                                      -65                 -60
atg gga att atg cts ttg cct cgg gaa tgt tgg aag gtc aaa gac agt      161
Met Gly Ile Met Leu Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser
            -55                 -50                 -45
aag aag tac aaa agc tgc aga gaa tca gta ctg cct gca caa gca tgt      209
Lys Lys Tyr Lys Ser Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys
        -40                 -35                 -30
aca gga gag tcc cct gtc tta tct gga gtc agg gtt ctg ggg atc cgc      257
Thr Gly Glu Ser Pro Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg
    -25                 -20                 -15
ctc tcg tgc gtg tta tcc cat ctc caa gcc tgg gac tcc tgg gac aat      305
Leu Ser Cys Val Leu Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn
-10                 -5                  1               5
cag aag gtg tgc tac ctg ggt gca ccc tgc ttt ggg aaa agg ctg agt      353
Gln Lys Val Cys Tyr Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser
            10                  15                  20
cca acc acc tgg ctc act ttt tgg gtg gga c                            384
Pro Thr Thr Trp Leu Thr Phe Trp Val Gly
        25                  30
```

<210> 536
<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..206

<221> sig_peptide
<222> 78..119
<223> Von Heijne matrix
score 4.30000019073486
seq FAFLAGCSGSCLW/SR

<400> 536

```
aactttaccc agatatacta tatgccaaac aatgtttgtc accagggata ccacaacaga     60
aaacaaatac actaaaa atg ttc gct ttc ctg gcc ggg tgc agt ggc tca      110
                   Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser
                                   -10                 -5
tgc ctg tgg tcc cgg cac ttc ggg aga ctg cgg cgg gcg gct ccc ttg      158
Cys Leu Trp Ser Arg His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu
            1               5                  10
agc cca gag ttt gag acc ggc ctg ggt aac atg gtg gaa ccc caa tgg g    207
Ser Pro Glu Phe Glu Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
    15                  20                  25
```

<210> 537
<211> 394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 268..393

<221> sig_peptide
<222> 268..318
<223> Von Heijne matrix
score 4.30000019073486
seq FLFVPHLISCNWC/EP

<400> 537

```
ttagcaaatc acagatgaag gtctcattac tatatgcaga gggtgccata agttacaatc     60
cctttgtgcc tctggctgct ccaacatcac agatgccatc ctgaatgctc taggtcagaa    120
ctgcccacgg cttaggtaaa catttcttgt ttagctcaaa aaatcatag aacaaaagtt    180
tccttcaccc atatttcttc cttggaactt tggaatttta aggtaggcac tgcagacgct    240
ttgaaatttt aaggtagtcc cttttag atg ccc acc tac ttc ctt ttt gta cct    294
                              Met Pro Thr Tyr Phe Leu Phe Val Pro
                                          -15                 -10
cat ttg att tca tgt aat tgg tgt gaa cca agg ggt aac aat ccc caa      342
His Leu Ile Ser Cys Asn Trp Cys Glu Pro Arg Gly Asn Asn Pro Gln
            -5                  1               5
att cca cta ctt gct atc cat act aga aaa aag aat caa cat ttt att      390
Ile Pro Leu Leu Ala Ile His Thr Arg Lys Lys Asn Gln His Phe Ile
    10                  15                  20
act t                                                                394
Thr
25
```

<210> 538
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 237..413

<221> sig_peptide
<222> 237..317
<223> Von Heijne matrix
score 4.30000019073486
seq LTSVSLXXXXXXG/SV

<221> misc_feature
<222> 308..309,375
<223> n=a, g, c or t

<400> 538
gaatcctcgc aaagaattgg caatgtcgtt gcctttctct ggcggaaggc tggcwactac 60
cctttgaatt tggaatgtat gtcacacagt tctagagtag aatgcaaact cagcactgtc 120
ctctttgaac caaaatgtct ccaaaaacaa gattctaatt tatacttaat atttccccca 180
gaagcccaat cattaaagcc acctttccag gaacagaagt gttttgaca ctgtga atg 239
Met
ctt tgg acc agt ttc cag aat cct ctt cag gta gtg ctt ctc acc agc 287
Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr Ser
-25 -20 -15
gtt tcc ctt ttd aww wtg gbn ndc mta ggt tca gtc cga atc awk cta 335
Val Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa Leu
-10 -5 1 5
tct cac tgg tca agc tca gcc ttc ttc ttc ctd att cwb nck kyw hwt 383
Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa Xaa
10 15 20
ctt tca cat gtg aca aaa caa atg cat ttg aa 415
Leu Ser His Val Thr Lys Gln Met His Leu
25 30

<210> 539
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..158

<221> sig_peptide
<222> 66..107
<223> Von Heijne matrix
score 4.30000019073486
seq LTCLCGCFIVLLV/CV

<400> 539
tacattcaag gttagtattg atatgcatgt atttgatcct gtcattgtgt tgttagctgt 60
ttatt atg ctg act tgt ttg tgt ggt tgc ttt ata gtg tta ctt gtc tgt 110
Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys
-10 -5 1
gta ctt aaa tgt gtt ttt gta gtg gct agt aat ggc ctt ttc ttt cct 158
Val Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
5 10 15
tt 160

<210> 540
<211> 327
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..326

<221> sig_peptide
<222> 207..293
<223> Von Heijne matrix
score 4.30000019073486
seq HLSILAFVAIAFG/VL

<400> 540
cattttttc atgtgttttt ttggctgcat aaatgtcttc ttttgagaag tgtctgttca 60
tgtccctcgc ccacttttg atggggttgt ttgtttttt cttgtaaatt tgtttgagtt 120

```
cattgtagat tctggatatt agccctttgt cagatgagta ggttgcgaaa attttctccc   180
atgttgtagg ttgcctgttc actctg atg gta gtt tct ttt gct gtg cag aag    233
                             Met Val Val Ser Phe Ala Val Gln Lys
                                             -25
ctc ttt agt tta att aga tcc cat ttg tca att ttg gct ttt gtt gcc     281
Leu Phe Ser Leu Ile Arg Ser His Leu Ser Ile Leu Ala Phe Val Ala
-20                 -15                 -10                 -5
att gct ttt ggt gtt ttg gac atg aag tcc ttg ccc acg cca ggg g       327
Ile Ala Phe Gly Val Leu Asp Met Lys Ser Leu Pro Thr Pro Gly
                1               5                  10
```

<210> 541
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..395

<221> sig_peptide
<222> 84..278
<223> Von Heijne matrix
score 4.30000019073486
seq FFSRLGATSVXRA/CT

<221> misc_feature
<222> 271,328,344..345,347
<223> n=a, g, c or t

<400> 541
```
cttctgcact cacagccgaa ggaaagcagc aggttggggc ttcttgtggc caacttcaga    60
gcctgtcacc aggaaaggta agc atg gga gga agg aag atg gcg aca gat gaa   113
                          Met Gly Gly Arg Lys Met Ala Thr Asp Glu
                          -65                 -60
gaa aat gtc tat ggt tta gaa gag aac gct cag tcc cgg cag gag tcc     161
Glu Asn Val Tyr Gly Leu Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser
-55                 -50                 -45                 -40
acg cgg agg ctc atc ctt gtt ggg aga aca ggg gcc ggg aag agc gcc     209
Thr Arg Arg Leu Ile Leu Val Gly Arg Thr Gly Ala Gly Lys Ser Ala
                -35                 -30                 -25
act ggg aac agc atc ctg ggc cag aga cgg ttc ttc tcc agg ctg ggg     257
Thr Gly Asn Ser Ile Leu Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly
            -20                 -15                 -10
gcc acg tct gtg anc agg gcc tgc acc acg grh agc cgc agg tgg gac     305
Ala Thr Ser Val Xaa Arg Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp
        -5                  1               5
aag tgc cac gtg gaa gtc gtr gnd ctm gga cat vwk can nmn ggg aag     353
Lys Cys His Val Glu Val Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys
10                  15                  20                  25
tgt cca aga cag atc ctg gct gtg agg aga gag gtc act gct a           396
Cys Pro Arg Gln Ile Leu Ala Val Arg Arg Glu Val Thr Ala
                30                  35
```

<210> 542
<211> 247
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..247

<221> sig_peptide
<222> 8..100
<223> Von Heijne matrix
      score 4.30000019073486
      seq ALALTXTLLPAPG/EH

<221> misc_feature
<222> 78,182,194
<223> n=a, g, c or t

<400> 542
```
atcaata atg cag ctt caa gtt ctg ggg aga ccg cag ggg gcc ccc cag       49
        Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln
            -30                 -25                 -20
ctg gct ccc cag gcc ttg gct cta act bnk acc ctc ctc cca gcc cca       97
Leu Ala Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro
    -15                 -10                 -5
gga gaa cac gat tck ccr atg stc att ggc cag ttt ccc cwa aac cct      145
Gly Glu His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro
  1               5                  10                  15
ccc tcc gag cac ccg ggc gcc agt ccc agg cgg wmr ngg acg ggc tgg      193
Pro Ser Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp
                20                  25                  30
nra ccc caa agc tgg gac cgg agg gtg agc ccg gca gag gca gag aca      241
Xaa Pro Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr
            35                  40                  45
cgc agg                                                              247
Arg Arg
```

<210> 543
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..221

<221> sig_peptide
<222> 87..209
<223> Von Heijne matrix
      score 4.30000019073486
      seq HLFTLGFLCSLCP/HP

<221> misc_feature
<222> 154
<223> n=a, g, c or t

<400> 543
```
tgctatgttc aatcttgtac aggtcttttg tggacatatg gtctcactcc tcttaggtat     60
ataccgagta gtgaaactgc caggtc atg gga gta tac acg tgt cca att ttt     113
                             Met Gly Val Tyr Thr Cys Pro Ile Phe
                                     -40                 -35
gtg cat tac tac gag aac cat gga cca acc ccw agt ttc cnt gcc ttt      161
Val His Tyr Tyr Glu Asn His Gly Pro Thr Pro Ser Phe Xaa Ala Phe
        -30                 -25                 -20
att tcc ttt cat cta ttt act ttg ggc ttt ctt tgt tcc cta tgc ccc      209
Ile Ser Phe His Leu Phe Thr Leu Gly Phe Leu Cys Ser Leu Cys Pro
    -15                 -10                 -5
cac ccc cac ggg                                                      221
```

```
His Pro His Gly
1

<210> 544
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 307..375

<221> sig_peptide
<222> 307..354
<223> Von Heijne matrix
      score 4.30000019073486
      seq SVSCCSSLWVSLS/KD

<221> misc_feature
<222> 302
<223> n=a, g, c or t


<400> 544
tcaatggaag aaggagwaaa aagagaagag gaaaatggga ccaatactgc tgatcatgtt      60
cgaaattcca gttgggcaaa aaacggctcc taccaaggtg ctcttcataa cgcctctgaa     120
gaagccacag aacaaaacat acgagctggt acccaggcag ttttgcaggt ggatcacttt     180
atggctattt ttaaaaataa aataatcatt aaatatttct gttcagtatt tcagtataca     240
gtatactttt cacaatataa aaatagaagc ttaatactgg gcattcatac tttttaaaga     300
gnatga atg aag aaa tcg gtt tcc tgc tgt agt tct cta tgg gta agt        348
       Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser
           -15                 -10                 -5
ctt agt aaa gac gag aat gct gaa atg                                   375
Leu Ser Lys Asp Glu Asn Ala Glu Met
        1               5

<210> 545
<211> 376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 260..376

<221> sig_peptide
<222> 260..349
<223> Von Heijne matrix
      score 4.30000019073486
      seq TVLLSGSPRAVVS/AV

<400> 545
tagtggacag cccaagctgc ttctcttaga atggctgtgg cttcacaagt gatgagaaga      60
gcatgcgctt gatttcagat ccccattaca agctcataat gaatgagtca caggagaaag     120
gtgrgacttg gggccctttc gtgcctgatg ggaagctcct gcmaccccgg ggagcccctc     180
cagactgtcc ttgcccacct ggctgcactg gcctctttat gccaacccag tgaggacagg     240
ttctgaggga cctggacag atg ctg ctg ccc cta gcc atg gct gga cga tgt      292
                     Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys
                     -30                 -25                 -20
tat aca gcc aag cac agc acw gtg ctg ctc tca gga agc cca agg gct       340
Tyr Thr Ala Lys His Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala
            -15                 -10                 -5
gtg gtc agt gca gtg gtg atg gtg ggc aca ggg tgc                       376
```

```
Val Val Ser Ala Val Val Met Val Gly Thr Gly Cys
            1                   5

<210> 546
<211> 109
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..107

<221> sig_peptide
<222> 30..86
<223> Von Heijne matrix
      score 4.30000019073486
      seq LRAFLLSVPLGKG/SA

<400> 546
cccacagcct tccctggtgt gcctgcagt atg cca tcc tgc tgc tac ctt agg        53
                                Met Pro Ser Cys Cys Tyr Leu Arg
                                                -15
gct ttt ctg ctc tct gtc cct ctg ggg aaa ggc tca gcc ctt aag gat       101
Ala Phe Leu Leu Ser Val Pro Leu Gly Lys Gly Ser Ala Leu Lys Asp
    -10                 -5                  1               5
ccc gtg ct                                                            109
Pro Val

<210> 547
<211> 306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 3..305

<221> sig_peptide
<222> 3..74
<223> Von Heijne matrix
      score 4.19999980926514
      seq LLLSSLWIVCCLH/LD

<400> 547
at atg gtt gct gac aag gag gtg cag aca agg acc ctc ttg ctt tcc        47
   Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser
                -20                 -15                 -10
tca cta tgg ata gtc tgt tgc ctc cat cta gat tct ctt att tca rrr        95
Ser Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa
                -5                  1               5
aaa tat cct ctc cat gca att agg aga tat tta tcg acg ctg aga aac       143
Lys Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu Arg Asn
        10                  15                  20
caa aga gcc gaa gaa cag gtt gca cgt ttt caa aaa ata cct aat ggt       191
Gln Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro Asn Gly
    25                  30                  35
gaa aat gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa       239
Glu Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu
40                  45                  50                  55
tta cca gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat       287
Leu Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn
                60                  65                  70
ggt cta aaa caa tgt gaa g                                             306
```

```
Gly Leu Lys Gln Cys Glu
            75

<210> 548
<211> 148
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..148

<221> sig_peptide
<222> 89..130
<223> Von Heijne matrix
      score 4.19999980926514
      seq HICLFFSFSXXFX/LF

<400> 548
aggatagctg aaaggagttc atctaactgg agtcccacta gaagtaagaa acccctattg    60
tttatttttt aataatgtaa tttttatt atg cat att tgt ctt ttt ttt tct      112
                               Met His Ile Cys Leu Phe Phe Ser
                                               -10
ttt tct ttw wct ttt tkt ctt ttc ttt ttt ttt ttt                     148
Phe Ser Xaa Xaa Phe Xaa Leu Phe Phe Phe Phe Phe
    -5                  1               5

<210> 549
<211> 374
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 240..374

<221> sig_peptide
<222> 240..296
<223> Von Heijne matrix
      score 4.19999980926514
      seq ILARLCRMQTCWC/LS

<400> 549
tacattcggc ccggccatgg cagcggcgcc cctgaaagtg tgcatcgtgg gctcggggaa    60
ctggggttca gctgttgcaa aarkrattgg taataatgtc aagaaacttc agaaatttgc   120
ctccacagtc aagatgtggg tcttttraar aaamcrgkkr akkggcagra aactgacaga   180
catcataaat aatgaccatg aaaatgtaaa atatcttcct ggacacaagc tgccagaaa    239
atg tgg ttg cca tgt caa atc tta gcg agg ctg tgc agg atg cag acc     287
Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr
                -15                 -10                 -5
tgc tgg tgt ttg tca ttc ccc acc agt tca ttc aca gaa tct gtg atg     335
Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met
            1               5                   10
aga tca ctg gga gag tgc cca aga aag cgc tgg ggg ggg                 374
Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly
    15                  20                  25

<210> 550
<211> 476
<212> DNA
<213> Homo sapiens

<220>
```

<221> CDS
<222> 147..476

<221> sig_peptide
<222> 147..398
<223> Von Heijne matrix
score 4.19999980926514
seq VTILVSLALAFLA/CI

<400> 550
```
agacacacgc gaggcgctgt cctttcagca ccacaagctc gggctgagga gggaggactc      60
ctggccgtcc tcctcckctt caaattggct tgaatctgct ctgaccccc acgagtgcag       120
cacagtctgg gaagaaaggc gtaagg atg gwg aag ctg arc agt aac ccc agc       173
                             Met Xaa Lys Leu Xaa Ser Asn Pro Ser
                                             -80
gag aag gga acc aag ccg cct tca gtt gag gat ggc ttc cag acc gtc        221
Glu Lys Gly Thr Lys Pro Pro Ser Val Glu Asp Gly Phe Gln Thr Val
-75                 -70                 -65                 -60
cct ctc atc act ccc ttg gag gtt aat cac tta cag ctg cct gct cca        269
Pro Leu Ile Thr Pro Leu Glu Val Asn His Leu Gln Leu Pro Ala Pro
                -55                 -50                 -45
gaa aag gtg att gtg aag aca aga acg gaa tat cag ccg gaa cag aag        317
Glu Lys Val Ile Val Lys Thr Arg Thr Glu Tyr Gln Pro Glu Gln Lys
            -40                 -35                 -30
aac aaa ggg aag ttc cgg gtg cca aaa atc gct gaa ttt acg gtc acc        365
Asn Lys Gly Lys Phe Arg Val Pro Lys Ile Ala Glu Phe Thr Val Thr
        -25                 -20                 -15
atc ctt gtc agc ctg gcc cta gct ttc ctt gcg tgc atc gtg ttc ctg        413
Ile Leu Val Ser Leu Ala Leu Ala Phe Leu Ala Cys Ile Val Phe Leu
    -10                 -5                  1               5
gtg gtt tac aaa gcc ttc acc tat gat cac agc tgc cca gag gat tcg        461
Val Val Tyr Lys Ala Phe Thr Tyr Asp His Ser Cys Pro Glu Asp Ser
                10                  15                  20
tct atr agc acc ggg                                                    476
Ser Xaa Ser Thr Gly
            25
```

<210> 551
<211> 231
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..229

<221> sig_peptide
<222> 77..139
<223> Von Heijne matrix
score 4.19999980926514
seq EVLSLLFXCIYWG/QY

<400> 551
```
catcctcatc ttcttcctct cttgttactt tggatatttg ctgaaaggtc gtcagttgct      60
ccacacaact tataaa atg ttc ats gcc gca gca gga gta gag gtc ctg agc      112
                  Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser
                      -20                 -15                 -10
ctc cta ttt tkc tgc atc tac tgg ggt caa tat gcc acc gat ggc att        160
Leu Leu Phe Xaa Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile
                -5                  1               5
ggc aac gag agt gtg aag atc ttg gcc aag ctg ctc ttc tcc tcc agc        208
Gly Asn Glu Ser Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser
        10                  15                  20
```

```
ttc ctc atc ttc ctg ctg atg gg                                       231
Phe Leu Ile Phe Leu Leu Met
    25                  30

<210> 552
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..229

<221> sig_peptide
<222> 125..202
<223> Von Heijne matrix
      score 4.19999980926514
      seq FLSFLSFFFFSFF/LF

<400> 552
agtttcactc cgaaagtsct tcttacagag caactccaag gatgggctga aaagcacata     60
gagaaaatgg aacagtgcga agttggaagg tccgtgcggg tggcagcgcc agtgtgggga    120
tgag atg ctc aca gga cgg ttt tta ggc ggc tca caa ggg ttt ttt ctt     169
     Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu
         -25                 -20                 -15
tct ttt ctt tct ttc ttt ttt ttt tcc ttt ttc ctt ttc ctt yct ttt      217
Ser Phe Leu Ser Phe Phe Phe Phe Ser Phe Phe Leu Phe Leu Xaa Phe
    -10                 -5                  1               5
ttt ttt ttt ttt                                                      229
Phe Phe Phe Phe

<210> 553
<211> 232
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 110..232

<221> sig_peptide
<222> 110..193
<223> Von Heijne matrix
      score 4.19999980926514
      seq FVFMSKLLLFSFS/FL

<400> 553
acgatcagat ctgakragaa ttgagccccc aaaagcagtt atcagactat ttgaaataaa     60
gatttatatt cacctttaat aacaatgtac cattaataac acatattac atg ttt att    118
                                                      Met Phe Ile
tkr taw rak atg aaa cag wcr ttt cat att ata gac ttt gtt ttc atg      166
Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe Val Phe Met
-25                 -20                 -15                 -10
agt aaa ctt tta tta ttt tca ttt tca ttt tta ara aaa gcr cgc atg      214
Ser Lys Leu Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys Ala Arg Met
                -5                  1               5
awt aca gca gca cct ggg                                              232
Xaa Thr Ala Ala Pro Gly
        10

<210> 554
<211> 141
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 31..141

<221> sig_peptide
<222> 31..84
<223> Von Heijne matrix
score 4.19999980926514
seq HILTAVLPLVSHQ/QN

<400> 554
```
ttacattcct cacttctagt ggtttgatta atg gtc aca cca gta cac atc ctg      54
                                 Met Val Thr Pro Val His Ile Leu
                                             -15
aca gcc gtg ctt cca ctt gtg tct cac cag caa aac cat ctg ggt gga      102
Thr Ala Val Leu Pro Leu Val Ser His Gln Gln Asn His Leu Gly Gly
-10                 -5                  1               5
agg ttt gca tct ctg gga tcc tca ggc att agg cac ggg                  141
Arg Phe Ala Ser Leu Gly Ser Ser Gly Ile Arg His Gly
            10                  15
```

<210> 555
<211> 376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 319..375

<221> sig_peptide
<222> 319..363
<223> Von Heijne matrix
score 4.19999980926514
seq ILHLATLLNLFIS/SN

<221> misc_feature
<222> 144..145,202,276..277
<223> n=a, g, c or t

<400> 555
```
ttctatttct gtgaagaatg tcacagaatg cagtctacat attgcataga atctgtagat    60
tgcattgggt agcatggaca ttttaacaat attgattctt ccaattcatg aacatgaaat   120
atctttccat tttttgaggt ctanncaatc tcttttatca gtgtktccta attctgatta   180
tagagatctt tcacatcttt gnttcaagtt gattcctacg tatttcactt tatttgtggc   240
tgttgtaaat gggattactt tttgcatttc tttchnnsaa ttgttcagtc agcatacagg   300
aatgatactg atttttgt atg ttg att tta cat ctt gca act tta cta aat      351
                    Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn
                    -15                 -10                 -5
ttg ttt atc agt tct aac agt ttt g                                    376
Leu Phe Ile Ser Ser Asn Ser Phe
                1
```

<210> 556
<211> 279
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

```
<222> 199..279

<221> sig_peptide
<222> 199..243
<223> Von Heijne matrix
      score 4.19999980926514
      seq LASFGPFRSSCFA/AR

<400> 556
cccttgttac tgctacccat cctacctgca ccctgctttt tccctcttgs cacgcttttt    60
ttcctctccc tcttaccccc accctgtaca aaatgcataa aggatggaaa aactactgca   120
gccagaagtc tttgaatgag gcatcaatgg atgaatattt aggcagctta gggctgtttc   180
gaaagctgac tgccaagg atg cct ctt gcc tct ttc ggg cca ttt cgg agc     231
                    Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser
                    -15                 -10                 -5
agt tgt ttt gca gcc agg tcc atc att tgg aaa tca gga agg caa ggg     279
Ser Cys Phe Ala Ala Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly
                1               5                   10

<210> 557
<211> 340
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 233..340

<221> sig_peptide
<222> 233..325
<223> Von Heijne matrix
      score 4.19999980926514
      seq FLLSFLSFRSPLC/HH

<400> 557
caaagaaatt agtggctaaa cgtagagaaa ttaagatgaa ggaactggca catggagcca    60
ctgtgtacta taaagtattt ttattggtat ttagtcttgc tgttattgtt gctaatgatt   120
gtattgaata attaccagct gttgttagtt atttgaaatt aggtgcctaa agcaacctct   180
catcttgcag aaagtcatct ttcttgaaac tttttaaaaa cttgcttgaa ac atg gag   238
                                                          Met Glu
                                                              -30
act tgg aat ggg acg tct atc ata gta gca cat ctg ara tcc ttc tca     286
Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser Phe Ser
            -25                 -20                 -15
ttc ctg ctg tca ttt ctg tcc ttt cgc agt cca ctt tgt cac cac ccc     334
Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His His Pro
        -10                 -5                  1
ctc ggg                                                             340
Leu Gly
    5

<210> 558
<211> 365
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 288..365

<221> sig_peptide
<222> 288..329
<223> Von Heijne matrix
```

score 4.19999980926514
seq QFLSLIFASCSST/TP

<400> 558
acatttgcaa ccttggccat ctgtccagaa cctgctccca cctcaggccc aggccaaccg 60
tgcactgctg caatgggctc tgagctggag acggcgatgg agaccctcat caacgtgttc 120
cacgcccact cgggcaaaga gggggacaag tacaagctga gcaagaagga gctgaaagag 180
ctgctgcaga cggagctctc tggcttcctg gatgtgaaag agcttatgct gtaggcaaca 240
gaagccctca agacttttga ggaggcctag aagagtccca taattca atg cag ttc 296
Met Gln Phe
ctc tcg ctc atc ttt gcc tcc tgc tcc tca acc acc ccc tta cct ctg 344
Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro Leu Pro Leu
-10 -5 1 5
amt cag tgc tgt acc ctt ccc 365
Xaa Gln Cys Cys Thr Leu Pro
10

<210> 559
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 103..354

<221> sig_peptide
<222> 103..261
<223> Von Heijne matrix
score 4.19999980926514
seq VLALVCHSASISV/FP

<400> 559
aatattataa tgaggctctg caggggcttg aacttaggtc cctgtaaggg agctactgtt 60
ccctggtatg acccactcta gctgagctgt gcagagactg ag atg gtc acc tca 114
Met Val Thr Ser
-50
aag agc agg gga ccc ckt gtc cag act ctg ggg cat gct ggc aac ctg 162
Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His Ala Gly Asn Leu
-45 -40 -35
agg agt ctg cgg gag tgg cct gat ctg tgc tgc ttg agg ctt ttt gtc 210
Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu Arg Leu Phe Val
-30 -25 -20
cca gat cac act gta ctt gct ctg gtg tgc cac agc gca tcc atc tct 258
Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser Ala Ser Ile Ser
-15 -10 -5
gtc ttc cct tct cag gtc acc tgc aga ctc cca agg aca ggg tca cat 306
Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg Thr Gly Ser His
1 5 10 15
ccc atc tgc gtc atc tct caa ggt gcc ttt cac gat cct cac cca aat 354
Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp Pro His Pro Asn
20 25 30

<210> 560
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 168..326

<221> sig_peptide

<222> 168..248
<223> Von Heijne matrix
score 4.19999980926514
seq RLVVLFASPXVRP/AS

<221> misc_feature
<222> 230
<223> n=a, g, c or t

<400> 560
attaagggac aataatggcc gctttcaagg tgtggatttt ggctccttga gcctgtctga 60
gcgaggggtg gcagcgccgg cgccccagaa tccgggacag aaagggtcbc aagagtcgcg 120
cttggtgmga gaaatcccag atcctgtgat gggggacacc agtgagg atg cct cga 176
Met Pro Arg
-25
tcc atc gat ksg aag gca ctg atc tgg act gtc agg ttg gtg gtc tta 224
Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu Val Val Leu
-20 -15 -10
ttt gcn agt cca awa gtg cgg cca gcg agc agc atg tct tca agg ctc 272
Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser Ser Arg Leu
-5 1 5
ctg ctc ccc gsc ctt cat tac tcg gac tgg act tgc tgg ctt cct gaa 320
Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp Leu Pro Glu
10 15 20
cgg aga ga 328
Arg Arg
25

<210> 561
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 69..341

<221> sig_peptide
<222> 69..230
<223> Von Heijne matrix
score 4.19999980926514
seq TVVFLTLLSVVIL/IF

<221> misc_feature
<222> 270..272,321..322
<223> n=a, g, c or t

<400> 561
ccttcaccag cagcccgtcc gactggaaag atctgcctct tctccaagaa actcaaccac 60
tagtgaca atg acc agc ctc ctg act act cct tct cca aga gaa gaa ctg 110
Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu
-50 -45
atg acc acc cca att tta cag ccc act gag gcc ctg tcc cca gaa gat 158
Met Thr Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp
-40 -35 -30 -25
gga gcc agc aca gca ctc att gca gtt gtt atc acc gtt gtc ttc ctc 206
Gly Ala Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu
-20 -15 -10
acc ctg ctc tcg gtc gtg atc ttg atc ttc ttt tac ctg tac aag aac 254
Thr Leu Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn
-5 1 5

```
aaa ggc agc tac gtm nnn tat gaa cct aca gaa ggt gag ccc agt gcc      302
Lys Gly Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala
    10                  15                  20
atc gtc cag atg gag adw nnc ttg gcc aag ggc agc gag                  341
Ile Val Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu
25                  30                  35
```

<210> 562
<211> 484
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 334..483

<221> sig_peptide
<222> 334..387
<223> Von Heijne matrix
score 4.19999980926514
seq LIYLVSSFLALNQ/AS

<400> 562

```
gttagttggg cagggctgaa gtgtatgtgg tgaggaaaag aggctcctac tgtagacagc    60
cttgttctac agatcctccc agaaatctct gggccaggtg gaacccaggg tcagagaggg   120
atgggagaga ggtttaattt tccatgataa ataaaaatct ataaaataat aaacaagaga   180
aaagagattg gaaacagcca ggttggagca gtgagtgagt aaggaaacct ggctgccctc   240
tccagattcc ccaggctctc agagaagatc agcagaaagt ctgcaagass ctaagaacca   300
tcagccctca gctgcacctc ctcccctcca agg atg aca aag gcg sgv ctc atc    354
                                     Met Thr Lys Ala Xaa Leu Ile
                                                 -15
tat ttg gtc agc agc ttt ctt gcc cta aat cag gcc agc ctc atc agt     402
Tyr Leu Val Ser Ser Phe Leu Ala Leu Asn Gln Ala Ser Leu Ile Ser
    -10                 -5                  1               5
cgc tgt gac ttg gcc cag gtg ctg cag ctg gag gac ttg gat ggg ttt     450
Arg Cys Asp Leu Ala Gln Val Leu Gln Leu Glu Asp Leu Asp Gly Phe
                10                  15                  20
gag ggt tac tcc ctg agt gac tgg ctg tgc tgg c                       484
Glu Gly Tyr Ser Leu Ser Asp Trp Leu Cys Trp
            25                  30
```

<210> 563
<211> 229
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 122..229

<221> sig_peptide
<222> 122..190
<223> Von Heijne matrix
score 4.19999980926514
seq QLILLGIFRGIRH/QI

<400> 563

```
gaaaggcctc gaaggcagcg tcctactcga ccaccaaggc aagacaagcc acctckattt    60
agacggctaa gagagaggga ggctgcttca aaatcaaatg aggtggtagc agtgcccaca   120
a atg gca cag tta ata atg tgg ctc aag aac cag tta ata ctc ttg ggg   169
  Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly
              -20                 -15                 -10
ata ttt cgg gga ata aga cac cag att tat cta atc aga act ctt cag     217
```

```
Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln
        -5                  1               5
atc agg caa tgg                                                 229
Ile Arg Gln Trp
10

<210> 564
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 80..352

<221> sig_peptide
<222> 80..169
<223> Von Heijne matrix
      score 4.19999980926514
      seq LAXTLSLTCSVSG/VS

<400> 564
actttctgag agtcctggac ctcctgtgca agaacatgaa acatctgtgg ttcttccttc    60
tcctggtggc aggtcccag atg ggt cct gtc cca ggt gca gct gca gga gtm    112
                     Met Gly Pro Val Pro Gly Ala Ala Ala Gly Val
                     -30                 -25                 -20
rgg ccc ayg amt ggc gaa ctt gcg grg acc ctg tcc ctc acc tgc agt     160
Xaa Pro Xaa Xaa Gly Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser
                -15                 -10                 -5
gtc tct ggt gtc tcc atc act agt tat tac tgg agc tgg atc cgc car     208
Val Ser Gly Val Ser Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln
            1               5                   10
gcc cca ggg aag ggg ccg gag tgg atc ggg cdk atc gat cat agc ggg     256
Ala Pro Gly Lys Gly Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly
    15                  20                  25
gat acc gac tac aat ccc tcc ctc cag agt cga gtc acc ctc tca gtg     304
Asp Thr Asp Tyr Asn Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val
30                  35                  40                  45
gac acg tcg aag aac cag ttc tca ctg agg ttg ctt tct gtg agc gca     352
Asp Thr Ser Lys Asn Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala
                50                  55                  60

<210> 565
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..201

<221> sig_peptide
<222> 85..192
<223> Von Heijne matrix
      score 4.19999980926514
      seq LPLFLCPLGMVET/SF

<400> 565
agttctgcgc tgtgagccgg ggcacaaaga gccctctgca ctagcgccgc agaccgcgga    60
ccagttggag gcatctgtcc accc atg tgg ttc cag aca cgt tca tgt ggc      111
                           Met Trp Phe Gln Thr Arg Ser Cys Gly
                               -35                 -30
cac cat gac ccc gtc ggc atc aca ggg gta acc aag gtg atc ctc cct     159
```

```
His His Asp Pro Val Gly Ile Thr Gly Val Thr Lys Val Ile Leu Pro
        -25                 -20                 -15
ctc ttc ctg tgt cca ctg ggg atg gta gag acc agc ttc ggg              201
Leu Phe Leu Cys Pro Leu Gly Met Val Glu Thr Ser Phe Gly
    -10                 -5                  1
```

<210> 566
<211> 422
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..422

<221> sig_peptide
<222> 87..413
<223> Von Heijne matrix
score 4.19999980926514
seq LVFLLMYLFPRQL/LI

<400> 566

```
ctctcccgct tctctcgctg tgaagatggc gctctccagg gtcttcaaag cttcaccttt     60
ctccaaaggc agatgtgaag aacttg atg tct tat gtg gta acc aag aca aaa     113
                             Met Ser Tyr Val Val Thr Lys Thr Lys
                                             -105
gcg att aat ggg aaa tac cat cgt ttc ttg ggt cgt cat ttc ccc cgc      161
Ala Ile Asn Gly Lys Tyr His Arg Phe Leu Gly Arg His Phe Pro Arg
-100                -95                 -90                 -85
ttc tat gtc ctg tac aca atc ttc atg aaa gga ttg cag atg tta tgg      209
Phe Tyr Val Leu Tyr Thr Ile Phe Met Lys Gly Leu Gln Met Leu Trp
                -80                 -75                 -70
gct gat gcc aaa aag gct aga aga ata aag aca aat atg tgg aag cac      257
Ala Asp Ala Lys Lys Ala Arg Arg Ile Lys Thr Asn Met Trp Lys His
            -65                 -60                 -55
aat ata aag ttt cat caa ctt cca tac cgg gag atg gag cat ttg aga      305
Asn Ile Lys Phe His Gln Leu Pro Tyr Arg Glu Met Glu His Leu Arg
        -50                 -45                 -40
cag ttc cgc caa gac gtc acc aag tgt ctt ttc cta ggt att att tcc      353
Gln Phe Arg Gln Asp Val Thr Lys Cys Leu Phe Leu Gly Ile Ile Ser
    -35                 -30                 -25
att cca cct ttt gcc aac tac ctg gtc ttc ttg cta atg tac ctg ttt      401
Ile Pro Pro Phe Ala Asn Tyr Leu Val Phe Leu Leu Met Tyr Leu Phe
-20                 -15                 -10                 -5
ccc agg caa cta ctg atc agg                                          422
Pro Arg Gln Leu Leu Ile Arg
                1
```

<210> 567
<211> 218
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..218

<221> sig_peptide
<222> 48..104
<223> Von Heijne matrix
score 4.19999980926514
seq LSLPSFLCTCCQF/FP

<400> 567
```
tttcctttct gttttgggag ggaagtggag ggagttcttt tttcttt atg tat aat      56
                                                    Met Tyr Asn
tat tac ttc ctt tca ttg ccg agt ttt ctt tgt acc tgt tgt caa ttc     104
Tyr Tyr Phe Leu Ser Leu Pro Ser Phe Leu Cys Thr Cys Cys Gln Phe
    -15                 -10                 -5
ttc cca cat gat cca att agc tct cag tac agt tct cca caa ggg aaa     152
Phe Pro His Asp Pro Ile Ser Ser Gln Tyr Ser Ser Pro Gln Gly Lys
1               5                   10                  15
cca tgt caa gta acc tac aag ttc ttg ttt att ttg ctt gga cac gtc     200
Pro Cys Gln Val Thr Tyr Lys Phe Leu Phe Ile Leu Leu Gly His Val
            20                  25                  30
tat ccc aga gat ggc ggg                                             218
Tyr Pro Arg Asp Gly Gly
        35
```

<210> 568
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 2..244

<221> sig_peptide
<222> 2..238
<223> Von Heijne matrix
score 4.19999980926514
seq LLLVSLLEHLSHV/HE

<400> 568
```
g atg cag ggg ggc aac tcc ggg gtc cgc aag cgc gaa gag gag ggc gac     49
  Met Gln Gly Gly Asn Ser Gly Val Arg Lys Arg Glu Glu Glu Gly Asp
                  -75                 -70                 -65
ggg gct ggg gct gtg gct gcg ccg ccg gcc atc gac ttt ccc gcc gag      97
Gly Ala Gly Ala Val Ala Ala Pro Pro Ala Ile Asp Phe Pro Ala Glu
            -60                 -55                 -50
ggc ccg gac ccc gaa tat gac gaa tct gat gtt cca gca kaa atc cag     145
Gly Pro Asp Pro Glu Tyr Asp Glu Ser Asp Val Pro Ala Xaa Ile Gln
        -45                 -40                 -35
gtg tta aaa gaa ccc cta caa cag cca acc ttc cct ttt gca gtt gca     193
Val Leu Lys Glu Pro Leu Gln Gln Pro Thr Phe Pro Phe Ala Val Ala
    -30                 -25                 -20
aac caa ctc ttg ctg gtt tct ttg ctg gag cac ttg agc cac gtg cat     241
Asn Gln Leu Leu Leu Val Ser Leu Leu Glu His Leu Ser His Val His
-15                 -10                 -5                  1
gaa cc                                                              246
Glu
```

<210> 569
<211> 142
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..140

<221> sig_peptide
<222> 78..128
<223> Von Heijne matrix
score 4.19999980926514

seq CFALCIILICVMS/CR

<400> 569

```
cacattagtt ttgaaactag ctctaatttc tcctaccagg aggaatttct tccttcttgg      60
caatactgtg gtattta atg gta ttt tac tgt ttt gca ctt tgt att ata        110
                   Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile
                           -15                 -10
ctt att tgt gtt atg tct tgt cgc cac ctg gg                              142
Leu Ile Cys Val Met Ser Cys Arg His Leu
    -5                  1
```

<210> 570
<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 12..206

<221> sig_peptide
<222> 12..140
<223> Von Heijne matrix
score 4.09999990463257
seq VLITQLCLGKGQS/EP

<400> 570

```
tcaatccttg a atg ctc tgg gag act gat ttg agt acc aat aaa act cca       50
             Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro
                         -40                -35
gtc tcc tgc aca gct ggc tct gcg tgt gct ctt tct cta ttg caa ttc         98
Val Ser Cys Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe
-30                 -25                 -20                 -15
cct gtc ttg ata act cag ctc tgt cta ggc aaa ggg caa agt gaa ccc        146
Pro Val Leu Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro
                -10                 -5                  1
att ggg cca tta caa gat ttt gtg tct ttg gaa agc act tca cat ttt        194
Ile Gly Pro Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe
        5                   10                  15
tat tct ttt ttt t                                                      207
Tyr Ser Phe Phe
    20
```

<210> 571
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 276..371

<221> sig_peptide
<222> 276..335
<223> Von Heijne matrix
score 4.09999990463257
seq LWCCSPSSRTSSS/LS

<221> misc_feature
<222> 251
<223> n=a, g, c or t

<400> 571
```
attctgcagc caactttgtt caccatctcc gcaatgcctt ggacgtcctg catagagagg    60
tgcccagagt cctggtcaac ctcgtggact tcctgaaccc cactatsrtg cggcaggtgt   120
tcctgggrra cccagacaag tgcccagtgc agcaggccag cgttttgtgt aactgcgttc   180
tgaccctgcg ggagaactcc caagagctag ccaggctggr ggccttcagc cgagcctacc   240
ggagcagcat nbcgagctgg tggggtcagg ccgct atg aca cgc agg agg act      293
                                      Met Thr Arg Arg Arg Thr
                                      -20                 -15
tct ctg tgg tgc tgc agc cct tct tcc aga aca tcc agc tcc ctg tcc     341
Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg Thr Ser Ser Ser Leu Ser
                -10                 -5                  1
tgg cgg atg ggc tcc cag ata cgt cct tct tt                          373
Trp Arg Met Gly Ser Gln Ile Arg Pro Ser
        5                   10
```

<210> 572
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..193

<221> sig_peptide
<222> 134..187
<223> Von Heijne matrix
score 4.09999990463257
seq WCFHAVFFTVCVC/VR

<400> 572
```
gtgacaaagt accacagact gggtggttga aacacagaaa tttattttct cacaatttcg    60
gaggctctag aagtctgaga tcaaggtgtt ggcaggtttg gtttattcta aggcctttct   120
ctatggcttg tag atg gcc ttc tat ctc tgg tgt ttt cat gcg gtc ttt      169
               Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe
                           -15                 -10
ttc act gtg tgt gtg tgt gtg cgg gg                                  195
Phe Thr Val Cys Val Cys Val Arg
    -5                  1
```

<210> 573
<211> 352
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..352

<221> sig_peptide
<222> 173..271
<223> Von Heijne matrix
score 4.09999990463257
seq PLIHLTLSGHSTC/FR

<400> 573
```
tcattcttgg gtgtttctcg cagaggggga tttggcaggg tcataggaca atagtggagg    60
gaaggtcagc agataaacaa gtgaacaaag gtttctggtt ttcctaggca gargaccctt   120
gcggccttcc gcagtgtttg tgtccctggg tacttgagat tagggagtgg tg atg act   178
                                                          Met Thr
ctt aac gag cat gct gcc ttc aag cat ctg ttt aac aaa gca cat ctt     226
Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala His Leu
    -30                 -25                 -20
```

```
gca cca ccc tta atc cat tta acb ctg agt gga cac agc aca tgt ttc      274
Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr Cys Phe
-15                 -10                 -5                  1
aga gag cac agg gtt ggg ggc aag gtc ata gat gaa cag cat ccc aag      322
Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His Pro Lys
            5                   10                  15
gca gaa gaa tct ttc tta gta cag gag ggg                              352
Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
        20                  25
```

<210> 574
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..121

<221> sig_peptide
<222> 35..112
<223> Von Heijne matrix
score 4.09999990463257
seq SLASFLLLTFLPS/LP

<400> 574

```
accttccttc tctccttctt tccttccctc cttc atg tct ttc tct tcc tct ctc     55
                                      Met Ser Phe Ser Ser Ser Leu
                                          -25                 -20
cct cca tct ctc cct cct tcc ctc gct tcc ttc ctc ctt ttg acc ttc      103
Pro Pro Ser Leu Pro Pro Ser Leu Ala Ser Phe Leu Leu Leu Thr Phe
                -15                 -10                 -5
ctt cct tcc ctc cct cgg                                              121
Leu Pro Ser Leu Pro Arg
            1
```

<210> 575
<211> 391
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..391

<221> sig_peptide
<222> 77..214
<223> Von Heijne matrix
score 4.09999990463257
seq GCAPLRWVPQIRG/CP

<221> misc_feature
<222> 31..32,314
<223> n=a, g, c or t

<400> 575

```
aaaaactgts sagacttttg cccgtccatt nncrctatct ctccccactc tgggtgtcct     60
acccaaggcg ctgtct atg cgt gcc cag ggc ctg tcc tgc gga tac cca gct    112
                  Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala
                      -45                 -40                 -35
cgc ccc ttg cag ccc ttt tta gag cat ctc gcg ggc tct ggc atc acc      160
Arg Pro Leu Gln Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr
```

```
                -30                 -25                 -20
aag cgc aca gcc ccg ggc tgc gct ccc cta agg tgg gtc cct cag atc      208
Lys Arg Thr Ala Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile
            -15                 -10                 -5
cgg ggc tgt cca tta acc agg ctg gcc caa aga ggc gca gac act cga      256
Arg Gly Cys Pro Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg
        1               5                   10
acc cgg gaa aac tta ttt tat tct cgg ttc ccg ggg ttg cag ctg cca      304
Thr Arg Glu Asn Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro
15                  20                  25                  30
gcg gct gak nac agt gcg tcc gct ttg tct ctc tgc act ccc cgc agc      352
Ala Ala Xaa Xaa Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser
                35                  40                  45
ccc cct ctc ccg ctt cct ctc ccg att aac tcc ccc ggg                  391
Pro Pro Leu Pro Leu Pro Leu Pro Ile Asn Ser Pro Gly
            50                  55
```

```
<210> 576
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..288

<221> sig_peptide
<222> 133..243
<223> Von Heijne matrix
      score 4.09999990463257
      seq SISFLPFQASIFG/KT

<400> 576
aaaggcacag cgcgggcgca ggcgcccaga ggcgacagga gacctcaggc ccagactcca     60
ctccccagct gtgaaaggac tgctggccag acccccaagc tagcccgcca ggcctccata    120
gagctgccca gc atg gct gca tcc agt acc agt cat ctt aaa aat aaa aca    171
              Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr
                  -35                 -30                 -25
aaa acc ttc ctt gcc ccc atg acc aac tgc cac tca att tcc ttt ctt      219
Lys Thr Phe Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu
                -20                 -15                 -10
cct ttc caa gca agt att ttt gga aag act cgt ctg cag tca ctg agg      267
Pro Phe Gln Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg
            -5                  1                   5
cct tcc cac cct tac ccc cac                                          288
Pro Ser His Pro Tyr Pro His
    10                  15

<210> 577
<211> 264
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 134..262

<221> sig_peptide
<222> 134..250
<223> Von Heijne matrix
      score 4.09999990463257
      seq FXSCXCVSTLAYT/KG
```

<400> 577
attacacagt agagggagga agctaaagga agtctatgga caggtgaggg agggkgagac 60
tggggaattt tctgattgtt cagaggaatc ttgaagatga tggaaatatc agatgtgcta 120
aagtttccta gta atg ccc aag gat gct gac ctg gct ttc agt gct tca 169
Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser
-35 -30
ttg ttt gaa aga gca gag tcc ctt tat act ctg att tca aaa ttt ktt 217
Leu Phe Glu Arg Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa
-25 -20 -15
tct tgt dtk tgt gtg tct acc ttg gca tat act aaa gga agg ggg gg 264
Ser Cys Xaa Cys Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
-10 -5 1

<210> 578
<211> 205
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..204

<221> sig_peptide
<222> 115..198
<223> Von Heijne matrix
score 4.09999990463257
seq MPFLFLTLFHCLG/RR

<221> misc_feature
<222> 94
<223> n=a, g, c or t

<400> 578
tgtagaaata cagwtgatgt ttaatagtga tcttgtatcc tatacccttg caaactccac 60
ttcttagttc cagttacttt attgtasytt tttnhttgty ytttactgtg tgtg atg 117
Met
ttt gtg aat aga acc tgt ttt aat tct tcc ttt cca atc tgg atg cct 165
Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met Pro
-25 -20 -15
ttt ctt ttt ctt aca tta ttc cac tgc tta gga cgt cgg g 205
Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
-10 -5 1

<210> 579
<211> 214
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..213

<221> sig_peptide
<222> 25..135
<223> Von Heijne matrix
score 4.09999990463257
seq HFLXAVSASSSXA/CL

<400> 579
gcctcctctw gcgctgtcct gtta atg gyg ggc agt agc cgc tgm vkg gga 51
Met Xaa Gly Ser Ser Arg Xaa Xaa Gly
-35 -30

```
ttg cag ata acc gct tcc cgc acg ggg aaa gtc tac cct gcc tgc cac       99
Leu Gln Ile Thr Ala Ser Arg Thr Gly Lys Val Tyr Pro Ala Cys His
        -25                 -20                 -15
ttt ctg skc gcc gtc agc gcc agt agc tcg cma gca tgt ctg tgg tac      147
Phe Leu Xaa Ala Val Ser Ala Ser Ser Ser Xaa Ala Cys Leu Trp Tyr
    -10                 -5                  1
cgc cca atm gct cgc aga ccg gct ggc ccc ggg ggg tca ctc agt tcg      195
Arg Pro Ile Ala Arg Arg Pro Ala Gly Pro Gly Gly Ser Leu Ser Ser
5                   10                  15                  20
gca caa gta cat cca gca g                                            214
Ala Gln Val His Pro Ala
                25
```

<210> 580
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..327

<221> sig_peptide
<222> 28..105
<223> Von Heijne matrix
score 4.09999990463257
seq VTFWLLCRICTFG/FH

<400> 580

```
tgtttgtgat cagtatccaa aggcaaa atg att ttg ttt gac cat tta cat tgt     54
                              Met Ile Leu Phe Asp His Leu His Cys
                                  -25                 -20
tca gca tca gga gtg act ttc tgg ttg ctt tgc agg atc tgt acg ttt      102
Ser Ala Ser Gly Val Thr Phe Trp Leu Leu Cys Arg Ile Cys Thr Phe
    -15                 -10                 -5
ggt ttt cat ggt ttt tct aaa tac aca gtt tca cgt gga aca cag cag      150
Gly Phe His Gly Phe Ser Lys Tyr Thr Val Ser Arg Gly Thr Gln Gln
    1               5                   10                  15
ggg gca gga avg tgv dgt gga tta cac cag aac tgg gaa cag tgg agg      198
Gly Ala Gly Xaa Xaa Xaa Gly Leu His Gln Asn Trp Glu Gln Trp Arg
                20                  25                  30
ggg ctt gtt ggg aag tct agt tct gcc gca gtt gtt ttc tgc ctt acs      246
Gly Leu Val Gly Lys Ser Ser Ser Ala Ala Val Val Phe Cys Leu Thr
            35                  40                  45
ttt gac ttg gtt acc agc ttt caa tta gca agt gca att gaa agt aca      294
Phe Asp Leu Val Thr Ser Phe Gln Leu Ala Ser Ala Ile Glu Ser Thr
    50                  55                  60
cat ttc cat gct ggg cgc gat ggc tca cac ctg t                        328
His Phe His Ala Gly Arg Asp Gly Ser His Leu
    65                  70
```

<210> 581
<211> 356
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 264..356

<221> sig_peptide
<222> 264..350
<223> Von Heijne matrix

score 4.09999990463257
seq LLLFPASLRLLCV/HP

<221> misc_feature
<222> 146
<223> n=a, g, c or t

<400> 581

```
gtckcatttt gcctttgwaa tggaagtcac ttccaagtgt ctgttctcta ggttttcctt     60
tttttctctt ttagaaattg gacacttcaa taaaatttgt aattacgtcc atctgwgtga    120
htattwgmat tyratgksca tatctnstgc cagattgtaa actccgcgag tgcacatatc    180
agatccatta tggttctcat catatcccta gctcctagcg cagtgcgggg cacgtataag    240
tgctcgaaag ctcccacgtg gtg atg gag cta agc ttg ccc cct tcc atg tgt    293
                          Met Glu Leu Ser Leu Pro Pro Ser Met Cys
                                          -25                 -20
gac tac cca amt ttc tgt ctc ctc ctc ttc ccg gcc tct ctc aga ctc      341
Asp Tyr Pro Xaa Phe Cys Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu
                -15                 -10                 -5
ctc tgt gtg cat ccc                                                  356
Leu Cys Val His Pro
            1
```

<210> 582
<211> 239
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..239

<221> sig_peptide
<222> 159..218
<223> Von Heijne matrix
score 4.09999990463257
seq TVGCAGLAGSCRG/IS

<400> 582

```
agttcctggg ctcccgcgga gsatgagacg ttgtgaatta gatgtgagaa gagggacgct     60
tggtctgcga ccaccaagac cccacaggat cgatgcaccc acccctgctg atgaccatga    120
ccatctaaar gggaaacatc atttgagggg ccctactc atg gat cag aag ccc ctc    176
                                          Met Asp Gln Lys Pro Leu
                                          -20                 -15
ttc act gtg ggg tgt gct ggg ttg gcg ggc agt tgc cgt gga atc agt      224
Phe Thr Val Gly Cys Ala Gly Leu Ala Gly Ser Cys Arg Gly Ile Ser
                -10                 -5                  1
ttc ctc agg acc cgc                                                  239
Phe Leu Arg Thr Arg
        5
```

<210> 583
<211> 144
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..142

<221> sig_peptide
<222> 8..76
<223> Von Heijne matrix

score 4.09999990463257
seq FILLLLIQDLTMS/PT

<400> 583
```
ttttaaa atg tca gtt aat gmt att ttt att ttc tat ttt atc tta tta       49
        Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu
                    -20                 -15                 -10
tta ttg ata caa gat ctc act atg tca ccc act gct gga atg cag tgg       97
Leu Leu Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp
                -5                  1               5
cat aat cat ggc cca cca caa gcc ttg cct tgc cca ctg aga abc cc       144
His Asn His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
        10                  15                  20
```

<210> 584
<211> 282
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..280

<221> sig_peptide
<222> 47..181
<223> Von Heijne matrix
score 4.09999990463257
seq ICLGSPLAECLLG/XX

<221> misc_feature
<222> 183,210
<223> n=a, g, c or t

<400> 584
```
ccttgtttaa gccgtgatcg tgacctcacc atgtgtagac agtgag atg tca ttt        55
                                                   Met Ser Phe
                                                   -45
ctc aat gtg gac atc aca gat tgc ctg tat aac ccc agt gtg tgt ccc      103
Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser Val Cys Pro
        -40                 -35                 -30
gtg gct cag agc agt ctg acc tgt gac ttc ata gat ggt atc tgc ttg      151
Val Ala Gln Ser Ser Leu Thr Cys Asp Phe Ile Asp Gly Ile Cys Leu
    -25                 -20                 -15
ggg tcg cct ttg gct gag tgt ctg ctt ggt gna gwa wkw ksc att ttk      199
Gly Ser Pro Leu Ala Glu Cys Leu Leu Gly Xaa Xaa Xaa Xaa Ile Xaa
-10                 -5                  1               5
ggr atc aat rns cym tgc ttt ccg tgt ggt gtg aag tgc gca ggt gtg      247
Gly Ile Asn Xaa Xaa Cys Phe Pro Cys Gly Val Lys Cys Ala Gly Val
            10                  15                  20
gtc ttg ggg ctg agc acc ctg tgg tat gtt gta gc                       282
Val Leu Gly Leu Ser Thr Leu Trp Tyr Val Val
        25                  30
```

<210> 585
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 242..388

<221> sig_peptide
<222> 242..352
<223> Von Heijne matrix
score 4.09999990463257
seq FTFLSPSFHSVHL/SE

<400> 585
```
tgcattttta aaaatagcta gaagaaaaga actttaatat tcccaaaaca aataaaatat    60
aaatgtttga ggtgagggat atcccaatta ccctgatttg gttatttattc attgtataca  120
gttttcaaaa tatcacatgt acccccaaaa tatgtaaaac tgttatatac aaataaataa   180
caaaactaaa aataacagct gtgcaaacat ttttaaaagg cttgctttaa atgggtttca   240
c atg aaa gta gga aag gac tct ctg gag tct tta cca tct tta tgt gag   289
  Met Lys Val Gly Lys Asp Ser Leu Glu Ser Leu Pro Ser Leu Cys Glu
          -35                 -30                 -25
aaa cac att ggt ccc agt ggt ctc ttt acc ttt ctt agt cca tcc ttt     337
Lys His Ile Gly Pro Ser Gly Leu Phe Thr Phe Leu Ser Pro Ser Phe
    -20                 -15                 -10
cac tct gta cat ctt tct gaa ctc aat gaa tta tac act att gct gcc     385
His Ser Val His Leu Ser Glu Leu Asn Glu Leu Tyr Thr Ile Ala Ala
-5                  1               5                   10
ggg                                                                 388
Gly
```

<210> 586
<211> 436
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 346..435

<221> sig_peptide
<222> 346..396
<223> Von Heijne matrix
score 4.09999990463257
seq VLISASLLRASQL/KI

<221> misc_feature
<222> 170
<223> n=a, g, c or t

<400> 586
```
tgtgctgtgt ggttaggaga aggagggatg ggagagagaa ggggaaggaa tgaggcatgg    60
agagagatca caaccatcgt ctcaatgaag cagcagcaca cacagggatg tgtggtcgwc   120
ccaagttcag gggagagagt ttaaaggcgg gatgatcata tgtgaagdhn tggcagcacc   180
aatatggcac tgtcaaagta aaagagaaat agatctgaac tggattttaa tgagaataat   240
agcaaatatt aacatttctt agatagtttg atatttattc tggaagtatc gctaccaaca   300
tcaacatctg ggaaagcdag tgggcatcaa aatcctacct ggcta atg gaa agc aaa   357
                                                  Met Glu Ser Lys
                                                          -15
gtt tta atc agt gca tca ctc cta cgg gcc tct caa tta aaa ata aaa     405
Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln Leu Lys Ile Lys
          -10                 -5                  1
tgr aac aaa atg aca aac ttc tta att ttg t                           436
Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
    5                   10
```

<210> 587
<211> 378
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 24..377

<221> sig_peptide
<222> 24..95
<223> Von Heijne matrix
      score 4.09999990463257
      seq RLPMLSLFRGSHX/XF

<400> 587
tcctgtcctg ggcgtacgtc aag atg gcg gcg tct gta tta aac acc gtg ctg      53
                          Met Ala Ala Ser Val Leu Asn Thr Val Leu
                                              -20                 -15
agg cgg ctt cct atg cta tct ctc ttc cga ggt tct cay vvg rbg ttc       101
Arg Arg Leu Pro Met Leu Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe
                -10                 -5                  1
agg ttc ccc tcc aga ctc ttt gca cca aag ctc cct ctg agg aag att       149
Arg Phe Pro Ser Arg Leu Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile
        5                   10                  15
ctt tgt cct cag ttc cca ttt ctc ctt ata agg atg agc cct gga aat       197
Leu Cys Pro Gln Phe Pro Phe Leu Leu Ile Arg Met Ser Pro Gly Asn
    20                  25                  30
atc tgg aat cag aag aat acc agg agc gat atg gtt ctc gcc ccg tct       245
Ile Trp Asn Gln Lys Asn Thr Arg Ser Asp Met Val Leu Ala Pro Ser
35                  40                  45                  50
ggg ctg act acc gcc gca acc aca agg gtg gtg tac ccc cac agc gga       293
Gly Leu Thr Thr Ala Ala Thr Thr Arg Val Val Tyr Pro His Ser Gly
                55                  60                  65
ctc gga aga cat gta ttc gtc gga ata aag ttg ttg gga atc cct gcc       341
Leu Gly Arg His Val Phe Val Gly Ile Lys Leu Leu Gly Ile Pro Ala
            70                  75                  80
cca tct gtc gag atc aca agt tgc atg ttg act tta g                     378
Pro Ser Val Glu Ile Thr Ser Cys Met Leu Thr Leu
        85                  90

<210> 588
<211> 413
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 185..412

<221> sig_peptide
<222> 185..238
<223> Von Heijne matrix
      score 4.09999990463257
      seq TLLTCLXLXGGEG/WK

<221> misc_feature
<222> 218,224
<223> n=a, g, c or t


<400> 588
aggaggcgca gttactgata tagccaaggt gggacactac tggagggagc tagaagggat      60
cagccagcca tgcctccagt tcaggtactt ggcattgcta agctcagaac aggacttgcc     120
agtgtctaga tgaaaaagag gagagatctc aagagggata accaattggc tggcaaagta     180
acaa atg aaa agt aac ctg act cta ttg acc tgc tta ncc ctg nat ggg      229
     Met Lys Ser Asn Leu Thr Leu Leu Thr Cys Leu Xaa Leu Xaa Gly
```

```
                 -15                 -10                 -5
ggg gaa gga tgg aaa gga gca gct gtt tgc ttt gaa acg gtg gaa cag       277
Gly Glu Gly Trp Lys Gly Ala Ala Val Cys Phe Glu Thr Val Glu Gln
            1               5                   10
ttt tgc agc ctt aga aaa tgg cat gta aca tac cta rcc aaa gac agc       325
Phe Cys Ser Leu Arg Lys Trp His Val Thr Tyr Leu Xaa Lys Asp Ser
    15                  20                  25
gga ctc tgt caa caa cag gag aag ctc tat acg aaa ttc ttg gtc tgc       373
Gly Leu Cys Gln Gln Gln Glu Lys Leu Tyr Thr Lys Phe Leu Val Cys
30                  35                  40                  45
ata aag gga gca tca aat gaa gaa att aag aaa acc tac a                 413
Ile Lys Gly Ala Ser Asn Glu Glu Ile Lys Lys Thr Tyr
                50                  55

<210> 589
<211> 210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 138..209

<221> sig_peptide
<222> 138..179
<223> Von Heijne matrix
      score 4.09999990463257
      seq LASPCVLVQGSGX/SL

<221> misc_feature
<222> 78,80,118
<223> n=a, g, c or t


<400> 589
gaagataata ataatgatta ttataataat gatgatgatt ccaaggaaaa aacctacagc     60
gaatgttcca tttctacnsn gcacgcagac actctcccta acactgataa cctgagcncc    120
cagcactgga cggaaga atg ctg gcg tct ccg tgt gta ctg gtt cag ggt       170
                   Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly
                                       -10                 -5
tct ggs bcc agc ctt gtc agg acc ccc tgg tgt cca gag c                210
Ser Gly Xaa Ser Leu Val Arg Thr Pro Trp Cys Pro Glu
            1               5                   10

<210> 590
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..177

<221> sig_peptide
<222> 40..96
<223> Von Heijne matrix
      score 4.09999990463257
      seq ILLLLITIIYSYL/ES

<400> 590
acaaggactg aaccagaagg aagaggacag agcaaagcc atg aac atc atc cta       54
                                           Met Asn Ile Ile Leu
                                                           -15
```

```
gaa atc ctt ctg ctt ctg atc acc atc atc tac tcc tac ttg gag tcg     102
Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr Ser Tyr Leu Glu Ser
                -10                 -5                  1
ttg gtg aag ttt ttc att cct cag agg aga aaa tct gtg gct ggg gag     150
Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys Ser Val Ala Gly Glu
        5                   10                  15
att gtt ctc att act gga gct ggg cat g                               178
Ile Val Leu Ile Thr Gly Ala Gly His
    20                  25

<210> 591
<211> 308
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..307

<221> sig_peptide
<222> 149..265
<223> Von Heijne matrix
      score 4.09999990463257
      seq PSLIAGLFVGCLA/GY

<221> misc_feature
<222> 272
<223> n=a, g, c or t


<400> 591
gcgagacggc tgggcgccga gtgggacagc gctggtgcgg agactgcttc cggactccag    60
gtaccgcgct tggcggcagc tggccccaga cttctgtctt ttcaagmkgc aagtraargc   120
tcggggctgc rraattgcaa ccttgcca atg gac ctg atc ggt ttt ggt tat      172
                               Met Asp Leu Ile Gly Phe Gly Tyr
                                               -35
gca gcc ctc gtg aca ttt gga agc att ttt gga tat aag cdg aga ggt     220
Ala Ala Leu Val Thr Phe Gly Ser Ile Phe Gly Tyr Lys Xaa Arg Gly
    -30                 -25                 -20
ggt gtt ccg tct ttg att gct ggt ctt ttt gtd gga tgt ttg gcc ggc     268
Gly Val Pro Ser Leu Ile Ala Gly Leu Phe Val Gly Cys Leu Ala Gly
-15                 -10                 -5                  1
tat nsa gct tac cgt gtc tcc aat gac aaa cga gat gta a               308
Tyr Xaa Ala Tyr Arg Val Ser Asn Asp Lys Arg Asp Val
            5                   10

<210> 592
<211> 219
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..219

<221> sig_peptide
<222> 16..72
<223> Von Heijne matrix
      score 4.09999990463257
      seq XTFLAAXRRLVTG/QT

<400> 592
acagttcatc cggaa atg gag ggg gtc gct ttv btc acc ttc ctc gct gcg     51
```

```
                  Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala
                                      -15                 -10
sgg cgg cgg ttg gta acc ggt cag acc agc ccg aga ggg acc tgg tgc        99
Xaa Arg Arg Leu Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys
        -5                  1               5
ctg tac cca ggc ttc tgt cgc tct gtc gcc tgc gct atg ccc tgc tgt       147
Leu Tyr Pro Gly Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys
10                  15                  20                  25
agt cac agg agc tgt aga gag gac ccc ggt aca tct gaa agc cgg gaa       195
Ser His Arg Ser Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu
                30                  35                  40
atg gtg cgt gtg cgg gac cac ggg                                       219
Met Val Arg Val Arg Asp His Gly
            45
```

<210> 593
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 105..215

<221> sig_peptide
<222> 105..167
<223> Von Heijne matrix
score 4
seq IGLIGLTVPCGWG/SL

<400> 593

```
aggaacattt tttattttat ttttatagag atagggtctc tttctgtagc ccaagctgga       60
gtactgtctt agtctgtttt tatgctgctg ataacgacat accc atg act ggg caa      116
                                                 Met Thr Gly Gln
                                                         -20
ttt aca aaa gaa ata ggt tta att gga ctt aca gtt cca tgt ggc tgg       164
Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val Pro Cys Gly Trp
        -15                 -10                 -5
gga agc ctc ata acc atg gca gaa ggc agg gag gag caa gtc acg tct       212
Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu Gln Val Thr Ser
    1                   5                   10                  15
ggg                                                                   215
Gly
```

<210> 594
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..160

<221> sig_peptide
<222> 89..130
<223> Von Heijne matrix
score 4
seq HLGFILSFHGLIA/NF

<400> 594

```
ctccatagtt ttaccttctc caggatgttg tatagatgga attgtacagt atgtagcctt       60
ttcacattgg cttctttcac taaataac atg cat tta gga ttc att ctt tct        112
                               Met His Leu Gly Phe Ile Leu Ser
```

```
                                                          -10
ttc cat ggt ttg ata gct aat ttc ttt ttt tgt ctg aat gca cca gcg g     161
Phe His Gly Leu Ile Ala Asn Phe Phe Phe Cys Leu Asn Ala Pro Ala
    -5                  1               5                   10
```

<210> 595
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 317..394

<221> sig_peptide
<222> 317..376
<223> Von Heijne matrix
score 4
seq GCVAAGVVIGAGA/AT

<221> misc_feature
<222> 149
<223> n=a, g, c or t

<400> 595

```
actcttccta tagcccagag ggcgagaggg cctgtggcct gggggaagga ggacgaggtt     60
ctgcctggmt cccagcagga cgctgtgcca tttgggaaca aaggaatagt ctgcctggaa    120
tccctgcaga tcttggggcc ggaggcagnt ccaacccttg gagcaggaag aaacgcaaag    180
ttgtcaagaa ccaagtcgag ctgcctcaga gccggcccgc agtagctgca gactccgccc    240
gcgacgtgtg cgcgcttctc tgggccagag cgagcctgtt ttgtgctcgg gttaagagat    300
ttgtccbagc tatacc atg ggc cgc act cgg gaa gct ggc tgc gtg gcc gct    352
                  Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala
                  -20                 -15                 -10
ggt gtg gtt atc ggg gct ggt gct gct act gtg tat aca gac tg           396
Gly Val Val Ile Gly Ala Gly Ala Ala Thr Val Tyr Thr Asp
            -5                  1               5
```

<210> 596
<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 228..407

<221> sig_peptide
<222> 228..341
<223> Von Heijne matrix
score 4
seq FKPXSCLSLLSNX/DY

<400> 596

```
tgagttttat gmttgattta tatcttttgg ttacaagtcc tttgtcagat atatgatttg     60
caaatatttt ctcactctgg gtaggttgtc tttttacttt cttgataatg tcctcttttg    120
ttgcttgtgt tatctccttt tttgtttttt attcttttta aagttatctc ttacaggaag    180
gattcctttt ttcttaaaaa agtttttcaa ttcttttttt ttttgag atg gag tct      236
                                                    Met Glu Ser
cac tct gtc gcc cag gct agg atg cgg ysg caw aat ctc agc tca ctg      284
His Ser Val Ala Gln Ala Arg Met Arg Xaa Xaa Asn Leu Ser Ser Leu
-35                 -30                 -25                 -20
caa cct ctg ccg cct ggg ttc aag cca tts tcc tgc ctm agc ctc ctg      332
```

```
Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu Ser Leu Leu
                -15                 -10                 -5
agt aay tsa gat tac agg cat gca cca cca ttc ctg gct aat ttt kgw      380
Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala Asn Phe Xaa
            1               5                   10
att ttt cat aga gat gga gtt tca cca                                  407
Ile Phe His Arg Asp Gly Val Ser Pro
    15                  20
```

<210> 597
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..272

<221> sig_peptide
<222> 90..254
<223> Von Heijne matrix
      score 4
      seq LHQGLCLPQRVHC/SL

<400> 597

```
gctgaccgrg cgcacsccgc ccccggsgcc atcttcccga ccgcgagccg tccaggtctc     60
agtgctrtgc ccccccccaga gcctagagg atg ttt cat ggg atc cca gcc acg     113
                                 Met Phe His Gly Ile Pro Ala Thr
                                 -55                 -50
ccg ggc ata gga gcc cct ggg aac aag ccg gag ctg tat gag gta cga      161
Pro Gly Ile Gly Ala Pro Gly Asn Lys Pro Glu Leu Tyr Glu Val Arg
        -45                 -40                 -35
caa cat ggc aga gct gtt tgc ggt ggt gaa gac aat gca agc cct gga      209
Gln His Gly Arg Ala Val Cys Gly Gly Glu Asp Asn Ala Ser Pro Gly
    -30                 -25                 -20
gaa ggc cta cat caa gga ctg tgt ctc ccc cag cga gta cac tgc agc      257
Glu Gly Leu His Gln Gly Leu Cys Leu Pro Gln Arg Val His Cys Ser
-15                 -10                 -5                  1
ctg ctc ccg gct cct gg                                               274
Leu Leu Pro Ala Pro
            5
```

<210> 598
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 343..417

<221> sig_peptide
<222> 343..408
<223> Von Heijne matrix
      score 4
      seq LFLSVLNFLFLLS/FS

<400> 598

```
gcatctagaa gtacaagttg atgattattg tccatttgat agagacactg gaagggtgtc     60
agtgtaaaca ctggccatgt gaagattgag cctgttgatg gtttcttttg tatcatagga    120
tgccacgtca ccaactaggg aattctgccc aatcagttga gccaaatagt gctgtcctat    180
tgtaaaattg tttaatctgt gtgcttgtgt gtgtgcttgt cagaatttgt gaatcataga    240
attgttttaa ctggaagaag acccccaaga tcatctgctt caaccccttc cttcctctct    300
```

```
tttccagaga ggttgcactt tacttgagct gtgactagga tt atg cca cat tct      354
                                               Met Pro His Ser
                                                       -20
ttt gta agt tgt aac cta ttt ttg tct gtr ttg aat ttc ctt ttt ttg     402
Phe Val Ser Cys Asn Leu Phe Leu Ser Val Leu Asn Phe Leu Phe Leu
        -15                 -10                 -5
cta agc ttt agc aca                                                 417
Leu Ser Phe Ser Thr
        1

<210> 599
<211> 329
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 240..329

<221> sig_peptide
<222> 240..317
<223> Von Heijne matrix
      score 4
      seq HHLLLSTLATIAG/NI

<400> 599
agaagactgg aactcagcaa gaaagtgatg aaaatgctct gagacataga aactctagac    60
ggcagcatag aaatggaaga aaaataccca gccagatcca gctcagagcc aagaaaatgt   120
acacaccaga tccccagcat tcccaattat cacaaaaggt gccttaattt ctatctacaa   180
gacaacccta caatcctcac aggccctgag ctcagtatag aaagttttct ggagtccat    239
atg gct gtt ttt ctc caa aag agg aaa cac aca atg aga cac cac cta     287
Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
    -25                 -20                 -15
ctc ctc agt aca ctg gct act ata gca ggc aac att tac aga             329
Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
-10                 -5                  1

<210> 600
<211> 311
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 169..309

<221> sig_peptide
<222> 169..246
<223> Von Heijne matrix
      score 4
      seq PVAVEALLRAVFG/VV

<400> 600
acagaggcgg caagactagg gtggaggaaa gctcaagggc catcgctggg tgcttcggtg    60
gcgggcagaa acgggactgg cagtgcccac acgtgtgcgt tctccccgtc cgcccgaagg   120
agctacctgt gcaccctgcc tccggctctc ctgagcagag agatcctg atg gct gac    177
                                                     Met Ala Asp
                                                         -25
tca gaa gca ctc ccc tcc ctt gct ggg gac cca gtg gct gtg gaa gcc     225
Ser Glu Ala Leu Pro Ser Leu Ala Gly Asp Pro Val Ala Val Glu Ala
            -20                 -15                 -10
ttg ctc cgg gcc gtg ttt ggg gtt gtt gtg gat gag gcc att cag aaa     273
Leu Leu Arg Ala Val Phe Gly Val Val Val Asp Glu Ala Ile Gln Lys
```

```
      -5                  1                   5
gga acc agt gtc tcc cag aag gtc tgc smg tgg aag ga                     311
Gly Thr Ser Val Ser Gln Lys Val Cys Xaa Trp Lys
10                  15                  20

<210> 601
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 159..419

<221> sig_peptide
<222> 159..266
<223> Von Heijne matrix
      score 4
      seq LAELPVSSPLCHA/VL

<221> misc_feature
<222> 365..366
<223> n=a, g, c or t


<400> 601
ctaagccttt tctaccctct tctcaaagta gagccgaata tgattcagag gagagtctgg       60
gaagtgatga tgatgacaat gatgatgatg atgatgtttt agcatcagat ttccatctcc      120
aggaacattc taattcaaat tcatatagtt ggtccttg atg cgg ttg gcg atg gtg      176
                                          Met Arg Leu Ala Met Val
                                              -35
caa ttg gtg ctc aac aat ttg aag act ttt tat ccc ttc gca gat cat        224
Gln Leu Val Leu Asn Asn Leu Lys Thr Phe Tyr Pro Phe Ala Asp His
-30                 -25                 -20                 -15
gat ctt gca gag ctt cca gtt agt tca cct ctt tgt cat gcg gtt cta        272
Asp Leu Ala Glu Leu Pro Val Ser Ser Pro Leu Cys His Ala Val Leu
                -10                 -5                  1
aaa act ctt caa tgt tgg gaa caa gtt ctt ctc cga cga ctt gaa atc        320
Lys Thr Leu Gln Cys Trp Glu Gln Val Leu Leu Arg Arg Leu Glu Ile
        5                   10                  15
cat ggt ggg cca cct caa aat tat atc gca agt cat acc gcc gan nag        368
His Gly Gly Pro Pro Gln Asn Tyr Ile Ala Ser His Thr Ala Xaa Xaa
    20                  25                  30
agt ttg tct gca ggt cct gca att ctt cgc cac aaa gct tta ctg gaa        416
Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg His Lys Ala Leu Leu Glu
35                  40                  45                  50
cct a                                                                  420
Pro

<210> 602
<211> 463
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 311..463

<221> sig_peptide
<222> 311..370
<223> Von Heijne matrix
      score 4
      seq LFILXYFXXYTLS/SG
```

```
<221> misc_feature
<222> 353..354
<223> n=a, g, c or t


<400> 602
tggcaaagac aaagagttga aacttatatg gcagaatcag agctcacaat ggtgctgggc      60
atttggggtt ttgagtcttc tctgaagatc tttgacatct ttagctttat tctacaggcc     120
acggggaact actggatatt tgaaagaagg aatttatctg tctatcttct atttatctat     180
ctgtaatcta tcatctaatc taggaaatga tagatctagg aagatgatag ctagataaat     240
atcagtcatc ttcctatcat ctgggaaata gatttatttt gttttattat tttaattaat     300
taatttaaaa atg ttt aaa tta ttt tta ttt tta ttt att tta ttw tat       349
           Met Phe Lys Leu Phe Leu Phe Leu Phe Ile Leu Xaa Tyr
           -20                 -15                 -10
ttc nng vat tac act tta agt tct ggg ata tat gtg cag aat gtg cag      397
Phe Xaa Xaa Tyr Thr Leu Ser Ser Gly Ile Tyr Val Gln Asn Val Gln
    -5                  1               5
gtt tgt tac ata ggt ata cac atg cca tgg tgg ttt gct gca ccc atg      445
Val Cys Tyr Ile Gly Ile His Met Pro Trp Trp Phe Ala Ala Pro Met
10                  15                  20                  25
aac ctg tca tct gca cta                                              463
Asn Leu Ser Ser Ala Leu
                30

<210> 603
<211> 269
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 182..268

<221> sig_peptide
<222> 182..244
<223> Von Heijne matrix
      score 4
      seq LIPLLSEILYALA/NI

<400> 603
tgtttacaaa agtatcttga atttgataga gcttatgttg agaaataatt tttaatcttt      60
taattccatt tttccatgaa ctttttgaag tccccgtata catacttttt catggtgaga     120
acacttataa tctactgtca gcaattttca aatataaaat atattattaa ctgtagtcac     180
c atg ata tac agt aga tct ctt gaa ctt att cct ctt ttg tct gaa att    229
  Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile
      -20                 -15                 -10
ttg tat gct ttg gcc aac atc tcc cca atc ccc cag acg g                269
Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr
-5                  1               5

<210> 604
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 297..350

<221> sig_peptide
<222> 297..344
<223> Von Heijne matrix
```

```
      score 4
      seq VIFYFVLFLGIMT/QR

<400> 604
aagaacatta tattttcaaa tggaataata ataccatcag tgaaataaat gttaaaattt     60
ttagggcaga gattaatgcc caccagaaag gtaactttga tgagggtagc aagcatgctt    120
tcactgaaaa gtattttttt ttcctctttt caagattctc ataattataa cccataaaac    180
taagttagac ttgtttctta tgtgcattta tgatttaatt aacgagagta cactttgtat    240
gacaaaatgc aattttaagg taaacactat ggagaataat ttcttttcct agtgaa atg    299
                                                               Met
gtg cac gtt ata ttt tat ttt gtt tta ttt cta ggg ata atg aca cag      347
Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr Gln
-15                 -10                 -5                  1
cgg g                                                                351
Arg

<210> 605
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..195

<221> sig_peptide
<222> 37..111
<223> Von Heijne matrix
      score 4
      seq LIYFFQLHSCCHD/KV

<400> 605
agtgaagaat ctaagkccag agaggtggta gttaac atg cac aaa ttc ttt aga       54
                                        Met His Lys Phe Phe Arg
                                        -25                 -20
cat ttc tat tca gat ttt ctg att tat ttc ttt cag ctc cat tca tgt      102
His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe Phe Gln Leu His Ser Cys
                -15                 -10                 -5
tgt cac gat aaa gtr act gcm cra agg gcc tat rtt cac tac agc agc      150
Cys His Asp Lys Val Thr Ala Xaa Arg Ala Tyr Xaa His Tyr Ser Ser
            1               5                   10
ctc tta act cct tac ctc tct cag cac ccc tgc ccc cat ccc ggg          195
Leu Leu Thr Pro Tyr Leu Ser Gln His Pro Cys Pro His Pro Gly
    15                  20                  25

<210> 606
<211> 426
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..425

<221> sig_peptide
<222> 63..140
<223> Von Heijne matrix
      score 4
      seq LLRELRYLSAATG/HP

<221> misc_feature
<222> 174
<223> n=a, g, c or t
```

```
<400> 606
ggaggagggg ttttcagggt cgtaggacgc cgttgggcac cacgctcgga gaagacagga      60
ca atg gcg gcc tta ggg tcc ccg tcg cac act ttt cga gga ctt ctg        107
   Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu
       -25                 -20                 -15
cgg gag ttg cgc tac ctg agc gcg gcc acc ggc cac cct atc gcg aca       155
Arg Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr
    -10                 -5                  1               5
ccg cgg cct atc ggt acc ntt gtg aag gct ttc cgt gca cat cgg gtc       203
Pro Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val
                10                  15                  20
acc agt gaa aag ttg tgc aga gcc caa cat gag ctt cat ttc caa gct       251
Thr Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala
            25                  30                  35
gcc acc tat ctc tgc ctc ctg cgt asa tcc gga aac atg tgg ccc tac       299
Ala Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr
        40                  45                  50
atc agg aat ttc atg gca agg gtg agc gct cgg tgg agg agt ctg ctg       347
Ile Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu
    55                  60                  65
gct tgg tgg gtc tca agt tgc ccc atc agc ctg gag gga agg gct ggg       395
Ala Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly
70                  75                  80                  85
agc cat gaa cat gga gaa tat cct tgg atg c                             426
Ser His Glu His Gly Glu Tyr Pro Trp Met
                90                  95

<210> 607
<211> 161
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 71..160

<221> sig_peptide
<222> 71..154
<223> Von Heijne matrix
      score 4
      seq VSLFLLVVLYHYA/AV

<400> 607
agttccggtc caggtctctg acttcgggct tgttcgctgg tggcgtcgga gccgagccgg      60
actggtcagg atg atc acg gac gtg cag ctc gcc atc ttc gcc aac atg        109
           Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met
                       -25                 -20
ctg ggc gtg tcg ctc ttc ttg ctt gtc gtt ctc tat cac tac gcg gcc       157
Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala
-15                 -10                 -5                  1
gtg g                                                                 161
Val

<210> 608
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 283..357
```

<221> sig_peptide
<222> 283..336
<223> Von Heijne matrix
score 4
seq LSFLCSLSQNALN/IS

<400> 608
```
tgaaccttgc ttttatacaa atcacttttt tgttatttga ggaacaagat aacattttct    60
tggcaggatt actatagtcc ccccaacaag ctctaccama gaagataata gaacttattg   120
agcttaaatg aattatagga magttcctga aaagtccaar gtaaatgtga agagaacccg   180
attctcttaa cctcacccaa cccagcactt gattctccct tgtttcctgg ttttcataca   240
cacactggga aaggamaagg aagaagaaac aaggatgtcg tt atg gct gaa gga      294
                                                Met Ala Glu Gly
                                                            -15
gct ttg agc ttc ctt tgc tct tta tcg caa aat gca ttg aat att tcc     342
Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala Leu Asn Ile Ser
                -10                 -5                   1
ctc att tct cgt aag                                                 357
Leu Ile Ser Arg Lys
        5
```

<210> 609
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 133..201

<221> sig_peptide
<222> 133..180
<223> Von Heijne matrix
score 4
seq SFLLCFTLVGTQL/RN

<400> 609
```
ttatatgttc tgcttatggg actttgcatg ttctacaaac tacaagtatc tttttctact    60
ctgaattgaa tttagctctg tttacggttt tcttttctgt gagcagaagt tcttaatgat   120
tactgtagtc aa atg tat cca tct ttt ctt tta tgc ttc aca ctc gta ggg   171
              Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly
                  -15                 -10                 -5
act cag tta aga aat tct tcc tta gcc atg                             201
Thr Gln Leu Arg Asn Ser Ser Leu Ala Met
            1               5
```

<210> 610
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 223..279

<221> sig_peptide
<222> 223..267
<223> Von Heijne matrix
score 4
seq SCTVGCATASSWG/CT

<400> 610

```
accgccttcc cacatcggat cgcagggctc ccaaaatggc gagtgagact gcggggactc    60
gctgagcagc ggaggggggag cgtgcagarm mgctgcggcc ctcacagtcc ggagcccggc  120
cgtgccgtgc cgtagggaac atgcactttt ccattcccga aaccgagtcc cgcagcgggg   180
acagcggcgg ctccgcctac gtggcctata acattcacgt ga atg gag tcc tgc     234
                                               Met Glu Ser Cys
                                               -15
act gtc ggg tgc gct aca gcc agc tcc tgg ggc tgy acg agc agg gg     281
Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys Thr Ser Arg
    -10                 -5                  1
```

<210> 611
<211> 241
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 28..240

<221> sig_peptide
<222> 28..156
<223> Von Heijne matrix
      score 4
      seq AAWCSLVLSFCRL/HK

<400> 611

```
agcttccggg tttcctgggc tactacg atg gcg atg agt ttc gag tgg ccg tgg     54
                              Met Ala Met Ser Phe Glu Trp Pro Trp
                                          -40                 -35
cag tat cgc ttc cca ccc ttc ttt acg tta caa ccg aat gtg gac act      102
Gln Tyr Arg Phe Pro Pro Phe Phe Thr Leu Gln Pro Asn Val Asp Thr
            -30                 -25                 -20
cgg cag aag cag ctg gcc gcc tgg tgc tcg ctg gtc ctg tcc ttc tgc      150
Arg Gln Lys Gln Leu Ala Ala Trp Cys Ser Leu Val Leu Ser Phe Cys
        -15                 -10                 -5
cgc ctg cac aaa cag tcc agc atg acg gtg atg gaa gct cag gag agc      198
Arg Leu His Lys Gln Ser Ser Met Thr Val Met Glu Ala Gln Glu Ser
        1               5                   10
ccg ctc ttc aac aac gtc aag cta cag cga aag ctt cct gtg g            241
Pro Leu Phe Asn Asn Val Lys Leu Gln Arg Lys Leu Pro Val
15                  20                  25
```

<210> 612
<211> 176
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..174

<221> sig_peptide
<222> 106..147
<223> Von Heijne matrix
      score 3.90000009536743
      seq RLHVHSLSPFSFA/CL

<400> 612

```
aagagccttg gaacatctct ctgaagaata aaacaaatct tttctgcatg tataatcgat    60
ataaatttga ttatattgta ctttttattt cgtgtgtgtg tgtac atg aga tta cat   117
                                                  Met Arg Leu His
gta cat tcc ctt tct ccc ttt tcc ttt gct tgt ctc cct ttt ctg tcc      165
Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu Pro Phe Leu Ser
```

```
-10                 -5                  1               5
ccc ccg ctg gg                                                   176
Pro Pro Leu

<210> 613
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 258..341

<221> sig_peptide
<222> 258..335
<223> Von Heijne matrix
      score 3.90000009536743
      seq RMCILQLLSAVLY/RF

<400> 613
catttctatk aaaatacaaa tttaaggctg tagatttaat atgtagtatg ttcattrrgt     60
tccaaataca ttctaatttc cactgtgatt tctwctttga ctcmtgaawt atttagvagg    120
tgwttttgwh ttabdwattt ctgactgtat ggggattttc tagttagttt wctactctta    180
atttgtcttc agagamaata ctccacaaga tttcagtctt tcaattttgt tgcaacttgc    240
tacaaacttg gcctaac atg ttg cat ttt wta tat atg atc caw gtg tgc       290
                   Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys
                       -25                 -20
ttg gaa aga atg tgc att ctg caa ttg ttg agt gct gtg ttg tat aga      338
Leu Glu Arg Met Cys Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg
-15                 -10                 -5                  1
ttt g                                                                342
Phe

<210> 614
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 48..152

<221> sig_peptide
<222> 48..137
<223> Von Heijne matrix
      score 3.90000009536743
      seq VGLLDTPLGAVSA/HH

<221> misc_feature
<222> 17
<223> n=a, g, c or t

<400> 614
agtcggagcg aaggvcntgg cggasagaac ggattgcagg gtcagcc atg tca tct       56
                                                    Met Ser Ser
                                                    -30
gag cct ccc cca cca cca cag ccc ccc acc cat caa gct tca gtc ggg      104
Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala Ser Val Gly
        -25                 -20                 -15
ctg ctg gac acc ccc ctc gga gcc gtg agc gct cac cat ccc ctc tgc      152
Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His Pro Leu Cys
    -10                 -5                  1               5
```

cc 154

<210> 615
<211> 272
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 185..271

<221> sig_peptide
<222> 185..244
<223> Von Heijne matrix
score 3.90000009536743
seq FLTSISFLALVLW/NV

<400> 615
```
caactataat agcttttaaa cttgtttctc tttccttttc cttcatttca gtccatctta     60
ttatctttga caaaataatt tctctgatgc ctgactgcct gccccccaac aacaaagctt    120
ttattatact tcttaactaa tcaactatwm cyttacccat ctagccaaag tagactaccc    180
atat atg ttt ctt gac cat gtc agg ttt tta acc tcc ata tct ttt ctt     229
     Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu
     -20                 -15                 -10
gct ctg gtc ctg tgg aat gtc ttt ctc aac tct acc cgt ctg g            272
Ala Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu
-5                  1               5
```

<210> 616
<211> 114
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..113

<221> sig_peptide
<222> 36..92
<223> Von Heijne matrix
score 3.90000009536743
seq PALLTSSELPALA/SQ

<400> 616
```
aggtttttag tcttgacctc ttgacctgct tatag atg aga gaa aag cca caa        53
                                       Met Arg Glu Lys Pro Gln
                                                       -15
cca gcg ctc ctg act tca agt gar ctg cct gcc ttg gcc tct caa ata      101
Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro Ala Leu Ala Ser Gln Ile
            -10                 -5                  1
cat tgc cgc gtc c                                                    114
His Cys Arg Val
    5
```

<210> 617
<211> 171
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 56..169

<221> sig_peptide
<222> 56..133
<223> Von Heijne matrix
score 3.90000009536743
seq VPVLCIWRAWLRA/EV

<400> 617
```
aaaatgacga tttctcagga aatcatttcg actcctcttt ccctgcccaa ggagg atg      58
                                                             Met
ccc cac aac cac ttg gag gga gat gct ttg ctg aga gtc cct gtc ctc      106
Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val Leu
-25                 -20                 -15                 -10
tgc atc tgg aga gct tgg ctc aga gct gag gtg gga ggg agg gct cct      154
Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala Pro
                -5                   1               5
ctt cca ggt cgc atg gg                                                171
Leu Pro Gly Arg Met
        10
```

<210> 618
<211> 240
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..240

<221> sig_peptide
<222> 160..225
<223> Von Heijne matrix
score 3.90000009536743
seq CLFWIXLPPHTCT/HT

<400> 618
```
caaaaaggaa aactgataat atcttaaaaa taatatttaa ctgagtgctg gagaaagggg      60
attgaaatgt gagctccttt atatttagc tttgccacgt cattgttttt ccctcagaaa       120
ctgtgaaata ctttaaatat gagttgttgg gaaagttaa atg aaa aat act ctt         174
                                           Met Lys Asn Thr Leu
                                                   -20
tat tat aat ttt tgt tta ttt tgg att ytc cta cct ccc cac aca tgc       222
Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu Pro Pro His Thr Cys
        -15                 -10                 -5
aca cac aca gac aca cat                                               240
Thr His Thr Asp Thr His
    1               5
```

<210> 619
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 97..255

<221> sig_peptide
<222> 97..201
<223> Von Heijne matrix
score 3.90000009536743
seq CTFLSLSLHPWGG/FF

<400> 619

```
acttcagaac tgggggagag ggagaggact ggaggcggga gggtggccgc tggccagtgc    60
gcactctttc ctctgcatcc ccttccctgc ggcccc atg tgc ctg aac ccc gcc     114
                                        Met Cys Leu Asn Pro Ala
                                        -35                 -30
tgc tcg gga ccg ctt tcc ctc cgt tcc cct cgg ctt ccc cct ctc ttt     162
Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro Arg Leu Pro Pro Leu Phe
                -25                 -20                 -15
tgc act ttt ctt tcc ctt tct ttg cat ccc tgg ggg ggt ttc ttt ttg     210
Cys Thr Phe Leu Ser Leu Ser Leu His Pro Trp Gly Gly Phe Phe Leu
            -10                 -5                   1
tgt gcc tgg att tct bkt ttc ctc ccg tgg gtg tgt gtg tgk gcg gg      257
Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp Val Cys Val Xaa Ala
    5                   10                  15

<210> 620
<211> 351
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 47..349

<221> sig_peptide
<222> 47..313
<223> Von Heijne matrix
      score 3.90000009536743
      seq RLLVACCLADIFR/IY

<400> 620
agcggagtak ygagtcggca acccggaggg tagaaatatt tctgtc atg gct cat       55
                                                   Met Ala His
tca aag act agg acc aat gat gga aaa att aca tat ccg cct ggg gtc     103
Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro Pro Gly Val
    -85                 -80                 -75
aag gaa ata tca gat aaa ata tct aaa gag gag atg gtg aga cga tta     151
Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val Arg Arg Leu
-70                 -65                 -60                 -55
aag atg gtt gtg aaa act ttt atg gat atg gac cag gac tct gaa gaa     199
Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp Ser Glu Glu
                -50                 -45                 -40
gaa aag gag ctt tat tta aac cta gct tta cat ctt gct tca gat ttt     247
Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala Ser Asp Phe
            -35                 -30                 -25
ttt ctc aag cat cct gat aaa gat gtt cgc tta ctg gta gcc tgc tgc     295
Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val Ala Cys Cys
        -20                 -15                 -10
ctt gct gat att ttc agg att tat gct cct gaa gct cct tac aca tcc     343
Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro Tyr Thr Ser
    -5                   1               5                  10
cct aag gg                                                          351
Pro Lys

<210> 621
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..117

<221> sig_peptide
```

```
<222> 40..93
<223> Von Heijne matrix
      score 3.90000009536743
      seq IAWTATPSSAAFA/QA

<400> 621
atatcctgcc tgmgcctggg mcgggtggag gtgtcctgc atg gmg tct tgt gaa        54
                                           Met Xaa Ser Cys Glu
                                                       -15
atc gcg tgg act gca aca ccc agc agc gcg gcc ttt gca caa gct ttt      102
Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala Phe Ala Gln Ala Phe
            -10                 -5                  1
ccc aca gcc tgc aac a                                                118
Pro Thr Ala Cys Asn
    5

<210> 622
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..220

<221> sig_peptide
<222> 83..157
<223> Von Heijne matrix
      score 3.90000009536743
      seq LLYILSRSSGRRG/KN

<400> 622
aaagatttga aggaagatgt aagctttacc aaaattaaaa agtaaaggga gtaagtgggg     60
ggaaaaggtg cagaacagtg ta atg tgt cac tac ttg tgg aaa aaa tta tac     112
                         Met Cys His Tyr Leu Trp Lys Lys Leu Tyr
                         -25                 -20
tca aca ctt ttg tat ata ctc agc aga tct tct gga aga aga ggt aag      160
Ser Thr Leu Leu Tyr Ile Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys
-15                 -10                 -5                  1
aat ctg ata act gca gtt gcc tcc agg gca ggg aat tta ggt gtc tgg      208
Asn Leu Ile Thr Ala Val Ala Ser Arg Ala Gly Asn Leu Gly Val Trp
            5                   10                  15
aca gaa aag ggg g                                                    221
Thr Glu Lys Gly
        20

<210> 623
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 344..430

<221> sig_peptide
<222> 344..424
<223> Von Heijne matrix
      score 3.90000009536743
      seq SRMVLLSSALLST/EN

<221> misc_feature
<222> 348..349
```

<223> n=a, g, c or t

<400> 623
```
gttattgca ttttbcacaa ctcattaaat ttaggcttat aagtagctgt atcctggttt    60
ggtttcactt gttttaatta ttttttgatg atttaagaca ctagccatat ggattcaagt  120
tttttagttt ttattttcct acaccatacc atagtagaac tattactgtt gttatttata  180
ttttttaaaa aattcacttg tttttctcga gaatttgtga ctgattttta tgttatactg  240
cataattcag taatttcaca cattaacaac atccagggtc atgtgaggat gagttttcta  300
gcttctgaaa tgttctgagg atgtaatttt ttaataagag gaa atg tnn tct cac    355
                                                Met Xaa Ser His
                                                        -25
aga cta ttt ggg tgt ttt cca agt gac ttg tca cga atg gtt ttg ctc    403
Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg Met Val Leu Leu
            -20                 -15                 -10
tct agt gca ctt ctg agt aca gaa aac ca                             432
Ser Ser Ala Leu Leu Ser Thr Glu Asn
        -5                  1
```

<210> 624
<211> 233
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..231

<221> sig_peptide
<222> 91..153
<223> Von Heijne matrix
score 3.90000009536743
seq YLCLHLCAFSTEG/WM

<400> 624
```
agaggaaaga gaaaaacatg taacatgtaa caaattgttt tcctaaatga caactcagaa   60
caatagaagg cattagaaga gaccttccat atg cgc cca tca cat tct tca gcc   114
                                 Met Arg Pro Ser His Ser Ser Ala
                                         -20                 -15
tac cta tgt ctg cac ctt tgt gct ttc agt act gaa ggt tgg atg aac    162
Tyr Leu Cys Leu His Leu Cys Ala Phe Ser Thr Glu Gly Trp Met Asn
            -10                 -5                  1
cgt ctg tcc tct tct cta agg ctg gct cct cta cct ttg tac cct ttt    210
Arg Leu Ser Ser Ser Leu Arg Leu Ala Pro Leu Pro Leu Tyr Pro Phe
    5                   10                  15
tgc cta ccc agc aat tca ccc ca                                     233
Cys Leu Pro Ser Asn Ser Pro
20                  25
```

<210> 625
<211> 380
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..378

<221> sig_peptide
<222> 10..57
<223> Von Heijne matrix
score 3.90000009536743
seq RLVWLGLRAPLGG/RQ

<400> 625

```
aaggaagaa atg tgg tcg cgg ttg gtg tgg ctg ggm ctt cgg gcc cct ctg      51
          Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu
                  -15                 -10                 -5
ggt ggg cgc cag ggc ttc acc tcc aag gcg gat cct cag ggc agt ggc        99
Gly Gly Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly
        1               5                   10
cgg atc acg gct gcg gtg atc gag cac ctg gag cgt cta gcg ctt gtg       147
Arg Ile Thr Ala Ala Val Ile Glu His Leu Glu Arg Leu Ala Leu Val
15                  20                  25                  30
gac ttc ggc agc cgc gag gca gtg gcg cga ctg gag aaa gct atc gcc       195
Asp Phe Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala
                35                  40                  45
ttc gcc gac cgg cta cgc gcc gtg gac aca gac ggg gtg gag ccc atg       243
Phe Ala Asp Arg Leu Arg Ala Val Asp Thr Asp Gly Val Glu Pro Met
            50                  55                  60
gaa tcg gtc ctg gag gac aga tgt cta tac ctg aga tcc gac aat gtg       291
Glu Ser Val Leu Glu Asp Arg Cys Leu Tyr Leu Arg Ser Asp Asn Val
        65                  70                  75
gta gaa ggc aac tgt gct gat gaa tta cta caa aac tcc cat cgc gtc       339
Val Glu Gly Asn Cys Ala Asp Glu Leu Leu Gln Asn Ser His Arg Val
    80                  85                  90
gtg gag gag tac ttt gtg gcc ccc cca ggt aat atc tct tt                380
Val Glu Glu Tyr Phe Val Ala Pro Pro Gly Asn Ile Ser
95                  100                 105
```

<210> 626
<211> 276
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 27..275

<221> sig_peptide
<222> 27..269
<223> Von Heijne matrix
score 3.90000009536743
seq AIVTCKSLASIHA/LP

<400> 626

```
atcctggttt tgggacagcg gcaatc atg gcg cca cct gtg aga tac tgc atc       53
                             Met Ala Pro Pro Val Arg Tyr Cys Ile
                                 -80                 -75
ccc ggc gaa cgt ctg tgt aac ttg gag gag ggc agc ccg ggc agc ggc       101
Pro Gly Glu Arg Leu Cys Asn Leu Glu Glu Gly Ser Pro Gly Ser Gly
        -70                 -65                 -60
acc tac acc cgc cac ggc tac atc ttt tcg tcg ctw rcc ggc tgt ctg       149
Thr Tyr Thr Arg His Gly Tyr Ile Phe Ser Ser Leu Xaa Gly Cys Leu
    -55                 -50                 -45
atg aag agc agc gag aat ggc gcg ctt cca gtg gtg tct gta gtg aga       197
Met Lys Ser Ser Glu Asn Gly Ala Leu Pro Val Val Ser Val Val Arg
-40                 -35                 -30                 -25
gaa aca gag tcc cag tta ctg cca gat gtg gga gct att gta acc tgt       245
Glu Thr Glu Ser Gln Leu Leu Pro Asp Val Gly Ala Ile Val Thr Cys
                -20                 -15                 -10
aag tct cta gca tca att cac gct ttg cca a                             276
Lys Ser Leu Ala Ser Ile His Ala Leu Pro
            -5                  1
```

<210> 627

<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 174..413

<221> sig_peptide
<222> 174..353
<223> Von Heijne matrix
score 3.90000009536743
seq RLLVARLHMASLA/RR

<221> misc_feature
<222> 7
<223> n=a, g, c or t

<400> 627
accggangtg gagcctggga gccttgacgt taggaacgaa gtctaacctg gatctggagc 60
cgggtgagat caaattggga atgctttcat aatgaacgtc aaccagtcag ttccacctgt 120
gccaccattt gggcagcccc agcccatcta cccagggtat catcagtcca gct atg 176
Met
-60
gtg ggc aat cag ggt cca cag ccc ccg cca ttc cct atg gag cct aca 224
Val Gly Asn Gln Gly Pro Gln Pro Pro Pro Phe Pro Met Glu Pro Thr
-55 -50 -45
atg gcc cag tac cag gct atc agc aaa cac ctc ccc aag gta tgt caa 272
Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys Gln
-40 -35 -30
gag ccc cac ctt cct cgg ggg cac ctc cag cct caa cag cac agg ctc 320
Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg Leu
-25 -20 -15
ctt gtg gcc agg ctg cat atg gcc agt ttg gca agg aga tgt aca gaa 368
Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr Glu
-10 -5 1 5
tgg gcc aag ctc cac tgt tca gat gca agg ctg ccc tgg gtc tca gc 415
Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser
10 15 20

<210> 628
<211> 318
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 214..318

<221> sig_peptide
<222> 214..297
<223> Von Heijne matrix
score 3.90000009536743
seq GVAGVCFFRRSDA/SE

<221> misc_feature
<222> 8
<223> n=a, g, c or t

<400> 628
amattgmnkh hataractct taccatcatt ttaactggat aaaaagtgaa gtgtctaaag 60

```
atgtatatat ttsgcacgtt tgarttcaca agaggaagaa caawtttcta gccasgawac    120
catgahagga ttccaaacag agattaaact tgtcctttga ggataggtaa tgagtccaga    180
attggtgggt tcttggtttt gctgacttca aga atg aag cca cag acc ctc gca     234
                                     Met Lys Pro Gln Thr Leu Ala
                                                     -25
gtg agt gtt aca gtt ctt aaa gat ggt gtg gct gga gtt tgt ttc ttc      282
Val Ser Val Thr Val Leu Lys Asp Gly Val Ala Gly Val Cys Phe Phe
    -20                 -15                 -10
aga cgt tca gat gcg tct gaa gtt tct tcc ttc tgg                      318
Arg Arg Ser Asp Ala Ser Glu Val Ser Ser Phe Trp
-5                  1               5
```

<210> 629
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 29..169

<221> sig_peptide
<222> 29..157
<223> Von Heijne matrix
score 3.90000009536743
seq KCLFLSFAHFLMG/RT

<400> 629

```
cattttgact ggtgtaagat gatatctc atg gtg gtt ttg att tgc ctt tct        52
                               Met Val Val Leu Ile Cys Leu Ser
                                               -40
ctc atg atc agt aat act gag ctt ttt ttc ata cgc ttc ttg act gca      100
Leu Met Ile Ser Asn Thr Glu Leu Phe Phe Ile Arg Phe Leu Thr Ala
-35                 -30                 -25                 -20
tgt atg cct tct ttt gaa aag tgt ctg ttc tta tct ttt gcc cac ttc      148
Cys Met Pro Ser Phe Glu Lys Cys Leu Phe Leu Ser Phe Ala His Phe
                -15                 -10                 -5
ttg atg gga aga acc cac cgt g                                        170
Leu Met Gly Arg Thr His Arg
            1
```

<210> 630
<211> 196
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..194

<221> sig_peptide
<222> 87..152
<223> Von Heijne matrix
score 3.90000009536743
seq SLLSDILFANIFS/HS

<400> 630

```
gccatttgta tatatttgav aaatatctat tcaaatacat tgcctgcttt aaaatactgt     60
tattggtctt tttatcattg gattgt atg agt tct tta tat att ttg gat att     113
                             Met Ser Ser Leu Tyr Ile Leu Asp Ile
                                     -20                 -15
agt ctc tta tca gat ata tta ttt gca aat att ttc tcc cat tct tgg      161
Ser Leu Leu Ser Asp Ile Leu Phe Ala Asn Ile Phe Ser His Ser Trp
```

```
             -10                  -5                  1
gac gtc ttt cca ctt tct ttt ctt ttc ttt tct tt                      196
Asp Val Phe Pro Leu Ser Phe Leu Phe Phe Ser
    5                   10
```

<210> 631
<211> 339
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 53..337

<221> sig_peptide
<222> 53..304
<223> Von Heijne matrix
score 3.90000009536743
seq SSLLIILLPNTQD/LR

<400> 631

```
agttccgacg aaaaatggcg gggtctcctg agttggtggt ccttgaccct cc atg gga     58
                                                          Met Gly
caa gga gct cgc ggc tgg cac aga gag cca ggc ctt ggt ctc cgc cac      106
Gln Gly Ala Arg Gly Trp His Arg Glu Pro Gly Leu Gly Leu Arg His
        -80                 -75                 -70
tcc ccg aga aga ctt tcg ggt gcg ctg cac ctc gaa gcg ggc tgt gac      154
Ser Pro Arg Arg Leu Ser Gly Ala Leu His Leu Glu Ala Gly Cys Asp
    -65                 -60                 -55
cga aat gct aca act gtg cgg ccg ctt cgt gca aaa shc ggg gac gct      202
Arg Asn Ala Thr Thr Val Arg Pro Leu Arg Ala Lys Xaa Gly Asp Ala
-50                 -45                 -40                 -35
ctg ccg gag gag att cgg gag ccc gct ctg cga gat gcg cag tgg gta      250
Leu Pro Glu Glu Ile Arg Glu Pro Ala Leu Arg Asp Ala Gln Trp Val
                -30                 -25                 -20
cgg gac cag tta gcc agt tct tta ctc atc atc ctc tta ccc aac acc      298
Arg Asp Gln Leu Ala Ser Ser Leu Leu Ile Ile Leu Leu Pro Asn Thr
            -15                 -10                 -5
cag gat ctt agg att cag aaa gat ccc aca cca ggc ccg gg               339
Gln Asp Leu Arg Ile Gln Lys Asp Pro Thr Pro Gly Pro
        1                   5                   10
```

<210> 632
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 171..431

<221> sig_peptide
<222> 171..314
<223> Von Heijne matrix
score 3.79999995231628
seq NSLLLLLCLYIYP/HS

<221> misc_feature
<222> 376..377
<223> n=a, g, c or t

<400> 632

```
actctgaaag cagtcttcac agaaactttt cacagaagtc aaatagttaa agcaaattct    60
agatacatgg tagagaccag gagaaaatat gaataacttt cttctaaaca aggagctcag   120
tggataaacc atacctctag attccttgct tccattttcc cagaaacaag atg agg     176
                                                       Met Arg
aag aga aag atc agt gtg tgt caa caa act tgg gcc tta tta tgc aag    224
Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu Cys Lys
    -45                 -40                 -35
aac ttt ctt aaa aaa tgg aga atg aaa aga gag tcc tta atg gaa tgg    272
Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met Glu Trp
-30                 -25                 -20                 -15
ctg aat tca ttg ctc cta cta ctt tgt ttg tat ata tat cct cat agt    320
Leu Asn Ser Leu Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro His Ser
                -10                 -5                  1
cat caa gta aat gaw tdd tct tca ctg ctt acc atg gac ctg gga cgg    368
His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu Gly Arg
        5                   10                  15
gta gat rnn tkt aat gaa tcc aga ttt tct gtt gta tac aca cct gtc    416
Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr Pro Val
    20                  25                  30
acc aac acg acc cct gg                                             433
Thr Asn Thr Thr Pro
35

&lt;210&gt; 633
&lt;211&gt; 154
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 54..152

&lt;221&gt; sig_peptide
&lt;222&gt; 54..143
&lt;223&gt; Von Heijne matrix
      score 3.79999995231628
      seq XFVFVCXLLKCMS/VP

&lt;400&gt; 633
cagttaagtg tatctgtgtg tgagcaagtt tatatgtgta cacatgtttg ccc atg      56
                                                           Met
                                                           -30
tgt act tgt ctt tgt gtg tgt ctg tat atg tay aat atg caa ttt tta    104
Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe Leu
                -25                 -20                 -15
kyt ttt gtg ttt gtk tgc gww ttg cta aag tgt atg agt gtg cct ttg    152
Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro Leu
            -10                 -5                  1
tg                                                                 154

&lt;210&gt; 634
&lt;211&gt; 390
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 34..390

&lt;221&gt; sig_peptide
&lt;222&gt; 34..126
&lt;223&gt; Von Heijne matrix
      score 3.79999995231628
```

seq PVCLLVLGMAGSG/KT

<221> misc_feature
<222> 224
<223> n=a, g, c or t

<400> 634
```
ctctatggtc gggtgggtgg ggccaggagg aag atg gcg gcg tcc gca gct gcc      54
                                     Met Ala Ala Ser Ala Ala Ala
                                         -30                 -25
gct gag ctc cag gct tct ggg ggt ccg cgg cac cca gtg tgt ctg ttg     102
Ala Glu Leu Gln Ala Ser Gly Gly Pro Arg His Pro Val Cys Leu Leu
                -20                 -15                 -10
gtg ttg gga atg gcg gga tcc ggg aaa acc act ttt gta cag agg ctc     150
Val Leu Gly Met Ala Gly Ser Gly Lys Thr Thr Phe Val Gln Arg Leu
            -5                  1               5
aca gga cac ctg cat gcc caa ggc act cca ccg tat gtg atc aac ctg     198
Thr Gly His Leu His Ala Gln Gly Thr Pro Pro Tyr Val Ile Asn Leu
    10                  15                  20
gat cca gca gta cat gaa gtt ccc tnt cct gcc aat att gat att cgt     246
Asp Pro Ala Val His Glu Val Pro Xaa Pro Ala Asn Ile Asp Ile Arg
25                  30                  35                  40
gat act gta aag tat aaa gaa gta atg aaa caa tat gga ctt gga ccc     294
Asp Thr Val Lys Tyr Lys Glu Val Met Lys Gln Tyr Gly Leu Gly Pro
                45                  50                  55
aat ggc ggc ata gtg acc tca ctc aat ctc ttt gst acc aga ttt gat     342
Asn Gly Gly Ile Val Thr Ser Leu Asn Leu Phe Xaa Thr Arg Phe Asp
            60                  65                  70
cag gtg atg aaa tta ttg aga agg ccc aga aca tgt cca aat atg tgt     390
Gln Val Met Lys Leu Leu Arg Arg Pro Arg Thr Cys Pro Asn Met Cys
        75                  80                  85
```

<210> 635
<211> 137
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 22..135

<221> sig_peptide
<222> 22..81
<223> Von Heijne matrix
score 3.79999995231628
seq VLLTHGLIHYSFT/HH

<400> 635
```
caacatgcag gtttgttact t atg tat gca tgt gcc atg ttg gtg tta tta      51
                        Met Tyr Ala Cys Ala Met Leu Val Leu Leu
                        -20                 -15
act cat gga ctc atc cat tac tca ttt act cat cat tta cat tac gta      99
Thr His Gly Leu Ile His Tyr Ser Phe Thr His His Leu His Tyr Val
-10                 -5                  1                   5
ttt atc cta att ctt ccc ctc cca ccc ccg cca cag gg                  137
Phe Ile Leu Ile Leu Pro Leu Pro Pro Pro Pro Gln
            10                  15
```

<210> 636
<211> 172
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 38..172

<221> sig_peptide
<222> 38..109
<223> Von Heijne matrix
      score 3.79999995231628
      seq SMCLLLDVSSXKS/TD

<400> 636
catcttgtag aaaaaagtta caaattaaca aaaaaga atg ggc ttt ctt ggc agc       55
                                         Met Gly Phe Leu Gly Ser
                                                         -20
ccc aga cag aga aac tca atg tgt ttg ctt tta gac gtc agc tct rcc       103
Pro Arg Gln Arg Asn Ser Met Cys Leu Leu Leu Asp Val Ser Ser Xaa
            -15                 -10                 -5
aag agc aca gat aat tth cya rtc gww wtt ttg att att tat tat ctg       151
Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa Leu Ile Ile Tyr Tyr Leu
        1               5                   10
att acc aga aaa ggg cca ggg                                           172
Ile Thr Arg Lys Gly Pro Gly
15                  20

<210> 637
<211> 253
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 100..252

<221> sig_peptide
<222> 100..228
<223> Von Heijne matrix
      score 3.79999995231628
      seq FNIFLAAPSPVWQ/PQ

<400> 637
acaagcactg caatgcagca accattgacc taactatgct tccttctcca ggtcatctca     60
agcagacccc tcactctgaa gcccccggat ccaagcagg atg agc tgc caa mct       114
                                           Met Ser Cys Gln Xaa
                                                           -40
mag ctt gct cdg acc ttg act tgg ctc atg atc cgt gga aga cat ccc       162
Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile Arg Gly Arg His Pro
            -35                 -30                 -25
tac ctg acc cgt cga tca gcc cga aac ttc aac atc ttt ttg gca gct       210
Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn Ile Phe Leu Ala Ala
        -20                 -15                 -10
ccg tcc cca gtt tgg cag cct cag agg acc cgc cga ccc cag k             253
Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg Arg Pro Gln
    -5                  1               5

<210> 638
<211> 185
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 32..184
```

<221> sig_peptide
<222> 32..133
<223> Von Heijne matrix
      score 3.79999995231628
      seq FHQMALXPGTSRA/QA

<400> 638
```
acgcggcaca cagtcccagt gctcagtcac c atg tgt cct gca tgg ctc cca        52
                                   Met Cys Pro Ala Trp Leu Pro
                                                   -30
tgt tgg acg gca cag acg gaa cat ctc gat cgt tac agg aag ttc cac      100
Cys Trp Thr Ala Gln Thr Glu His Leu Asp Arg Tyr Arg Lys Phe His
        -25                 -20                 -15
cag atg gcg ctg tyt cca ggg aca tct agg gca cag gcc tta ctt tat      148
Gln Met Ala Leu Xaa Pro Gly Thr Ser Arg Ala Gln Ala Leu Leu Tyr
    -10                 -5                  1               5
aac gaa gtc cta gag aga ttt atg ttc acc cgg ctg c                    185
Asn Glu Val Leu Glu Arg Phe Met Phe Thr Arg Leu
                10                  15
```

<210> 639
<211> 206
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..204

<221> sig_peptide
<222> 73..126
<223> Von Heijne matrix
      score 3.79999995231628
      seq RICTFLLPSHSTS/GP

<400> 639
```
ttggatgacc ttaatgcttc aggacttagt aagaaataag cccgagtact tgtgaaatgt     60
taggctttgt tg atg aat gtc atg aag aga ata tgt acc ttt ctg ttg cct    111
              Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro
                          -15                 -10
tca cac tct acc tct ggc cct ctg tgc tgt tca aat gcc cat ctt cct      159
Ser His Ser Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro
-5                  1               5                   10
gct acc tcc tct acc ttg aaa cat tgc agg gct tgg agg gaa gcg bv       206
Ala Thr Ser Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
            15                  20                  25
```

<210> 640
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..506

<221> sig_peptide
<222> 21..383
<223> Von Heijne matrix
      score 3.79999995231628
      seq SLATLPFLSTVVT/DK

<221> misc_feature
<222> 495
<223> n=a, g, c or t

<400> 640
```
aagtcacatg agccaccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag      53
                      Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
                              -120                -115
cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag       101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
-110                -105                -100                -95
gtt ttc aag atg gca gca tct atg cat ggt cag ccc agt cct tct cta       149
Val Phe Lys Met Ala Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu
                -90                 -85                 -80
gaa gat gca aaa ctc aga aga cca atg gtc ata gaa atc ata gaa aaa       197
Glu Asp Ala Lys Leu Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys
            -75                 -70                 -65
aat ttt gac tat ctt aga aaa gaa atg aca caa aat ata tat caa atg       245
Asn Phe Asp Tyr Leu Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met
        -60                 -55                 -50
gcg aca ttt gga aca aca gct ggt ttc tct gga ata ttc tca aac ttc       293
Ala Thr Phe Gly Thr Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe
    -45                 -40                 -35
ctg ttc aga cgc tgc ttc aag gtt aaa cat gat gct ttg aag aca tat       341
Leu Phe Arg Arg Cys Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr
-30                 -25                 -20                 -15
gca tca ttg gct aca ctt cca ttt ttg tct act gtt gtt act gac aag       389
Ala Ser Leu Ala Thr Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys
                -10                 -5                  1
ctt ttt gta att gat gct ttg tat tca gat aat ata agc aag gaa aac       437
Leu Phe Val Ile Asp Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn
        5                   10                  15
tgt gtt ttc aga agc tca ctg att ggc ata gtt tgt ggw gtt ttc tat       485
Cys Val Phe Arg Ser Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr
    20                  25                  30
ccc agt tct ntg gct ttt act a                                         507
Pro Ser Ser Xaa Ala Phe Thr
35                  40
```

<210> 641
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 295..483

<221> sig_peptide
<222> 295..408
<223> Von Heijne matrix
score 3.79999995231628
seq LVVCVSVTVFVWS/CC

<221> misc_feature
<222> 54
<223> n=a, g, c or t

<400> 641
```
accattcgga agaggcggag tcttcttccg aggaccattc ggaagaaggc gganctacct      60
ctcatcagga ccagtctgac tgcacctgca tccttagctc agagcatccc cggagcatct     120
```

```
taagagctga gcgcastgac aactaggggc cggaccgtcg caggaggcgt ccgctggata    180
ccttccccct tccctgacct agagctctac agctgctgcc tcggtactga ccgagggttc    240
ccagagctgt ctyaccattg caaaaacgtt atagcaacag cctctgatta cgac atg      297
                                                            Met
gct gag atc acc aat atc cga cct agc ttt gat gtg tca ccg gtg gtg      345
Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val Val
        -35                 -30                 -25
gcc ggc ctc atc ggg gcc tct gtg ctg gtg gtg tgt gtc tcg gtg acc      393
Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val Thr
    -20                 -15                 -10
gtc ttt gtc tgg tca tgc tgc crc cag cag gca gag aag aag cac aag      441
Val Phe Val Trp Ser Cys Cys Xaa Gln Gln Ala Glu Lys Lys His Lys
-5                  1               5                   10
aac cca cca tac aag ttt att cac atg ctc aaa ggc wtc agc              483
Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
            15                  20                  25
```

<210> 642
<211> 309
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 235..309

<221> sig_peptide
<222> 235..279
<223> Von Heijne matrix
score 3.79999995231628
seq ILTMLILLIHEHG/IF

<400> 642

```
attratctat gtgtctgttg ttatacgaat atcatgctgt tttggtttct atatccttgt     60
aatatgtttt gaagtcaggt agtgtgatgc ctccagattt gttctttttg gtcaggattg    120
ctttggctgw tttgggttcw wttwtggttc catacaaatt ttaggattat tttttctatg    180
tctgtgaaaa gtggcatggg tattacattc aatctgtaga ttgctttgga tagt atg      237
                                                            Met
                                                            -15
gtc att tta act atg tta att ctt tta atc cat gag cat ggt att ttc      285
Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile Phe
                -10                 -5                  1
ttt tca ctt gtt tgt gtc ctc ttc                                      309
Phe Ser Leu Val Cys Val Leu Phe
        5                   10
```

<210> 643
<211> 245
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 147..245

<221> sig_peptide
<222> 147..233
<223> Von Heijne matrix
score 3.79999995231628
seq LTHTHTCTPPSTA/HP

<221> misc_feature
<222> 61

<223> n=a, g, c or t

<400> 643
aacagacccc acccggcaca acctgctcac atacacacac acaataacac acacccaatc 60
nyacgcaccc sactcagcat aacctgctca cacaatcaca cacacaatca cacacaccct 120
acccagtaca gcccactcag acacac atg ttc tca cac aat cac tca tac aca 173
Met Phe Ser His Asn His Ser Tyr Thr
-25
tac aca cca cag cac agc ccg ctc aca cac aca cac aca tgc acc cca 221
Tyr Thr Pro Gln His Ser Pro Leu Thr His Thr His Thr Cys Thr Pro
-20 -15 -10 -5
ccc agc aca gct cac cca cgc ggg 245
Pro Ser Thr Ala His Pro Arg Gly
1

<210> 644
<211> 211
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..209

<221> sig_peptide
<222> 144..188
<223> Von Heijne matrix
score 3.79999995231628
seq XMILLCFLAVSNF/NK

<400> 644
atactctttc tacattctgc tccgctttag ctgcgagagt ttaccaactc aaatctggcc 60
caagcctgga cagtctagat aaggaagcgg atcacaaaaa caaattggtc tgtgtgtgtg 120
tgcgtgcgtg cacgcgcctg tgt atg ttt kat atg att tta ctt tgt ttt ttg 173
Met Phe Xaa Met Ile Leu Leu Cys Phe Leu
-15 -10
gca gtt tcg aat ttt aat aaa ctt tta tgg gga gva ag 211
Ala Val Ser Asn Phe Asn Lys Leu Leu Trp Gly Xaa
-5 1 5

<210> 645
<211> 98
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..98

<221> sig_peptide
<222> 6..83
<223> Von Heijne matrix
score 3.79999995231628
seq LPLACFSLFGXLP/QG

<400> 645
ttcaa atg ttt tta att tta ggg aaa ttt tct cga gtt atg ggt tta cca 50
Met Phe Leu Ile Leu Gly Lys Phe Ser Arg Val Met Gly Leu Pro
-25 -20 -15
ctt gct tgc ttc tct ctc ttt ggc wtt ctt cct cag ggg ctc ctt atc 98
Leu Ala Cys Phe Ser Leu Phe Gly Xaa Leu Pro Gln Gly Leu Leu Ile
-10 -5 1 5

```
<210> 646
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 258..347

<221> sig_peptide
<222> 258..314
<223> Von Heijne matrix
      score 3.79999995231628
      seq LAXLPGXXHGGLS/AV

<221> misc_feature
<222> 294
<223> n=a, g, c or t


<400> 646
ctttcttttc cggayycagc agtggcgcct aaagtctgcg aggaggaagt cgcctctgtg     60
ccccggagtt cagaggtcta aggaagagga gataaatata tgaaggtgct gtttggcaca    120
gaatttaata gggaagaaag agacagtata actcaccagt gctgggtctc atcatcctgc    180
aatttcdgaa caactatgaa tacaaaaaga attttaaaat cccagtcctg cctagaaagg    240
ggaagtcatc tctaaat atg gtg gcc ctg ggg cag ctg gcc tdc ctg cca       290
                   Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro
                                   -15                 -10
ggc nbc tdc cat ggg ggc ctt tct gca gtg act gtg gtt ctt ccc att      338
Gly Xaa Xaa His Gly Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile
        -5                  1               5
tta ctc tgt                                                          347
Leu Leu Cys
    10

<210> 647
<211> 143
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..143

<221> sig_peptide
<222> 78..122
<223> Von Heijne matrix
      score 3.79999995231628
      seq VSFVCLLFRNVYS/NL

<400> 647
aaactggggt gagatgatat ctcaatgtag ttttcattta catctctaat gatcaataat     60
gttgagcaat ttttcat atg ccc gtt tca ttt gtc tgt ctt ctt ttc aga      110
                   Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg
                   -15                 -10                 -5
aat gtt tat tca aat cta ttg cct tct ttt ttt                          143
Asn Val Tyr Ser Asn Leu Leu Pro Ser Phe Phe
                1               5

<210> 648
<211> 232
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 41..232

<221> sig_peptide
<222> 41..121
<223> Von Heijne matrix
score 3.79999995231628
seq LPLLLPAHHGRHG/SG

<400> 648
```
aaaaagtgct cgggacaagg mcatagggct gagagtagcc atg ggc tct gga gga       55
                                            Met Gly Ser Gly Gly
                                                    -25
gac agc ctc ctg ggg ggc agg ggt tcc ctg cct ctg ctg ctc cct gct      103
Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro Leu Leu Leu Pro Ala
        -20                 -15                 -10
cat cat ggg agg cat ggc tca gga ctc ccc gcc cca gat cct agt cca      151
His His Gly Arg His Gly Ser Gly Leu Pro Ala Pro Asp Pro Ser Pro
    -5                  1               5                   10
ccc cca gga cca gct gtt cca ggg ccc tgg ccc tgc cag gat gag ctg      199
Pro Pro Gly Pro Ala Val Pro Gly Pro Trp Pro Cys Gln Asp Glu Leu
                15                  20                  25
cca agc ctc agg cca gcc acc tcc cac cac ttt                          232
Pro Ser Leu Arg Pro Ala Thr Ser His His Phe
            30                  35
```

<210> 649
<211> 133
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..132

<221> sig_peptide
<222> 4..78
<223> Von Heijne matrix
score 3.79999995231628
seq LLGRSGFSFQVSG/WG

<400> 649
```
act atg gcg gtt gga gga acg gca gtg atc aca cgt cgg ctg ctg gga       48
    Met Ala Val Gly Gly Thr Ala Val Ile Thr Arg Arg Leu Leu Gly
    -25                 -20                 -15
aga tct gga ttc tcg ttt cag gtt tcg ggg tgg ggg tgg gga gaa agg       96
Arg Ser Gly Phe Ser Phe Gln Val Ser Gly Trp Gly Trp Gly Glu Arg
-10                 -5                  1               5
gtc gat gat ttc ctt ttt tcg tcg ggt ata gac ggr a                    133
Val Asp Asp Phe Leu Phe Ser Ser Gly Ile Asp Gly
            10                  15
```

<210> 650
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 317..418

```
<221> sig_peptide
<222> 317..379
<223> Von Heijne matrix
      score 3.79999995231628
      seq ALSSLAHHPRTSG/QK

<400> 650
ggagtggaca cggaggggcc tagaggaggc ccctagaggg gcggaggggc cgatggaaag     60
ggaaaggtgg cctgtcctcc cctcccgaca ccaggggagg agccccagcc ccgcgacgag    120
gaggaagcgg actgragctg ctgaggcagt ttgacctggc ctggcagtac gggccctgca    180
ccgggatcac acggctgcag cgctggtgtc gggccaagca gatgggcttg gagcctcccc    240
cagaggtgtg gcaggtgctg aagacccacc ccggagaccc ccgcttccag tgcagtctct    300
ggcatctcta tcccct atg agg cac cac gta aga yct cct gcc ctt agc tct    352
                  Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser
                      -20                 -15                 -10
ctt gct cac cac cca aga acc tca gga cag aag cga gag ccc att gct      400
Leu Ala His His Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala
                -5                   1               5
cct gct cag ctc agc ccg g                                            419
Pro Ala Gln Leu Ser Pro
        10

<210> 651
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..396

<221> sig_peptide
<222> 52..270
<223> Von Heijne matrix
      score 3.79999995231628
      seq LAGNLALSPTGNA/KK

<400> 651
ttggaagtgg tgtggagacg gaggacagga gcagtgccca agcagcgagg g atg ctg      57
                                                         Met Leu
atc ttg aat ggc ttc cgg ggc cat gcc aca gat tcc gtg aag aac tcc      105
Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys Asn Ser
    -70                 -65                 -60
atg gaa agc atg aac act gac atg gtg atc atc cca ggg ggt ctg acc      153
Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly Leu Thr
-55                 -50                 -45                 -40
tca cag ctt cag gtg ctg gat gtc gtg gtc tac aag cca ctg aat gac      201
Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu Asn Asp
                -35                 -30                 -25
agt gtg cgg gcc cag tac tcc aac tgg ctt ctg gct ggg aac ctg gcg      249
Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn Leu Ala
            -20                 -15                 -10
ctg agc cca acc ggg aat gct aag aag cca ccc ctg ggc ctc ttt ctg      297
Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu Phe Leu
        -5                   1               5
gag tgg gtc atg gtc gcg tgg aat agc atc tca agt gag tcc atc gtc      345
Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser Ile Val
10                  15                  20                  25
caa ggg whc aaa gaa gtg cca tat ctc crg caa ctt gga gga gga aga      393
Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly Gly Arg
                30                  35                  40
cga                                                                  396
```

```
Arg

<210> 652
<211> 170
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 67..168

<221> sig_peptide
<222> 67..141
<223> Von Heijne matrix
      score 3.79999995231628
      seq YCLSNCLLXXSWG/LH

<400> 652
tgtatacaca taaccagata ttctcctaag tttttcaaaa taatagaaac agatattttg    60
ggattc atg atc tgt acc act gtt tat att acc atg gct cct tac tgt      108
       Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys
       -25                 -20                 -15
cta tca aac tgt tta ctt thw caw agt tgg ggc ctg cat ttg tat aga     156
Leu Ser Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg
    -10                 -5                  1               5
ttt cta gcc ccc at                                                   170
Phe Leu Ala Pro

<210> 653
<211> 178
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 131..178

<221> sig_peptide
<222> 131..172
<223> Von Heijne matrix
      score 3.79999995231628
      seq VSLCVAALFPLQA/YG

<400> 653
agagtacctg aaaaccttag agaaccctgg ggaaatattt atagccaggc ttcttggaga    60
ctctgggaac aggaaagtca ggaaccctgc ctttcaggaa ctgctgtatc tcagtcggct   120
tcttcatttc atg gtt tct ctc tgt gta gct gct tta ttt cct ctt cag      169
           Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln
                           -10                 -5
gct tac ggg                                                          178
Ala Tyr Gly
    1

<210> 654
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..119

<221> sig_peptide
```

<222> 36..107
<223> Von Heijne matrix
score 3.79999995231628
seq FVYLLLRNLXSYS/LP

<400> 654
tgtggttttg attggcattt ccctgatcat tactg atg ttg agc att ttt tca 53
Met Leu Ser Ile Phe Ser
-20
ttt ttt tgt agg cca ttt gta tat ctt ctt ttg aga aat ctc krt tca 101
Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu Leu Arg Asn Leu Xaa Ser
-15 -10 -5
tat tct ttg ccc acc acg gg 121
Tyr Ser Leu Pro Thr Thr
1

<210> 655
<211> 370
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..370

<221> sig_peptide
<222> 89..319
<223> Von Heijne matrix
score 3.79999995231628
seq LGLQCDAVNLAFG/RR

<400> 655
acttcgccat tttcctccgg aagtgcggat cccagcggcg gtcgtgtagc tgagcagscc 60
tggggcttgg ttctatgtcc ctgtggct atg ttt cca gtg tcc tct ggg tgt 112
Met Phe Pro Val Ser Ser Gly Cys
-75 -70
ttc caa gag caa caa gaa acg aat aaa tct ctg ccc cgc agc gcc tcc 160
Phe Gln Glu Gln Gln Glu Thr Asn Lys Ser Leu Pro Arg Ser Ala Ser
-65 -60 -55
acc cca gag acc cgg acc aag ttc aca cag gac aat ctg tgc cry gcc 208
Thr Pro Glu Thr Arg Thr Lys Phe Thr Gln Asp Asn Leu Cys Xaa Ala
-50 -45 -40
cag cgc gag cgc ctg gac tcg gcc aac ctg tgg gtk ctk gtg gac tgc 256
Gln Arg Glu Arg Leu Asp Ser Ala Asn Leu Trp Val Leu Val Asp Cys
-35 -30 -25
atc ctt cgc gac acc tcc gag gac ctg gga ctc cag tgt gac gcc gtg 304
Ile Leu Arg Asp Thr Ser Glu Asp Leu Gly Leu Gln Cys Asp Ala Val
-20 -15 -10
aac ctg gcc ttc ggg cgc cgc tgt gag gaa ctg gag gac gcg cgg cac 352
Asn Leu Ala Phe Gly Arg Arg Cys Glu Glu Leu Glu Asp Ala Arg His
-5 1 5 10
aag ctg cag yac cac ctg 370
Lys Leu Gln Xaa His Leu
15

<210> 656
<211> 197
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 137..196

```
<221> sig_peptide
<222> 137..181
<223> Von Heijne matrix
      score 3.79999995231628
      seq LVHSFLWLSSILY/IY

<400> 656
attgtatcgt tcttatgcct ttgcatcctc atagcttagc tcccacatat cagtgagaac    60
atacaatgtt tggttttcca ttcctgagtt acttcactta gaataatagt ctccaatctc   120
atccaggtca ctgcaa atg cca ttg gtt cat tcc ttc tta tgg ctg agt agt   172
                  Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser
                  -15                 -10                 -5
atc cta tat ata tac cac ctg cgg g                                    197
Ile Leu Tyr Ile Tyr His Leu Arg
            1               5

<210> 657
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..246

<221> sig_peptide
<222> 79..150
<223> Von Heijne matrix
      score 3.79999995231628
      seq XVFXFXFLXRXLX/XX

<400> 657
tttttgacat cytattaata gccattctgg ctggtgtcag gtggtatctc attgtggttt    60
cgattttgga tttctcta atg att agt aat ggt aag ttt ttt tgt ttt ttt     111
                    Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe
                                    -20                 -15
ttk gtt ttt kgt ttt tkg ttt ttg ara cgg asy ttg cyc tkg ycg ccc     159
Xaa Val Phe Xaa Phe Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro
            -10                 -5                  1
agg ctg gag tgc aat ggm aar ayc tcg gcy cac tgm aac ctc cgc ctc     207
Arg Leu Glu Cys Asn Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu
    5                   10                  15
ctg agt yca agc aat tcy ctk gcc tca gcc ccc cga ggg                 246
Leu Ser Xaa Ser Asn Ser Leu Ala Ser Ala Pro Arg Gly
20                  25                  30

<210> 658
<211> 335
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 31..333

<221> sig_peptide
<222> 31..300
<223> Von Heijne matrix
      score 3.70000004768372
      seq LRVRLTLPHSIRS/DS

<221> misc_feature
```

```
<222> 320
<223> n=a, g, c or t

<400> 658
acacgcgcct cttcacgagg tggaaacaag atg gag gat tcg gcc tcg gcc tcg      54
                                 Met Glu Asp Ser Ala Ser Ala Ser
                                 -90                 -85
ctg tct tct gca gcc gct act gga acc tcc acc tcg act cca gcg gcc      102
Leu Ser Ser Ala Ala Ala Thr Gly Thr Ser Thr Ser Thr Pro Ala Ala
        -80                 -75                 -70
ccg aca gca cgg aag cag ctg gat aaa gaa cag gtt aga aag gca gtg      150
Pro Thr Ala Arg Lys Gln Leu Asp Lys Glu Gln Val Arg Lys Ala Val
    -65                 -60                 -55
gac gct ctc ttg acg cat tgc aag tcc agg aaa aac aat tat ggg ttg      198
Asp Ala Leu Leu Thr His Cys Lys Ser Arg Lys Asn Asn Tyr Gly Leu
-50                 -45                 -40                 -35
ctt ttg aat gag aat gaa agt tta ttt tta atg gtg gta tta tgg aaa      246
Leu Leu Asn Glu Asn Glu Ser Leu Phe Leu Met Val Val Leu Trp Lys
                -30                 -25                 -20
att cca agt aaa gaa ctg agg gtc aga ttg acc ttg cct cat agt att      294
Ile Pro Ser Lys Glu Leu Arg Val Arg Leu Thr Leu Pro His Ser Ile
            -15                 -10                 -5
cga tca gat tca gaa gat atc tgt tna ttt acg aag gat gg               335
Arg Ser Asp Ser Glu Asp Ile Cys Xaa Phe Thr Lys Asp
        1               5                   10

<210> 659
<211> 197
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 20..196

<221> sig_peptide
<222> 20..106
<223> Von Heijne matrix
      score 3.70000004768372
      seq LIELNLXSPVALQ/WP

<400> 659
attcaacaag caatcaggt atg aat gca gaa ggg gct tcc cca gga aaa gaa      52
                     Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu
                                     -25                 -20
acg aac aca gga aca ttg ata gag cta aat ctg mcc agc cct gta gcc      100
Thr Asn Thr Gly Thr Leu Ile Glu Leu Asn Leu Xaa Ser Pro Val Ala
            -15                 -10                 -5
ctc cag tgg cca ctt tcc agc ccc tct tgc ctg agg atc ctc agc aac      148
Leu Gln Trp Pro Leu Ser Ser Pro Ser Cys Leu Arg Ile Leu Ser Asn
        1               5                   10
aag gtg ccc agg aac ctg agg tgg cag aaa cac tac tcc acc cac cag g    197
Lys Val Pro Arg Asn Leu Arg Trp Gln Lys His Tyr Ser Thr His Gln
15                  20                  25                  30

<210> 660
<211> 272
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
```

<222> 28..270

<221> sig_peptide
<222> 28..216
<223> Von Heijne matrix
score 3.70000004768372
seq MAAAAALRAPAQS/SV

<400> 660
atttggcct gtcaggtcca tccggcg atg ctg ggt ctg gac gag ctc ggg agg 54
Met Leu Gly Leu Asp Glu Leu Gly Arg
-60 -55
agt ggt tgt ggc cat tgc aca cag gcg gat ctg agg ttc ggc gac gcc 102
Ser Gly Cys Gly His Cys Thr Gln Ala Asp Leu Arg Phe Gly Asp Ala
-50 -45 -40
gct ggy csc gaa ccc cgg gmc agg mca acg cac agg aac acc gcc gca 150
Ala Gly Xaa Glu Pro Arg Xaa Arg Xaa Thr His Arg Asn Thr Ala Ala
-35 -30 -25
gcc cgc gtt ccc ccc ccg ccc aga gtc atg gcg gca gca gcc gct ctg 198
Ala Arg Val Pro Pro Pro Pro Arg Val Met Ala Ala Ala Ala Ala Leu
-20 -15 -10
agg gcg cct gct cag agc agt gtg acc ttt gaa gat gtg gct gta aac 246
Arg Ala Pro Ala Gln Ser Ser Val Thr Phe Glu Asp Val Ala Val Asn
-5 1 5 10
ttt tcc ctg gag gaa tgg agt ctt ct 272
Phe Ser Leu Glu Glu Trp Ser Leu
15

<210> 661
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 263..409

<221> sig_peptide
<222> 263..340
<223> Von Heijne matrix
score 3.70000004768372
seq WGNLSFHLQEAHG/SE

<400> 661
tgaaaacaaa catctactaa tgttgtcaga tggttaggaa gcaagattct gcaactatag 60
agggtaagtg tttctttggt tctgtgggtc ctctctaaaa ctctaagatc ttgaggggtg 120
catttcagaa agtgcagcgt gacccgcagt ttgtgggaag ccatggagct cggcactgcc 180
atcctaatac ttcctaaagc acaaaacccc agagacaatc tggggtcagg agagtggaag 240
gggcttgtct gccacactgg tg atg agt gcc ctg aaa gac ttc aga gaa ttt 292
Met Ser Ala Leu Lys Asp Phe Arg Glu Phe
-25 -20
ctg aac tgg tgg gga aac ctc tct ttt cat ctt cag gaa gct cat gga 340
Leu Asn Trp Trp Gly Asn Leu Ser Phe His Leu Gln Glu Ala His Gly
-15 -10 -5
agt gaa att gca gaa atg gga gct ggt att cta gag gaa aaa aat tat 388
Ser Glu Ile Ala Glu Met Gly Ala Gly Ile Leu Glu Glu Lys Asn Tyr
1 5 10 15
ggv caa caa wat cac tgt aac ta 411
Gly Gln Gln Xaa His Cys Asn
20

<210> 662
<211> 146

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..145

<221> sig_peptide
<222> 38..127
<223> Von Heijne matrix
      score 3.70000004768372
      seq PPSLFLSLPPSLS/PP

<400> 662
awbwcccgcc cacacgtggc caacctttgc gttttta atg tct ctw ccc cct ttt      55
                                         Met Ser Leu Pro Pro Phe
                                         -30                 -25
ttc cac cct tct ccc gct ccc tct ctc gct ccc cct ccc tcc ctc ttt      103
Phe His Pro Ser Pro Ala Pro Ser Leu Ala Pro Pro Pro Ser Leu Phe
                -20                 -15                 -10
ctt tcc ctc cct ccc tct ctt tct ccc cct cta ccc gcc cgg g            146
Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro Leu Pro Ala Arg
            -5                  1               5

<210> 663
<211> 65
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 10..63

<221> sig_peptide
<222> 10..48
<223> Von Heijne matrix
      score 3.70000004768372
      seq MFFLCGFLYLCFI/SF

<400> 663
caatatgct atg ttt ttc ctt tgt ggt ttt ctg tat cta tgt ttt atc tca    51
          Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser
                      -10                 -5                   1
ttt ttt ttt ttt tt                                                   65
Phe Phe Phe Phe
            5

<210> 664
<211> 182
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 30..182

<221> sig_peptide
<222> 30..155
<223> Von Heijne matrix
      score 3.70000004768372
      seq ALGIFLCPGETLS/AS

<400> 664
```

```
cgggatgccg gagccctcgg gccttggag atg aag gca ggc ccc tgc tcc tgc        53
                                Met Lys Ala Gly Pro Cys Ser Cys
                                        -40                 -35
cag gag gga ggg agg cag tgg gct cat ggg tcg gtg cct ttg cag ccg       101
Gln Glu Gly Gly Arg Gln Trp Ala His Gly Ser Val Pro Leu Gln Pro
            -30                 -25                 -20
aca gca cgc ctt gcg gcc ctg ggg atc ttt ctg tgc ccc ggc gag acc       149
Thr Ala Arg Leu Ala Ala Leu Gly Ile Phe Leu Cys Pro Gly Glu Thr
            -15                 -10                 -5
ctt tcg gcc tca ctg cat tgg aac ccc att ggg                           182
Leu Ser Ala Ser Leu His Trp Asn Pro Ile Gly
        1               5
```

<210> 665
<211> 320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 160..318

<221> sig_peptide
<222> 160..228
<223> Von Heijne matrix
score 3.70000004768372
seq TNLLCLTFQRCQS/YN

<400> 665

```
tacatcagaa accagaggcg gaaaactttc cacggtgata tgcataaaca aatatttcat      60
atttttttaca gaaagtctgg ctattgccta tagaaagaca aaaactggta acagccttat     120
tccagctaaa tttgaatgcc aggttgacac taatcatgg atg ctt tcc cag agc        174
                                          Met Leu Ser Gln Ser
                                                      -20
ttt cag aaa aac aaa acc aac ctg ttg tgt tta act ttc caa aga tgt       222
Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu Thr Phe Gln Arg Cys
            -15                 -10                 -5
cag agt tac aat tgg ctg aat att ttt gaa gct aca tat atg acg act       270
Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala Thr Tyr Met Thr Thr
        1               5                   10
ctc ttc att tca gta att aam aca aat ttt tta aaa aga tac ctc ctg       318
Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu Lys Arg Tyr Leu Leu
15                  20                  25                  30
gg                                                                    320
```

<210> 666
<211> 273
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 180..272

<221> sig_peptide
<222> 180..254
<223> Von Heijne matrix
score 3.70000004768372
seq QLLGCMVLYDCFS/FK

<400> 666

```
aagttgttgc atgtgtcaat ggttgttcct ttttatttct gagtaatgtt ccatgatatg      60
aatgtaccac agtttgttta accattcacc cactgaagga cgtttggatt gtttctaagt     120
```

```
tttgactgtg gcaagtaaag atgctatgaa cattcatgta cacatgaatt tgtaggcat      179
atg ttt tta ttt tgc tgg gag aaa agc cca aga atg cag ttg ctg ggt      227
Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly
-25                 -20                 -15                 -10
tgt atg gta ttg tat gat tgt ttt tct ttt aag aaa ctg ccg ggg g        273
Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly
                -5                  1               5
```

<210> 667
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..148

<221> sig_peptide
<222> 8..97
<223> Von Heijne matrix
score 3.70000004768372
seq FVCFFHVFYCVFC/NV

<400> 667

```
atttgt atg tct ttt ata tct gtt att ttt cct tta atc ctt tta aac       49
       Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn
       -30                 -25                 -20
cgt ttt tca ttt gtt tgt ttc ttt cat gtc ttt tac tgt gtt ttc tgc      97
Arg Phe Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys
    -15                 -10                 -5
aac gtc tct tct ttg ttc tcc tat cag ttt ctt ctt cat ttc tgt gat     145
Asn Val Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp
1               5                   10                  15
gac t                                                               149
Asp
```

<210> 668
<211> 122
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 16..120

<221> sig_peptide
<222> 16..108
<223> Von Heijne matrix
score 3.70000004768372
seq LGMGMGFFSGVKS/WI

<400> 668

```
caaggaatta cagaa atg cat gaa tac tta cct aga aac ttt cat gac ttt      51
                 Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe
                     -30                 -25                 -20
aat tct ccc aac tct aaa tta ggc atg gga atg ggc ttt ttc tca ggt      99
Asn Ser Pro Asn Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly
                -15                 -10                 -5
gtc aaa tct tgg att gga ggt ga                                     122
Val Lys Ser Trp Ile Gly Gly
            1
```

<210> 669

```
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 38..286

<221> sig_peptide
<222> 38..145
<223> Von Heijne matrix
      score 3.70000004768372
      seq ILMRDFSPSGIFG/AF

<400> 669
tcgcgcggtc ccgcacagcg gacaccagga ctccaaa atg gcg tca rtt gta cca      55
                                         Met Ala Ser Xaa Val Pro
                                                 -35
gtg aag gac aag aaa ctt ctg gag gtc aaa ctg ggg gag ctg cca agc      103
Val Lys Asp Lys Lys Leu Leu Glu Val Lys Leu Gly Glu Leu Pro Ser
-30                 -25                 -20                 -15
tgg atc ttg atg cgg gac ttc agt cct agt ggc att ttc gga gcg ttt      151
Trp Ile Leu Met Arg Asp Phe Ser Pro Ser Gly Ile Phe Gly Ala Phe
                -10                 -5                  1
caa aga ggt tac tac cgg tac tac aac aag tac atc aat gtg aag aag      199
Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys Tyr Ile Asn Val Lys Lys
        5                   10                  15
ggg agc atc tcg ggg att acc atg gtg ctg gca tgc tac gtg ctc ttt      247
Gly Ser Ile Ser Gly Ile Thr Met Val Leu Ala Cys Tyr Val Leu Phe
    20                  25                  30
agc tac tcc ttt tcc tac aag cat ctc aag cac gag tcg gg               288
Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys His Glu Ser
35                  40                  45

<210> 670
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 89..160

<221> sig_peptide
<222> 89..142
<223> Von Heijne matrix
      score 3.70000004768372
      seq GALLWMAWDGQLS/RP

<400> 670
cgtcaacatt cttttcattc tgggcctgag cgcgtggatc aagccgctgc ccttgcaact      60
gctgagcctg aagctggact tgccggtg atg gtg ata tcg gcc ggg gca ctg       112
                               Met Val Ile Ser Ala Gly Ala Leu
                                                   -15
ctg tgg atg gcg tgg gac ggc cag ctc agc cgc ccc gaa ggc gcc cgt      160
Leu Trp Met Ala Trp Asp Gly Gln Leu Ser Arg Pro Glu Gly Ala Arg
-10                 -5                  1                   5

<210> 671
<211> 137
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 44..136

<221> sig_peptide
<222> 44..97
<223> Von Heijne matrix
      score 3.70000004768372
      seq LELLGSSYNPISA/SP

<400> 671
gaattttctt cttctgctca ggctggagta caatggcaca atc atg gtt cac tgt      55
                                                Met Val His Cys
                                                            -15
aat ctt gaa ctc ctg ggc tca agt tat aat ccc atc tca gcc tct cca     103
Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile Ser Ala Ser Pro
            -10                 -5                      1
gta gct agg act ata tca tgc ccc gct att gtg g                       137
Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val
        5                   10

<210> 672
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 111..491

<221> sig_peptide
<222> 111..374
<223> Von Heijne matrix
      score 3.70000004768372
      seq CDLLLARFGLIQS/MK

<400> 672
gcccgcgctt gttgtgctga ggccgaggga gtcgccattt tggatggtga accctgaagt    60
cggtgtctgc tgcgttcacg gcaggattcg gttaggagga acagcacagc atg ctg      116
                                                       Met Leu
ggc tct gga ttt aaa gct gag cgc tta aga gtg aat ttg aga tta gtc     164
Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg Leu Val
    -85                 -80                 -75
ata aat cgc ctt aaa cta ttg gag aaa aag aaa acg gaa ctg gcc cag     212
Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu Ala Gln
-70                 -65                 -60                 -55
aaa gca agg aag gag att gct gac tat ctg gct gct ggg aaa gat gaa     260
Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys Asp Glu
                -50                 -45                 -40
cga gct cgg atc cgt gtg gag cac att atc cgg gaa gac tac ctc gtg     308
Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr Leu Val
            -35                 -30                 -25
gag gcc atg gag atc ctg gag ctg tac tgt gac ctg ctg ctg gct cgg     356
Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu Ala Arg
        -20                 -15                 -10
ttt ggc ctt atc cag tct atg aag gaa cta gat tct ggt ctg gct gaa     404
Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu Ala Glu
    -5                  1               5                   10
tct gtg tct aca ttg atc tgg gct gct cct cga ctc cag tca gaa gtg     452
Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser Glu Val
                15                  20                  25
gct gag ttg aaa ata gtt gct gat cag ctc tgt cca agt at              493
Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser
```

30 35

<210> 673
<211> 263
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 102..263

<221> sig_peptide
<222> 102..230
<223> Von Heijne matrix
score 3.70000004768372
seq VWCLXLKLVPALC/IS

<400> 673
```
tcccagcaga agggyyagcg cctggctgtc agcagcgtgt gcctcaggag ggatctgcgg     60
tgacggggtt gttacttcag taggatgagg aagagtcaca a atg cgg ggt tgg mmg    116
                                              Met Arg Gly Trp Xaa
                                                          -40
gct cct gct tgg aga sgh ytg arc acy agg aga cta cca atg ggg agc      164
Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg Leu Pro Met Gly Ser
            -35                 -30                 -25
agg cac ggt gcc agc ccg gcc tct gcc gtc tgg tgt ctg tmc ctc aag      212
Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp Cys Leu Xaa Leu Lys
        -20                 -15                 -10
tta gtc cca gct ttg tgc att agc ggg ctc acc ctc gga atc cag gga      260
Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr Leu Gly Ile Gln Gly
    -5                  1               5                   10
ttc                                                                  263
Phe
```

<210> 674
<211> 263
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 115..261

<221> sig_peptide
<222> 115..216
<223> Von Heijne matrix
score 3.70000004768372
seq RLTILXFHDNTWG/ST

<221> misc_feature
<222> 136,139..140
<223> n=a, g, c or t

<400> 674
```
gtcatttatg ccatattctg tccactagaa atgaattact aagtctggcc caaactcaag     60
tggaggcgaa ttaagctgca tctcataagg gaaagagtat cgaagaactt ctgt atg      117
                                                            Met
tat ttt aaa acc act aca nta nnb cat agt gca cat atg ctt ctg caa      165
Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu Gln
            -30                 -25                 -20
att tgc ttt ttt cgc tta aca atc tta gkt ttc cat gac aat aca tgg      213
Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr Trp
```

```
        -15                 -10                 -5
ggg tca act tca ttc tct twa gtt gck gca atg cta ttc cac tac cgg      261
Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr Arg
    1               5                   10                  15
gg                                                                   263

&lt;210&gt; 675
&lt;211&gt; 107
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 30..107

&lt;221&gt; sig_peptide
&lt;222&gt; 30..101
&lt;223&gt; Von Heijne matrix
      score 3.70000004768372
      seq LLFLFFLFLFFFF/FF

&lt;400&gt; 675
tgcactggca cacactcaca gctctgacc atg tca tca aac ata cag aga ctg       53
                                Met Ser Ser Asn Ile Gln Arg Leu
                                                -20
ggc ttc cct ctg ctt ttt ctt ttt ttt ctt ttt ctt ttt ttt ttt ttt      101
Gly Phe Pro Leu Leu Phe Leu Phe Phe Leu Phe Leu Phe Phe Phe Phe
    -15                 -10                 -5
ttt ttt                                                              107
Phe Phe
1

&lt;210&gt; 676
&lt;211&gt; 276
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 70..276

&lt;221&gt; sig_peptide
&lt;222&gt; 70..270
&lt;223&gt; Von Heijne matrix
      score 3.70000004768372
      seq LVLPLPMLPTSNR/KR

&lt;400&gt; 676
gtcacagcac cctcctgaaa actgcagctt ccttctcacc ttgaagaata atcctagaaa     60
actcacaaa atg tgt gat gct ttt gta ggt acc tgg aaa ctt gtc tcc agt    111
          Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser
                      -65                 -60                 -55
gaa aac ttt gat gat tat atg aaa gaa gta gga gtg ggc ttt gcc acc      159
Glu Asn Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr
            -50                 -45                 -40
agg aaa gtg gct ggc atg gcc aaa cct aac atg atc atc agt gtg aat      207
Arg Lys Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn
        -35                 -30                 -25
ggg gat gtg atc acc att ccc cac ctg gtc ctc ccc ctt ccc atg ctg      255
Gly Asp Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu
    -20                 -15                 -10
cca act tct aac cgc aag agg                                          276
Pro Thr Ser Asn Arg Lys Arg
```

```
-5                  1

<210> 677
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 337..441

<221> sig_peptide
<222> 337..399
<223> Von Heijne matrix
      score 3.59999990463257
      seq GQLLSFLLGTYLG/RR

<400> 677
gggattcaag gaggcccatc atgtcagaat gctgtgggtt ggcaggaggc atcacaatga      60
aattttccat gttcccaaat ttgatattca cagtactaca tataatttct cagggaagat     120
agggttggac acgatggaaa tattttggtg aaccattcgt tcccttgggt ttctttctca     180
tttggggagt gtggtttaca atgattggag caaaagtttc ctgaatcttt ttcttgtttc     240
cattttattg catggtaaaa cacaatttat ccactttctt gtcaatgagt atctagttag     300
attcctgttt tttggctaat tcaaataaaa ctatga atg ttt ttg tac cgg tct       354
                                         Met Phe Leu Tyr Arg Ser
                                             -20
ttt ggt ggg cag ttg ctt tcc ttt ctc ttg ggt aca tac cta gga agg       402
Phe Gly Gly Gln Leu Leu Ser Phe Leu Leu Gly Thr Tyr Leu Gly Arg
-15                 -10                 -5                  1
agg gaa gtt gct ggg cca cag cat ggc cag ttt tct aaa                   441
Arg Glu Val Ala Gly Pro Gln His Gly Gln Phe Ser Lys
            5                   10

<210> 678
<211> 191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 135..191

<221> sig_peptide
<222> 135..182
<223> Von Heijne matrix
      score 3.59999990463257
      seq FFCLCAFNSFLLS/PE

<400> 678
aagtgtgtgt tgctgcggca scacggaggc caaggacctc acggkwstaa aagatgacga      60
gactggcttc gggagaaaca ccatccagaa gagacctttc aaaaaacttc tagagactcc     120
ccaagacgta tgag atg ama ggc ttc ttc tgt ctg tgt gcg ttt aac tca       170
                Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser
                    -15                 -10                 -5
ttt ctc ctt agc ccc gag ggg                                           191
Phe Leu Leu Ser Pro Glu Gly
                1

<210> 679
<211> 235
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 31..234

<221> sig_peptide
<222> 31..228
<223> Von Heijne matrix
      score 3.59999990463257
      seq LTSFLSIXIFVNP/TR

<400> 679
atttttcacc actgcatagt gttacattgt atg att ttc cca cat tgc atg tac       54
                                 Met Ile Phe Pro His Cys Met Tyr
                                         -65                 -60
tgt tta gag tgt ata act aag aat gga ttg cta ggt tta aag gtg ctt       102
Cys Leu Glu Cys Ile Thr Lys Asn Gly Leu Leu Gly Leu Lys Val Leu
            -55                 -50                 -45
cca ctc tat ggg ata atg cta att ttt ttc cct aaa gtg gtt tat aac       150
Pro Leu Tyr Gly Ile Met Leu Ile Phe Phe Pro Lys Val Val Tyr Asn
        -40                 -35                 -30
aat caa ccc ttg cac tac aag tca gta atg gtg ttt cag ttg act tca       198
Asn Gln Pro Leu His Tyr Lys Ser Val Met Val Phe Gln Leu Thr Ser
    -25                 -20                 -15
ttc ttg tcg att tka att ttt gtc aac ccc act cgg g                     235
Phe Leu Ser Ile Xaa Ile Phe Val Asn Pro Thr Arg
-10                 -5                  1

<210> 680
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 173..409

<221> sig_peptide
<222> 173..334
<223> Von Heijne matrix
      score 3.59999990463257
      seq LMAXLLTVEVTHP/NS

<221> misc_feature
<222> 305
<223> n=a, g, c or t


<400> 680
taatcgaaaa gctcagtgcg caggcgcgaa gaagctggca ggggcacgag ccgggggcgg      60
gtttgaagac gcgtcgttgg gttttggagg ccgtgaaaca gccgtttgag tttggctgcg     120
ggtggagaac gtttgtcagg ggcccggcca agaaggaggc ccgcctgtta cg atg gtg     178
                                                          Met Val
tcc atg agt ttc aag cgg aac cgc agt gac cgg ttc tac agc acc cgg       226
Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser Thr Arg
        -50                 -45                 -40
tgc tgc ggc tgt tgc cat gtc cgc rcc ggg acg atc atc ctg ggg acc       274
Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu Gly Thr
    -35                 -30                 -25
tgg tac atg gta gta aac cta ttg atg gca nbt ttg ctg act gtg gaa       322
Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr Val Glu
-20                 -15                 -10                 -5
gtg act cat cca aac tcc atg cca gct gtc aac att cag tat gaa gtc       370
Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr Glu Val
```

```
                1                   5                   10
atc ggt aat tac tat tcg tct gag aga atg gct gat aat g                  410
Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
        15                  20                  25
```

<210> 681
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..302

<221> sig_peptide
<222> 21..113
<223> Von Heijne matrix
      score 3.59999990463257
      seq STFALTIXRXXSC/SS

<221> misc_feature
<222> 102
<223> n=a, g, c or t

<400> 681

```
gagttkgact gtgaagaaac atg gcg gcc gcg acg ttg act tcg aaa ttg tac      53
                      Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr
                          -30                 -25
tcc ctg ctg ttc cgc agg acc tcc acc ttc gcc ctc acc atc akc cgt       101
Ser Leu Leu Phe Arg Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg
-20                 -15                 -10                 -5
ngg gsg tca tgt tct tcg rgc gcg cct tcg atc aag gcg cgg acg cta       149
Xaa Xaa Ser Cys Ser Ser Xaa Ala Pro Ser Ile Lys Ala Arg Thr Leu
                1               5                   10
tct acg acc aca tca acg agg gga agc tgt gga aac aca tca agc aca       197
Ser Thr Thr Thr Ser Thr Arg Gly Ser Cys Gly Asn Thr Ser Ser Thr
        15                  20                  25
agt atg aga aca agt agt tcc ttg gag gcc ccc atc cag gcc aga agg       245
Ser Met Arg Thr Ser Ser Ser Leu Glu Ala Pro Ile Gln Ala Arg Arg
    30                  35                  40
acc agg tcc acc cag cag ctg ttt gcc cag agc tgg agc ctc agc dtg       293
Thr Arg Ser Thr Gln Gln Leu Phe Ala Gln Ser Trp Ser Leu Ser Xaa
45                  50                  55                  60
aag atg atg c                                                         303
Lys Met Met
```

<210> 682
<211> 328
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..327

<221> sig_peptide
<222> 79..201
<223> Von Heijne matrix
      score 3.59999990463257
      seq LHTSVTLFLLSYC/DC

<221> misc_feature

```
<222> 258
<223> n=a, g, c or t


<400> 682
agatgattcc ctgattctcc agagagatta cacacttcgt ttgtggctaa ggttactgtg      60
acccaatgaa agaagaaa atg aaa gcc ata aag aaa agt ctt aca gaa gaa       111
                    Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu
                        -40                 -35
gaa tac ctg tac ctg gac ttt tct cac caa aca gaa gga tgc atc ttt       159
Glu Tyr Leu Tyr Leu Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe
-30                 -25                 -20                 -15
cct ctt cat aca tct gta act tta ttt ctg tta tct tac tgt gac tgt       207
Pro Leu His Thr Ser Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys
                -10                  -5                   1
aaa atc ttt aaa att tgc tta gtt gtc acc aaa gag gtg agt aga gat       255
Lys Ile Phe Lys Ile Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp
        5                   10                  15
avn tca cta cta aga gat gac ctg atc cag gat gtt gaa ata cag att       303
Xaa Ser Leu Leu Arg Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile
    20                  25                  30
att tca agg cag gag ctc cca cca a                                     328
Ile Ser Arg Gln Glu Leu Pro Pro
35                  40

<210> 683
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 386..445

<221> sig_peptide
<222> 386..427
<223> Von Heijne matrix
      score 3.59999990463257
      seq FLCVCYFIRKSTS/FF

<221> misc_feature
<222> 307
<223> n=a, g, c or t


<400> 683
ttaacatctt ccactgaaaa gaaaagataa tgatataaat aaagcaattt aaatcaagtc      60
taaggtatag gaaggtattt aagaaagaag caaacattct ctagatgttg ttatccaaaa     120
tatattctct tttgcagttt actgaaataa tttcttcagt gtgtgggaat ttcctttgca     180
tccagcttta ctatagagat gacatcacac caacagtgac acgacttgtt tacaagaggg     240
tggtataaac agcaaatgtt cttccttaaa acagatttct tgttgaactt caacagaaaa     300
agaagcngta aatgtagaag gaagaacagg agatagtctt taacatgtag ggtaaaatct     360
aaggtagagg agagagcagc tgata atg ttt tta tgt gtt tgc tac ttt att       412
                            Met Phe Leu Cys Val Cys Tyr Phe Ile
                                            -10
agg aag tct act tcc ttc ttt tcc ata tct agt ag                        447
Arg Lys Ser Thr Ser Phe Phe Ser Ile Ser Ser
-5                  1               5

<210> 684
<211> 217
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 5..217

<221> sig_peptide
<222> 5..139
<223> Von Heijne matrix
      score 3.59999990463257
      seq AWWLLLPVWKLGG/QL

<400> 684
tcaa atg ggg aag ccg aga ggt ggt gag atg ctt gag gtt gta aag act        49
     Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr
     -45                 -40                 -35
gtc tcc act ttc act ttg gga ggg tgg aaa ggg act gct cct gtg tcc          97
Val Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser
-30                 -25                 -20                 -15
tgc gcc tgg tgg ctg ctt ctc cca gtt tgg aag ctg gga ggg cag ctt         145
Cys Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu
                -10                 -5                  1
gag cgc agg aag aat cca aag gaa tac tgt ctt ggc tcc tgg gtg tgg         193
Glu Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp
        5                   10                  15
ctc agt cct cag ctg gct cca agg                                         217
Leu Ser Pro Gln Leu Ala Pro Arg
    20                  25

<210> 685
<211> 132
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..130

<221> sig_peptide
<222> 77..124
<223> Von Heijne matrix
      score 3.59999990463257
      seq FTFISTLLFVFLG/VV

<400> 685
tgaaatccta gcttgaatat ttacattagt cttgtttctc aaacttgact ctttggtttg     60
atcgacattt tcccta atg ctg att ttc acc ttt att tct act ttg ctg ttt    112
                  Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe
                      -15                 -10                 -5
gta ttc ttg gga gtt gtg gg                                           132
Val Phe Leu Gly Val Val
                1

<210> 686
<211> 260
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 120..260

<221> sig_peptide
<222> 120..230
```

<223> Von Heijne matrix
score 3.59999990463257
seq PGSGLCSMAAVQA/GN

<400> 686
acatctcctt ggccccgccc cactcccgcg gggctattgt ccccggtaaa ctgcagtttc 60
tggttcgaga ctccaatcct gtttcgaatt gctgcttgct gcccccttggg ctggggata 119
atg gaa gtt ctt tcb mtt ccc aac tct ttc cag acc caa gca ctc tgg 167
Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp
-35 -30 -25
gac tca ctc cat agt cca gga gtt cca ggt tcc gga tta tgt tcc atg 215
Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met
-20 -15 -10
gca gca gtc caa gca gga aac caa gcc atc tac tct gcc tcg ggg 260
Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly
-5 1 5 10

<210> 687
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 332..472

<221> sig_peptide
<222> 332..457
<223> Von Heijne matrix
score 3.59999990463257
seq LLTQAGFPRRGEA/AP

<400> 687
tgtgtatgtg tgaaaatcag gaagagccag cggggagtgt gtgttgccat cgcgtctccg 60
cctgcagggg cgggacccca ggaggaggga gaggacagag ccactgcaga ggaccagact 120
gggaaaacaa cgatatggca ggagccagtc ttggggcccg cttctaccgg cagatcaaaa 180
gacatccggg gctgggacag aaagaacaac ccggagccct ggaaccgcct gagccccaat 240
gaccaataca agttccttgc agtttccact gactataaga agctgaagaa ggaccggcca 300
gacttctaag ccaggctggg ctgccagtgc c atg caa gcc aca gcc agc cag 352
Met Gln Ala Thr Ala Ser Gln
-40
ccc atc cac ttc ttc crs tcc tcc ccg cag gcc cca agg cat cac tcc 400
Pro Ile His Phe Phe Xaa Ser Ser Pro Gln Ala Pro Arg His His Ser
-35 -30 -25 -20
ggc cac cct gtc ccg cta ctg ctt aca cag gcc ggg ttc cca cgc aga 448
Gly His Pro Val Pro Leu Leu Leu Thr Gln Ala Gly Phe Pro Arg Arg
-15 -10 -5
ggg gag gct gct cca ccc cta ctc c 473
Gly Glu Ala Ala Pro Pro Leu Leu
1 5

<210> 688
<211> 107
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 5..106

<221> sig_peptide
<222> 5..94
<223> Von Heijne matrix

score 3.59999990463257
seq LCTFTLNLTAVRT/IX

<400> 688
```
acac atg cga ggg tak aac tgh gtg ttc agg gtt ttc tct gaa agc ctg      49
     Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu
     -30                 -25                 -20
aag gga ttg tgt acw ttt aca ttg aac ttg act gca gtt aga acc att      97
Lys Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile
-15                 -10                 -5                  1
arc cta gat g                                                        107
Xaa Leu Asp
```

<210> 689
<211> 377
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 258..377

<221> sig_peptide
<222> 258..353
<223> Von Heijne matrix
score 3.59999990463257
seq RLTISTXLSTSXX/FM

<400> 689
```
aaacacaaca accagattcc tcctctaaag aagcccctgg gagcacagct catcaccatg     60
gactggacct ggaggttcct ctttttggtg acagcagcta cagatgtcca gtcccaggtc    120
cagctggtgc aagtctgggt actgaggtga agaggcctgg gtcctcggtg aaggtctcct    180
gtaagacttc tggaggcacc ttcagtagta atgccatcac gtgggtgcga caggcccctg    240
gacaagggct tgagtgg atg ggr agg atc atc ccc atg gtt gaa aaa gcg       290
                   Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala
                           -30                 -25
gac acc gca cag aag ttc cag ggc aga ctc act att agt aca dkv cta      338
Asp Thr Ala Gln Lys Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu
    -20                 -15                 -10
tcg acg agc asa gsc ttc atg gaa ctg agc agt ctg aga                  377
Ser Thr Ser Xaa Xaa Phe Met Glu Leu Ser Ser Leu Arg
-5                  1               5
```

<210> 690
<211> 388
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 53..388

<221> sig_peptide
<222> 53..253
<223> Von Heijne matrix
score 3.59999990463257
seq IIMVFVFICFCYL/HY

<400> 690
```
ataaattcag tagttacctt agtagacaaa tcatttgaac caagttgcgg ac atg aat     58
                                                          Met Asn
ctt gtt att tgt gtc cta ctt ttg tcc att tgg aaa aat aat tgc atg      106
Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn Cys Met
```

```
-65                 -60                 -55                 -50
act aca aac caa acc aat gga tct tct act aca gga gat aaa cct gtt     154
Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys Pro Val
                -45                 -40                 -35
gaa tca atg cag aca aaa ttg aac tac ctt aga aga aat cta ctc att     202
Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu Leu Ile
            -30                 -25                 -20
tta gtt ggt att atc atc atg gtt ttt gtc ttt atc tgt ttt tgt tat     250
Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe Cys Tyr
        -15                 -10                 -5
ctc cat tat aat tgt ctg agc gat gat gcg tcc aaa gca gga atg gtc     298
Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly Met Val
    1               5                   10                  15
aag aaa aaa ggc ata gca gcc aag tca tct aaa aca tca ttc agt gaa     346
Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe Ser Glu
                20                  25                  30
gcc aag aca gcc tct caa tgc agt tca gaa aca caa acc ggg             388
Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly
            35                  40                  45
```

<210> 691
<211> 408
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 304..408

<221> sig_peptide
<222> 304..387
<223> Von Heijne matrix
score 3.59999990463257
seq IFFSLTLSGCKFS/KL

<400> 691

```
cttgacttct gtgcactcac aggcttgatc aacaccacaa ggaagctgcc aaggccatcc      60
tctgaaacca cagcccgagc tctatgttgg cccctttttag ccatggctgg aatggctgag    120
acacaggaca ccaagtccct aggctgtaca cagcactggg accctgggcc ctgcccatgg     180
aacaattttt tcctcctaaa tcttcaggcc tgtgatggga ggggctaccg caaaggtctc     240
tgacatgccc cagatacatt ttccctattg tcttggggat taacatttgg ctcctcgtta     300
ctt atg caa att tct gca gcc agc ttg aat ttc tcc tca aaa aat gga       348
    Met Gln Ile Ser Ala Ala Ser Leu Asn Phe Ser Ser Lys Asn Gly
                -25                 -20                 -15
att ttc ttt tct tta aca ttg tca ggc tgc aaa ttt tcc aaa ctt tta       396
Ile Phe Phe Ser Leu Thr Leu Ser Gly Cys Lys Phe Ser Lys Leu Leu
            -10                 -5                  1
tgc cct ttt ggg                                                       408
Cys Pro Phe Gly
    5
```

<210> 692
<211> 322
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 106..321

<221> sig_peptide
<222> 106..261
<223> Von Heijne matrix

```
      score 3.59999990463257
      seq LVWDCLLPPPSFF/LL

<221> misc_feature
<222> 284..285
<223> n=a, g, c or t


<400> 692
tgttacctgt gtgcatatat tatatctact taagttttat tctaaataag gagcttgtga     60
tarttgtttc cgttttgtaa ttagaaggta ttatatgttc ctatc atg att ttt gag    117
                                                  Met Ile Phe Glu
                                                              -50
cct gtg gtt ctg aaa cca gtg ttt cta aat att ttt ttc ttt tca cat      165
Pro Val Val Leu Lys Pro Val Phe Leu Asn Ile Phe Phe Phe Ser His
            -45                 -40                 -35
cat gta ttt aca gtg ttt ttc agt ggt agt cat gtt gac atc ctg agt      213
His Val Phe Thr Val Phe Phe Ser Gly Ser His Val Asp Ile Leu Ser
        -30                 -25                 -20
cgc aca gtt ctt gtt tgg gac tgt ctt ctt cct cct cct tcc ttc ttc      261
Arg Thr Val Leu Val Trp Asp Cys Leu Leu Pro Pro Pro Ser Phe Phe
    -15                 -10                 -5
ctc ctt ctt ctt tct tct tcc tnn tcc ttv ctc ctc ctt vct dct tct      309
Leu Leu Leu Leu Ser Ser Ser Xaa Ser Xaa Leu Leu Leu Xaa Xaa Ser
1               5                   10                  15
tcc tcc tcc cgg g                                                    322
Ser Ser Ser Arg
            20

<210> 693
<211> 153
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 93..152

<221> sig_peptide
<222> 93..134
<223> Von Heijne matrix
      score 3.59999990463257
      seq LVPLLSHLLFKFT/WP

<400> 693
ctttttagt aggggagctt gataatggaa aacagtatga ggaattgtca cactgtatga      60
gattttaaac taaggcataa gaatgaaacc gg atg tta gtt cct ctt tta tca      113
                                    Met Leu Val Pro Leu Leu Ser
                                                        -10
cac ttg ctc ttc aag ttt acc tgg cca aaa tkg tcc cag g                153
His Leu Leu Phe Lys Phe Thr Trp Pro Lys Xaa Ser Gln
        -5                  1               5

<210> 694
<211> 234
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 23..232

<221> sig_peptide
```

```
<222> 23..169
<223> Von Heijne matrix
      score 3.59999990463257
      seq FGVLSGLXQXVSP/GK

<400> 694
aagcgcggga cgcwrcaaag tc atg gac cgc aac ccc tcg ccg ccg ccg ccg      52
                         Met Asp Arg Asn Pro Ser Pro Pro Pro Pro
                                         -45                 -40
ggt cgc gac aag gag gag gag gag gag gtg gcc ggt gga gac tgc ata      100
Gly Arg Asp Lys Glu Glu Glu Glu Glu Val Ala Gly Gly Asp Cys Ile
                -35                 -30                 -25
ggg agc acg gtc tac agc aaa cac tgg ctc ttc ggc gtc ctc agc gga      148
Gly Ser Thr Val Tyr Ser Lys His Trp Leu Phe Gly Val Leu Ser Gly
            -20                 -15                 -10
ctc akc cag rtt gtt agc cct gga aaa cac caa aat cta ggc tca grt      196
Leu Xaa Gln Xaa Val Ser Pro Gly Lys His Gln Asn Leu Gly Ser Xaa
        -5                  1               5
gmt gag gag cag ctg acg gag ctt gat gaa cga aat gg                   234
Xaa Glu Glu Gln Leu Thr Glu Leu Asp Glu Arg Asn
10                  15                  20

<210> 695
<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 344..454

<221> sig_peptide
<222> 344..412
<223> Von Heijne matrix
      score 3.59999990463257
      seq LGCHFFSLALLNT/GP

<221> misc_feature
<222> 285,342..343
<223> n=a, g, c or t


<400> 695
tgttatatgg gtctcttgaa gacaatatac agttgggtct ttcttcttta ttcaacttac      60
cactctgtgc cttttaagtg gggcatttag ctaakwtaca ttcaaggtta atattgatat      120
gtgcatattt gatcctgtca tsatgttamc tggtcgttat tcagactaga ttgtgtagtt    180
tttttatagt gtgtcagtag ttacgttttg tggtggtcag tgacagtgat tttttttcccc    240
atgtttagca tccctttaag gacctattgt aaagcaggtc tagtngtaac aaatttcctt    300
ggcatttact tatcaggaaa ggatcttttt ttctcctttg cnn atg aag ctt agt      355
                                                Met Lys Leu Ser
                                                            -20
ttg gct gga tat gaa att ctt ggt tgt cat ttc ttt tct tta gca ctg      403
Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe Ser Leu Ala Leu
                -15                 -10                 -5
cta aat aca ggc ccc caa tat ctt ttg gct tat agg gtt tct gct gaa      451
Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg Val Ser Ala Glu
            1               5                   10
agg t                                                                455
Arg

<210> 696
<211> 153
<212> DNA
```

```
<213> Homo sapiens

<220>
<221> CDS
<222> 8..151

<221> sig_peptide
<222> 8..127
<223> Von Heijne matrix
      score 3.59999990463257
      seq ITALSQSLQPLRK/LP

<400> 696
agacaag atg gcg acg tcc gtg ggg cac cga tgt ctg gga tta ctg cac       49
        Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His
        -40                 -35                 -30
ggg gtc gcg ccg tgg cgg agc agc ctc cat ccc tgt gag atc act gcc       97
Gly Val Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala
    -25                 -20                 -15
ctg agc caa tcc cta cag ccc tta cgg aag ctg cct ttt aga gcc tct      145
Leu Ser Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser
-10                 -5                  1               5
ygc acg gg                                                           153
Xaa Thr

<210> 697
<211> 493
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 116..493

<221> sig_peptide
<222> 116..262
<223> Von Heijne matrix
      score 3.59999990463257
      seq YCLVTLVFFYSSA/SF

<400> 697
aaaagctgac gacttcggtc tgcgccggaa gtgcatgagc tgccgatgtg gtgcttagtg     60
attgcggttt cggtcgctct cccgtgtttc ccgggctggg tatttgcctc gcacc atg     118
                                                             Met
gcg ccc aag ggc aaa gtg ggc acg aga ggg aag aag cag ata ttt gaa      166
Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe Glu
            -45                 -40                 -35
gag aac aga gag act ctg aag ttc tac ctg cgg atc ata ctg ggg gcc      214
Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly Ala
        -30                 -25                 -20
aat gcc att tac tgc ctt gtg acg ttg gtc ttc ttt tac tca tct gcc      262
Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser Ala
    -15                 -10                 -5
tca ttt tgg gcc tgg ttg gcc ctg ggc ttt agt ctg gca gtg tat ggg      310
Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr Gly
1               5                   10                  15
gcc agc tac cac tct atg agc tcg atg gca cga gca gcg ttc tct gag      358
Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser Glu
            20                  25                  30
gat ggg gcc ctg atg gat ggt ggc atg gac ctc aac atg gag cag ggc      406
Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln Gly
        35                  40                  45
atg gca gag cac ctt aag gat gtk atc cta ctg aca gcc atc gtg cag      454
```

```
Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln
    50                  55                  60
gtg ctc agc tgc ttc tct ctc tat gtc tgg tcc ttc tgg                493
Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp
65                  70                  75

<210> 698
<211> 174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..172

<221> sig_peptide
<222> 8..94
<223> Von Heijne matrix
      score 3.59999990463257
      seq AFNKAVWFTPCSC/QE

<400> 698
aacaaag atg gcg gcg gtg act gtg acg gtg acg aag acg gcg gcg gcg      49
        Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala
                        -25                 -20
gcg acg gca ttt aac aag gcg gtg tgg ttt act cca tgc agt tgt cag      97
Ala Thr Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln
-15                 -10                 -5                  1
gag gta agt agc agg ctg ccg gct cgg acg gcg gcg acg cgg cag gac     145
Glu Val Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp
            5                   10                  15
agg gcg gat aag aag gag cgg ccc tgt gg                              174
Arg Ala Asp Lys Lys Glu Arg Pro Cys
        20                  25

<210> 699
<211> 300
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 199..300

<221> sig_peptide
<222> 199..255
<223> Von Heijne matrix
      score 3.59999990463257
      seq PGSAICLWHSTLG/GX

<221> misc_feature
<222> 261
<223> n=a, g, c or t


<400> 699
attttgtctc ggcagcggtg gccgwagctc catcgcattt tatgtttctg gcgagaaggg     60
aacggagttt tcatcaggta gattggtttt trtgcggccg tcctccaccg tttcctccag    120
gacagcacct agtcgtggcc ggaggagtct catagctgtc agaaagaata agactgattt    180
tatgggaaaa ttaagcag atg ctc cag ttt gag aaa cct gga tct gcg atc      231
                    Met Leu Gln Phe Glu Lys Pro Gly Ser Ala Ile
                                    -15                 -10
tgt ttg tgg cac agc act ttg gga ggy ymn ggc ggg cgt gag att gds     279
```

```
Cys Leu Trp His Ser Thr Leu Gly Gly Xaa Gly Gly Arg Glu Ile Xaa
            -5                  1               5
agt ttg aga cca gcc tgc ggg                                         300
Ser Leu Arg Pro Ala Cys Gly
    10                  15

<210> 700
<211> 159
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 86..157

<221> sig_peptide
<222> 86..139
<223> Von Heijne matrix
      score 3.59999990463257
      seq LAILLKWVSNSKS/FL

<400> 700
ttttatagct atcacaaatg agattgcttt cttaattttt tttcagatta atcatagtta     60
acaaatagaa actattgatt ttygt atg ttg att tcg tat ctt gca att tta      112
                            Met Leu Ile Ser Tyr Leu Ala Ile Leu
                                        -15             -10
cta aaa tgg gtt agc aat tct aag agt ttt ttg gtg aag gca tcg gg       159
Leu Lys Trp Val Ser Asn Ser Lys Ser Phe Leu Val Lys Ala Ser
            -5                  1               5

<210> 701
<211> 274
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..273

<221> sig_peptide
<222> 46..90
<223> Von Heijne matrix
      score 3.59999990463257
      seq LQTLAFWSAYVPC/QT

<400> 701
agtgtgtccg gaattggtgg gttcttggtc tcactgagtt ctaga atg aag ctg cag     57
                                                  Met Lys Leu Gln
                                                  -15
acc ctc gca ttc tgg tca gcc tat gtg cca tgc cag acc cag gac cgg      105
Thr Leu Ala Phe Trp Ser Ala Tyr Val Pro Cys Gln Thr Gln Asp Arg
    -10                 -5                  1               5
gat gcc ccg cgc ctc acc ctg gag cag att gac ctc ata cgc cgc atg      153
Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu Ile Arg Arg Met
                10                  15                  20
tgt gcc tcc tat tct gag ctg gag ctt gtg acc tcg gct aaa gct ctg      201
Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala Lys Ala Leu
            25                  30                  35
aac gac act cag aaa ttg gcc tgc ctc atc ggt gta gag ggt ggc cac      249
Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val Glu Gly Gly His
        40                  45                  50
tcg ctg gac aat agc ctc tcc agg g                                    274
Ser Leu Asp Asn Ser Leu Ser Arg
```

55 60

<210> 702
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 107..175

<221> sig_peptide
<222> 107..148
<223> Von Heijne matrix
score 3.5
seq PACLSSFVIPSLL/SP

<400> 702
```
ttgctttcta agacacttac tttcatcggc actttcagat ttttgaatta tactttctca      60
atttgatttt tcaagtgagt tattaggata taggtgggag tggaga atg cct gcc        115
                                                   Met Pro Ala
tgc ctt tct tcc ttt gtc att ccc tct ctc ctt tct ccc tcc tcc cct       163
Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro Ser Ser Pro
    -10                 -5                  1               5
ccc tcc ata ggg                                                       175
Pro Ser Ile Gly
```

<210> 703
<211> 298
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 197..298

<221> sig_peptide
<222> 197..244
<223> Von Heijne matrix
score 3.5
seq SFAGSCTILGASS/HS

<400> 703
```
ttttcatgtg tctgttggct gcataaatgt cttcttctga gaagtgtctg ttcatatcct      60
tcgcccactt gttgatgagg ttgttttttt cttgtaaatt tgtttgtgtt cattgtaagt     120
tctggatatt agccctttgt cagatgagta gattgtaaaa attttctccc attctacagg     180
ttgcctgttc actctg atg gta gtt tct ttt gct ggt tct tgc aca att cta     232
                  Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu
                      -15                 -10                 -5
ggc gcc agt agc cat tca ttc ccc att gaa gtc agc ctg ttc cca gtg       280
Gly Ala Ser Ser His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val
                1               5                   10
gac tgt ggc ttc ctc ttg                                               298
Asp Cys Gly Phe Leu Leu
        15
```

<210> 704
<211> 136
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> 41..136

<221> sig_peptide
<222> 41..100
<223> Von Heijne matrix
score 3.5
seq AVSQSWLAAPSTS/WV

<400> 704
```
ttcttattaa agatttattt ttgtagagac agatgtctca atg tgt tgc cca ggc       55
                                            Met Cys Cys Pro Gly
                                            -20
tgg aac gca gtg tcg caa tct tgg ctc gct gca cct tcc acc tcc tgg      103
Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala Pro Ser Thr Ser Trp
-15                 -10                 -5                  1
gtt caa gag att ctc gta ctt cag cct cca ggg                          136
Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
            5                   10
```

<210> 705
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 225..431

<221> sig_peptide
<222> 225..386
<223> Von Heijne matrix
score 3.5
seq IRCPLIFLXXVSG/TX

<400> 705
```
agaggactay gcgagagcgt ctacggttgt gccaaaggaa aaaaaatgtt cctaagaaaa     60
gagtatacaa agttgtgttc atcaaagtct ggaacccaaa ggtgtccctc caaagctgta    120
cacgacagag aaaacgcgaa ctgaaagaag aagcaggtcc caaggggcca ggcgcctcct    180
ccacctcctc ctcctcctag gattaacctc catttcagct aatc atg gga gag att     236
                                                 Met Gly Glu Ile
aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa      284
Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys
-50                 -45                 -40                 -35
aab dtw atk gtg gat gat gat gac agt aag ata tgg tcg chc tat gac      332
Xaa Xaa Xaa Val Asp Asp Asp Asp Ser Lys Ile Trp Ser Xaa Tyr Asp
                -30                 -25                 -20
gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg cyc yct gtc      380
Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Xaa Xaa Val
            -15                 -10                 -5
agt gga act gha gat gtc ttt ttc cgg cag att ttg gct ctg act gga      428
Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr Gly
        1               5                   10
tgg gg                                                               433
Trp
15
```

<210> 706
<211> 419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

```
<222> 284..418

<221> sig_peptide
<222> 284..331
<223> Von Heijne matrix
      score 3.5
      seq SHSHLSLVGHSRA/CG

<400> 706
attgaaaatc attaaaaatc ttagcaattg ttttaaatta tctaattttt ttctccaaat     60
aatatctatt ttagcagcca aatcaccaca aatcattggt ttttatcttt agttgtgggt    120
gcacagcggg tgcgtgtatt ttggggcatg tgaggtgtct tgatgcgttc atgcagtgtg    180
taacagtcac atcagggtaa atgggacatc tttcacctca agcatttatc cttcgtgtta    240
tggacaccct cagctggaaa ggggggctgc gtcgtgagta tga atg gat gca agt      295
                                                Met Asp Ala Ser
                                                    -15
cat agc cac ctg agc ctg gtg ggg cac agc agg gcc tgt gga gtc aca      343
His Ser His Leu Ser Leu Val Gly His Ser Arg Ala Cys Gly Val Thr
        -10                 -5                  1
tcc cgg cct cat gct cgg cat agg gga cgc tgc tta ggt cca tgc agt      391
Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu Gly Pro Cys Ser
5                   10                  15                  20
cgc tca ggg ccc agg ctg tgc agc gcc a                                419
Arg Ser Gly Pro Arg Leu Cys Ser Ala
                25

<210> 707
<211> 382
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 200..382

<221> sig_peptide
<222> 200..301
<223> Von Heijne matrix
      score 3.5
      seq LISHDPWPRGAFA/LS

<221> misc_feature
<222> 365
<223> n=a, g, c or t


<400> 707
gttacttatg gttgagagag aatatttttc agattttatt ggacattgat atttgtaaat     60
tgttcattcc ttttgcccag ttttctattg agtggttcat agtttctcat gggtatccaa    120
gagttctgga tatgtagagg tggagggtca atctcatcay ttccttgttt taaaaatctt    180
ccatggtttt gtcatcact atg ggc tca aac gcc gtg gtg tgg cat aca aag      232
                    Met Gly Ser Asn Ala Val Val Trp His Thr Lys
                                    -30                 -25
ccc tca ctt ctg aac cac cct gct tcc agc ctc atc tcc cat gat ccc      280
Pro Ser Leu Leu Asn His Pro Ala Ser Ser Leu Ile Ser His Asp Pro
            -20                 -15                 -10
tgg cca cgc ggt gcg ttt gcg ctt tca tgt cca agt gct tcc ttc atg      328
Trp Pro Arg Gly Ala Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met
        -5                  1                   5
ttg ttt tct tcc tta caa tgc cct ttc cct tat tgd naa aca gag tgc      376
Leu Phe Ser Ser Leu Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys
10                  15                  20                  25
aac gwg                                                              382
```

Asn Xaa

<210> 708
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 215..382

<221> sig_peptide
<222> 215..268
<223> Von Heijne matrix
score 3.5
seq ACLFRAVADQVYG/DQ

<400> 708
```
aagtgacgct acaggggcca gctatgctcc cgggagtgtt gatgttttcc agtcattccg      60
gctgacagcg ttcaagttgg aatcctggag gggaggtgtt tttcctgtcg tacgtgggac     120
aggccacgct gtccgtccgc agtaccgacg cctgcagcag gagcattggt ttgaaaaggc     180
cctacgagac aagaagggct tcatcatcaa gcag atg aag gag gat ggc gcc tgt     235
                                      Met Lys Glu Asp Gly Ala Cys
                                                  -15
ctc ttc cgg gct gta gct gac cag gtg tat gga gac cag gac atg cat      283
Leu Phe Arg Ala Val Ala Asp Gln Val Tyr Gly Asp Gln Asp Met His
    -10                 -5                  1               5
gag gtt gtg cga aag cat trc atg gac tat ctg atg aag aat gcc gac      331
Glu Val Val Arg Lys His Xaa Met Asp Tyr Leu Met Lys Asn Ala Asp
                10                  15                  20
tay ttc tcc arc tat gtc aca gag gac ttt acc acc tac att akc agg      379
Tyr Phe Ser Xaa Tyr Val Thr Glu Asp Phe Thr Thr Tyr Ile Xaa Arg
            25                  30                  35
aag cg                                                               384
Lys
```

<210> 709
<211> 149
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..147

<221> sig_peptide
<222> 76..138
<223> Von Heijne matrix
score 3.5
seq VLIMIXEAXNVWC/GD

<221> misc_feature
<222> 123..124
<223> n=a, g, c or t

<400> 709
```
acctaatatt aaaaatcttc ttctctaaaa gtggcatata accctgatca agaggtcatg      60
ggctcagttt gatat atg gtt cac ctc att ctt act gaa gtc ctc att atg     111
                 Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met
                     -20                 -15                 -10
atc akc gag gcn nsg aat gtg tgg tgt ggg gat tcg gg                   149
Ile Xaa Glu Ala Xaa Asn Val Trp Cys Gly Asp Ser
```

```
           -5                  1

<210> 710
<211> 167
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 15..167

<221> sig_peptide
<222> 15..155
<223> Von Heijne matrix
      score 3.5
      seq CLXFGILASEVYS/WN

<400> 710
atatttcatg gcga atg tac cac aat tta ttt gct ctg ttg ttg ata gac       50
                Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp
                        -45                 -40
att cat gtt gtt cta gtt ttt tac tgc ctg gat ctc tta atg att cat       98
Ile His Val Val Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His
-35                 -30                 -25                 -20
att ttc tat tgt aaa tac tgc ctt gka ttt ggk att tta gca agt gaa      146
Ile Phe Tyr Cys Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu
                -15                 -10                 -5
gtc tat tct tgg aac att tac                                          167
Val Tyr Ser Trp Asn Ile Tyr
            1

<210> 711
<211> 215
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..215

<221> sig_peptide
<222> 84..170
<223> Von Heijne matrix
      score 3.5
      seq SPLCSXSSGYCXA/FP

<400> 711
ccgcttttgg ctgcatcagc cggggattgc cggcgccagg tgctgggggc gactcggaca     60
gcgggagcgt ggggtggagt agg atg gag tct ccc tcc cga gct ggg ggt gtr    113
                          Met Glu Ser Pro Ser Arg Ala Gly Gly Val
                                          -25                 -20
grc ctm vga aag gct gct tcg ccg ctg tgt tcg gmv agc tct gga tac      161
Xaa Leu Xaa Lys Ala Ala Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr
                -15                 -10                 -5
tgc rgg gct ttt ccg cgg agg agc gcc cgc cgg cat ctg cat ccg gga      209
Cys Xaa Ala Phe Pro Arg Arg Ser Ala Arg Arg His Leu His Pro Gly
            1               5                   10
cac ggg                                                              215
His Gly
    15

<210> 712
<211> 241
```

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 59..241

<221> sig_peptide
<222> 59..133
<223> Von Heijne matrix
score 3.5
seq LISLSVLMPVQHS/PD

<400> 712
```
actatccttt cctcattgaa ttgctgtgat acctttgttg caaatcagct gtctgcag       58
atg tgg agg tat gtt tct aga ctt tct tct gtt cca ttg atc agc ttg      106
Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
-25                 -20                 -15                 -10
tct gtc ttg atg cca gta cag cac tcc cct gat ttt tgt agc ttt att      154
Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
                -5                  1               5
gta agt aca gtt atc cct tgg ttt cct tgg gga att ggt tcc agg acc      202
Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
        10                  15                  20
ctc atg gat ata aaa atc ctg gga tgc tcg agt cca ggg                  241
Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
    25                  30                  35
```

<210> 713
<211> 376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 276..374

<221> sig_peptide
<222> 276..365
<223> Von Heijne matrix
score 3.5
seq NLLKLSSHSPTCA/CK

<221> misc_feature
<222> 154,217
<223> n=a, g, c or t

<400> 713
```
tatgtacatt tgtcaaaact cagaaaatgt atatataata tgtgtgcata tgattttaag      60
tagttttaca taaaaagata agcaaatatt ggatgctggt taacactaag catgctgaaa     120
tatttagagg gaagagtatt attgtctaca atyngcttta aagacaccaa aaataaggtg     180
grttaattwa wkggsywwgg grmdwtggat aaatggnkag awatgtgata aagcaagtct     240
aatagaattt tgtggcagaa tctaatggcg gctat atg gat gtt agc tgt aaa       293
                                       Met Asp Val Ser Cys Lys
                                       -30                 -25
att ctt tac aat gtg att gaa aaa ttt tgc aat aat ctg ttg aag ctt      341
Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys Asn Asn Leu Leu Lys Leu
                -20                 -15                 -10
tct tcc cat tcc cct act tgt gct tgc aaa cta aa                       376
Ser Ser His Ser Pro Thr Cys Ala Cys Lys Leu
            -5                  1
```

<210> 714
<211> 304
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 216..302

<221> sig_peptide
<222> 216..275
<223> Von Heijne matrix
score 3.5
seq SHLSGSSLQLCVA/QF

<400> 714
```
gtatgtgtga tttgatttta tttgcccttt gaactatgac ccaatactcc ccaaacctgt     60
tattcagttt ttgcccagag ttattatatc tggggaataa acagaggaca cacacccaga    120
ggctgccagt agcaaaaatc actgtaattc aaaaagcatg acactacggt agtgaaatta    180
tcacactttt ctttgcatag agcagtttac ttgtg atg att ttc aaa gat gtg       233
                                       Met Ile Phe Lys Asp Val
                                       -20                 -15
ttc tcc cac ttg tca ggt tca tct ctt caa ctg tgt gtc gca caa ttt      281
Phe Ser His Leu Ser Gly Ser Ser Leu Gln Leu Cys Val Ala Gln Phe
                -10                 -5                  1
ctc gaw ctc agt gct gtt gac at                                       304
Leu Xaa Leu Ser Ala Val Asp
        5
```

<210> 715
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 91..240

<221> sig_peptide
<222> 91..222
<223> Von Heijne matrix
score 3.5
seq SFSFLFFFFLSFF/FF

<400> 715
```
gtttgtgatt aagtgatttc ctctagtggt atgctttgac tcctctttag cttttgtgta     60
aatactatag gtttttgctt tgtggttaac atg aag ctt aca aaa aat atc tta     114
                                 Met Lys Leu Thr Lys Asn Ile Leu
                                                 -40
twa gta ata ata ggc tgt ttt aag ctg ata gcc tac aaa aac tct gta      162
Xaa Val Ile Ile Gly Cys Phe Lys Leu Ile Ala Tyr Lys Asn Ser Val
    -35                 -30                 -25
ctg tac ttt tac tct aac ttc tca ttt tct ttt ctt ttc ttt ttt ttc      210
Leu Tyr Phe Tyr Ser Asn Phe Ser Phe Ser Phe Leu Phe Phe Phe Phe
-20                 -15                 -10                 -5
ctt tct ttc ttt ttt ttc ttt ttt ttt ttt tt                           242
Leu Ser Phe Phe Phe Phe Phe Phe Phe Phe
                1               5
```

<210> 716
<211> 375
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 100..375

<221> sig_peptide
<222> 100..360
<223> Von Heijne matrix
      score 3.5
      seq VAGXMLAPGGTLA/DD

<400> 716
ctggcgtyag ttccggtcgc agaggagaca ccgccgcagt tgccggtaca tcggggattt     60
ctggctcttt cctcttcgcc ttaaattcgg gtgtcttttt atg aat aat caa aag      114
                                            Met Asn Asn Gln Lys
                                                    -85
cag caw rag cca acg cta tca ggc cag cgt ttt aaa act aga aaa aga      162
Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg
    -80                 -75                 -70
gat gaa aaa gag agg ttt gac cct act cag ttt caa gac tgt att att      210
Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile
-65                 -60                 -55
caa ggc tta act gaa acc ggt act gat ttg gaa gca gta gct aag ttt      258
Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu Ala Val Ala Lys Phe
-50                 -45                 -40                 -35
ctt gat gct tct gga gca aaa ctt gat tac cgt cga tat gca gaa aca      306
Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr
                -30                 -25                 -20
ctc ttt gac att ctg gtg gct ggt kga atg ctg gcc cca ggt ggt aca      354
Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu Ala Pro Gly Gly Thr
            -15                 -10                 -5
ctg gca gat gac atg atg cvg                                          375
Leu Ala Asp Asp Met Met Xaa
    1               5

<210> 717
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 324..428

<221> sig_peptide
<222> 324..374
<223> Von Heijne matrix
      score 3.5
      seq LEIKLPFLPFAQQ/ID

<400> 717
aacagtctat ttctgtttgt aaatattagt atttctgtgg attctgtact tgttccttgt     60
tatcctttca ttctcttagg ttcatttggt ctgatggatt caggtaccat tgaaattctg    120
atagtttcaa aatcttttat ctccaggttt gatctctctt gtgaactctg gaactgtatt    180
cccaattgtc aattggacat ccctacgtat gggacctcag atatttcaaa catgatgtgt    240
ccaagtctgt atcacttctg gccatcatat tgttctttta tttttccaaa tttcacatca    300
ccagtaacaa actagctgtg atc atg gca gat agc ctg gaa ata aaa ctc ccc    353
                          Met Ala Asp Ser Leu Glu Ile Lys Leu Pro
                                  -15                 -10
ttt tta ccc ttt gca cag caa att gac atc aaa tcc tgt ttc tac ttt      401
Phe Leu Pro Phe Ala Gln Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe
    -5                  1               5
ttt ttt ttw aac wat kgc ttc cct agg g                                429
```

```
Phe Phe Xaa Asn Xaa Xaa Phe Pro Arg
10                  15

<210> 718
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..348

<221> sig_peptide
<222> 4..108
<223> Von Heijne matrix
      score 3.5
      seq ATAAATAASATTG/AS

<221> misc_feature
<222> 155
<223> n=a, g, c or t


<400> 718
tga atg gac aga aaa tgg acc tgg aag aga ggg caa agg tca cat ctg        48
    Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu
    -35                 -30                 -25
gag tca ggc cag gct gcc ccg gcc act gca gca gct acg gca gca tct        96
Glu Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Ala Thr Ala Ala Ser
-20                 -15                 -10                 -5
gcc aca acg ggg gca agt gtg tgg aga agc aca atg ggc wac ctg tgt       144
Ala Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys
                1               5                   10
gat tgc acc anb dca cct tat gaa ggg ccc ttt tgc aaa aaa gag gtt       192
Asp Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val
        15                  20                  25
tct gct gtt ttt gag gct ggc acg tcg gtt act tac atg ttt caa gaa       240
Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu
    30                  35                  40
ccc tat cct gtg acc aag aat ata agc ctc tca tcc tca gct att tac       288
Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr
45                  50                  55                  60
aca gat tca gct cca tcc aag gaa aac att gca ctt agc ttt gtg aca       336
Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr
                65                  70                  75
acc caa gca ccg gg                                                    350
Thr Gln Ala Pro
            80

<210> 719
<211> 305
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 84..305

<221> sig_peptide
<222> 84..212
<223> Von Heijne matrix
      score 3.5
      seq VLSIKHLPPQLRA/FQ
```

<400> 719
```
gtttttteet tttcatttca gcctgactgc cggaatcaga gccgcgggtg agatccccag     60
ccctgtgagc ctgtaggagt aga atg gct ccc caa atg tat gag ttc cat ctg    113
                          Met Ala Pro Gln Met Tyr Glu Phe His Leu
                                      -40                 -35
cca tta tcc cca gag gag ttg ttg aaa agt gga ggg gtg aat cag tat     161
Pro Leu Ser Pro Glu Glu Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr
            -30                 -25                 -20
gtt gtg caa gag gta ctg tcc atc aaa cat ctt cca cca cag ctt aga     209
Val Val Gln Glu Val Leu Ser Ile Lys His Leu Pro Pro Gln Leu Arg
        -15                 -10                 -5
gct ttt cag gct gcc ttt cga gct cag ggg ccc ctg gct atg ctg cag     257
Ala Phe Gln Ala Ala Phe Arg Ala Gln Gly Pro Leu Ala Met Leu Gln
    1               5                   10                  15
cac ttt gat act atc tac agc att ttg cat cac ttt cga agt ata gat     305
His Phe Asp Thr Ile Tyr Ser Ile Leu His His Phe Arg Ser Ile Asp
                20                  25                  30
```

<210> 720
<211> 257
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..257

<221> sig_peptide
<222> 6..50
<223> Von Heijne matrix
score 3.5
seq AVQVVGSWPSVQP/RE

<400> 720
```
aaaag atg gct gct gtg caa gtt gtc ggt tcg tgg cct tcc gtg cag ccg      50
      Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro
      -15                 -10                 -5
cgg gag gca ccg cgg gaa gca atc cct gag cga ggc aat ggg ttt cgc       98
Arg Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg
1               5                   10                  15
ctc ttg tct gcc agg ctc tgc gcc ctg cgc ccg gat gac agc agc tcc      146
Leu Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser
            20                  25                  30
gcc cgm acc gag atc cac ctg mtc ttc gat cag ctc atc tcc gag aac      194
Ala Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn
        35                  40                  45
tac agc gag ggc agt ggc gtg gcc ccg gag gac gtw agt gct ctt ctt      242
Tyr Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu
    50                  55                  60
gtc cag gct tgc ggg                                                  257
Val Gln Ala Cys Gly
65
```

<210> 721
<211> 360
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 217..360

```
<221> sig_peptide
<222> 217..306
<223> Von Heijne matrix
      score 3.5
      seq FLFFLQFSFPLYY/LF

<221> misc_feature
<222> 316,319
<223> n=a, g, c or t


<400> 721
ggcatgttta tatactcatt ccctggtgat tgtattttgc atacttgatt tttacctaag     60
catttatctt ttttccttta ttttctgttg ctttgtcttt ttgtaatgcc tcctggggca    120
atttctttga tttttatctt gcagttcttc tattgagttt tgcatgttgg ctatcatgtt    180
ttaaattttc atttttcata gtattctgtc ctatgg atg ttt cat ggc tgt cat      234
                                        Met Phe His Gly Cys His
                                        -30                 -25
att tta tct ttt ctg agg ata tca act aga ggt ttt ctt ttt ttt ctt      282
Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg Gly Phe Leu Phe Phe Leu
                -20                 -15                 -10
caa ttt tcc ttt cct ctg tat tat ctc ttt cgg ngg ntt ttc cct cag      330
Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe Arg Xaa Xaa Phe Pro Gln
            -5                  1                   5
tct ttc atg ttg gag gca ttt gtc aga tgt                              360
Ser Phe Met Leu Glu Ala Phe Val Arg Cys
    10                  15

<210> 722
<211> 191
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 64..189

<221> sig_peptide
<222> 64..141
<223> Von Heijne matrix
      score 3.5
      seq LVLYAPWVPPLLL/AF

<400> 722
ttctcctctt gtgaaggcag ctcctcagat ccagggagta tctgcacgga cctcatttat     60
gtt atg tat aga cat tcc aaa cag cgt aat aat gtc cca tgc ctt gta      108
    Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val
        -25                 -20                 -15
ctc tac gcc cct tgg gtc cct ccc ctc ctc cta gct ttc tgg ggc tgg      156
Leu Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp
    -10                 -5                  1                   5
tgg ctc ctg gag cag ggt ctt ttt ttt ttt ttt tt                       191
Trp Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe
                10                  15

<210> 723
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 63..473
```

<221> sig_peptide
<222> 63..212
<223> Von Heijne matrix
      score 3.5
      seq ITYGVFLCIDCSG/SH

<400> 723
```
tttttttttc gtcgactctt accggttggc tgggccagct gcgccgcggc tcacagctga      60
cg atg ggg gac ccc agc aag cag gac atc ttg acc atc ttc aag cgc        107
   Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg
   -50                 -45                 -40
ctc cgc tcg gtg ccc act aac aag gtg tgt ttt gat tgt ggt gcc aaa       155
Leu Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys
-35                 -30                 -25                 -20
aat ccc agc tgg gca agc ata acc tat gga gtg ttc ctt tgc att gat       203
Asn Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp
                -15                 -10                 -5
tgc tca ggg tcc cac cgg tca ctt ggt gtt cac ttg agt ttt att cga       251
Cys Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg
            1               5                   10
tct aca gag ttg gat tcc aac tgg tca tgg ttt cag ttg cga tgc atg       299
Ser Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met
    15                  20                  25
caa gtc gga gga aac gct agt gca tct tcc ttt ttt cat caa cat ggg       347
Gln Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly
30                  35                  40                  45
tgt tcc acc aat gac acc aat gcc aag tac aac agt cgt gct gct cag       395
Cys Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln
                50                  55                  60
ctc tat agg gag aaa atc aaa tcg ctc gcc tct caa gca aca cgg aag       443
Leu Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys
            65                  70                  75
cat ggc act gat ctg tgg ctt gat agt tgt                               473
His Gly Thr Asp Leu Trp Leu Asp Ser Cys
        80                  85
```

<210> 724
<211> 139
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 60..137

<221> sig_peptide
<222> 60..125
<223> Von Heijne matrix
      score 3.5
      seq LLLHLVFHQRTLI/SL

<400> 724
```
tttagcattc aagccgtgat tagtgctttc tcttctcccc agcctgcctt tcagaacag       59
atg cct ctc cct ccc aat cag tcc cct cta ctg ctg cac ctg gtg ttt       107
Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
        -20                 -15                 -10
cat caa agg acc ctg att tcc ctc ccg ccg cc                            139
His Gln Arg Thr Leu Ile Ser Leu Pro Pro
    -5                  1
```

<210> 725
<211> 187

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 125..187

<221> sig_peptide
<222> 125..163
<223> Von Heijne matrix
      score 3.5
      seq MFLTFFFCTQVHG/PS

<400> 725
```
tcttcgggaa ctctcactct ctcataaact actttattac catcccacca tatcctgtcc    60
tctttttttg gcctacttag atctgttttc ctttcttgcc ttaaatggga attgctagag   120
gmat atg ttt cta act ttt ttt ttc tgc aca caa gtt cat ggt cct tct    169
     Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser
                 -10                 -5                  1
ata ctt gat agc cca gct                                             187
Ile Leu Asp Ser Pro Ala
        5
```

<210> 726
<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 39..206

<221> sig_peptide
<222> 39..80
<223> Von Heijne matrix
      score 3.5
      seq VTLWIFQFFLCLT/CK

<221> misc_feature
<222> 154
<223> n=a, g, c or t

<400> 726
```
aatataaata ccaaatacat aaatagtttt ggtgttag atg gtc act tta tgg att    56
                                          Met Val Thr Leu Trp Ile
                                                          -10
ttt caa ttt ttc ttg tgt ttg act tgt aaa gct tat aat tta aga aac     104
Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys Ala Tyr Asn Leu Arg Asn
            -5                  1               5
tgt aat gat ggg aag ggh wga gsm tca gwg gtg ctt gga ttg gaa caa     152
Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa Val Leu Gly Leu Glu Gln
    10                  15                  20
mnr cta cct gaa tct gct ggt atg gta caw ttt tta ggt ttg aaa cac     200
Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa Phe Leu Gly Leu Lys His
25                  30                  35                  40
agg tgg g                                                           207
Arg Trp
```

<210> 727
<211> 164
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 54..164

<221> sig_peptide
<222> 54..95
<223> Von Heijne matrix
      score 3.5
      seq VLWAGPXVPLLCA/AX

<400> 727
agacaatggg gmmaatgtca cacatcacag accaagaggc ctaggaggav aag atg        56
                                                           Met
gtt ttg tgg gct ggg ccc akg gtc ccc ctg ctg tgt gca gcc tas gga      104
Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa Gly
            -10                 -5                  1
ctt ggt gcc ctg cat ccc aga tgc tct agt caa ggc ttg agg ctt gcr      152
Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu Ala
    5                   10                  15
sct tct gaa gcc                                                      164
Xaa Ser Glu Ala
20

<210> 728
<211> 321
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 139..321

<221> sig_peptide
<222> 139..261
<223> Von Heijne matrix
      score 3.5
      seq FNIGLLWVPXXXG/AV

<400> 728
catggaaatc actccaatca gaccggcccg aggatacgct ttcttgtgat ccgcagcagc     60
gccattagca tcataaacca ggtgattggc tggatctact ttgtggcctg gtccatctcc    120
ttctaccctc aggtgmtc atg aat tgg agg cgg aaa agt gtc att ggt ctg      171
                    Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu
                        -40                 -35
agc ttc gac ttc gtg gct ctg aac ctg acg ggc ttc gtg gcc tac agt      219
Ser Phe Asp Phe Val Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser
-30                 -25                 -20                 -15
gta ttc aac atc ggc ctc ctc tgg gtg ccc twc wtc daa gga gca gtt      267
Val Phe Asn Ile Gly Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val
                -10                 -5                  1
tct cct caa ata ccc caa cgg agt gaa ccc cgt gaa cag caa cga cgt      315
Ser Pro Gln Ile Pro Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg
        5                   10                  15
ctt ctt                                                              321
Leu Leu
    20

<210> 729
<211> 472
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> 25..471

<400> 729
gacttccctc tagaatcctc caac atg gag cct ctt gca gct tac ccg cta        51
                           Met Glu Pro Leu Ala Ala Tyr Pro Leu
                           1               5
aaa tgt tcc ggg ccc aga gca aag gta ttt gca gtt ttg ctg tct ata       99
Lys Cys Ser Gly Pro Arg Ala Lys Val Phe Ala Val Leu Leu Ser Ile
10                  15                  20                  25
gtt cta tgc aca gta acg cta ttt ctt cta caa cta aaa wtc ctc aaa      147
Val Leu Cys Thr Val Thr Leu Phe Leu Leu Gln Leu Lys Xaa Leu Lys
                30                  35                  40
cct aaa atc aac agc ttt tat gcc ttt gaa gtg aag gat gca aaa gga      195
Pro Lys Ile Asn Ser Phe Tyr Ala Phe Glu Val Lys Asp Ala Lys Gly
            45                  50                  55
aga act gtt tct ctg gaa aag tat aaa ggc aaa gtt tca cta gtt gta      243
Arg Thr Val Ser Leu Glu Lys Tyr Lys Gly Lys Val Ser Leu Val Val
        60                  65                  70
aac gtg gcc agt gac tgc caa ctc aca gac aga aat tac tta ggg ctg      291
Asn Val Ala Ser Asp Cys Gln Leu Thr Asp Arg Asn Tyr Leu Gly Leu
    75                  80                  85
aag gaa ctg cac aaa gag ttt gga cca tcc cac ttc agc gtg ttg gct      339
Lys Glu Leu His Lys Glu Phe Gly Pro Ser His Phe Ser Val Leu Ala
90                  95                  100                 105
ttt ccc tgc aat cag ttt gga gaa tcg gag ccc cgc cca agc aag gaa      387
Phe Pro Cys Asn Gln Phe Gly Glu Ser Glu Pro Arg Pro Ser Lys Glu
                110                 115                 120
gta gaa tct ttt gca aga aaa aac tac gga gta act ttc ccc atc ttc      435
Val Glu Ser Phe Ala Arg Lys Asn Tyr Gly Val Thr Phe Pro Ile Phe
            125                 130                 135
cac aag att aag att cta gga tct gaa gga gaa ctg c                    472
His Lys Ile Lys Ile Leu Gly Ser Glu Gly Glu Leu
        140                 145

<210> 730
<211> 465
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 70..465

<400> 730
actcggggag actccaaaca gtgagcctag agctggagac tagcgttaac cggcggggcg     60
gccggtttt atg aat gaa gct atg gct aca gat tcc cca aga aga ccc agt    111
          Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser
          1               5                   10
cgt tgt act ggt gga gtt gtg gtt cgc ccc cag gct gtc aca gag cag      159
Arg Cys Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln
15                  20                  25                  30
tcc tac atg gaa agt gtt gtg act ttt ctg cag gat gtt gtg cca cag      207
Ser Tyr Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln
                35                  40                  45
gct tac agt gga aca cct cta aca gaa gaa aag gag aaa ata gtc tgg      255
Ala Tyr Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp
            50                  55                  60
gtc aga ttt gaa aat gca gat tta aat gat aca tca aga aat ctg gaa      303
Val Arg Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu
        65                  70                  75
ttt cat gaa ata cat agt act ggg agt gaa ccg cct ttg ttg att atg      351
```

```
Phe His Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met
    80                  85                  90
att ggc tac agt gat gga atg cag gtc tgg agc atc cct atc akt ggc      399
Ile Gly Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly
95                  100                 105                 110
gaa sac aag agc tct tct ctg ttc gac atg gcc caa ttc gag cgg cta      447
Glu Xaa Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu
                115                 120                 125
gaa tct tgc ctg ctc cac                                              465
Glu Ser Cys Leu Leu His
            130
```

<210> 731
<211> 345
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 207..344

<400> 731

```
agacgcgacg gtgctgggat cccgggaggg akcggaacgg acctgggctt ggtcgcctcc     60
aagccggcgg gaccgagtgc tttaggccgc tygaaagaaa gttgctccga cccgggaaaa    120
ggagaagatg aaggaagcca aggatgcccg ctataccaat gggcacctct tcaccaccat    180
ttcagtttca ggcatgacca tgtgct atg cct gta aca aga gca tca cag cca     233
                             Met Pro Val Thr Arg Ala Ser Gln Pro
                             1               5
agg aag ccc tca tct gcc caa caa cag aaa gcg gcc ctg ctg aak aac      281
Arg Lys Pro Ser Ser Ala Gln Gln Gln Lys Ala Ala Leu Leu Xaa Asn
10                  15                  20                  25
aac acc gcc ttg cag tcc gtt tct ctt cga agt aag aca acc atc cgg      329
Asn Thr Ala Leu Gln Ser Val Ser Leu Arg Ser Lys Thr Thr Ile Arg
                30                  35                  40
gag cgg cca agc tcg g                                                345
Glu Arg Pro Ser Ser
            45
```

<210> 732
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 274..396

<400> 732

```
agcaaccaag tcgcacctgg agctgtccta gcgcctagtt ctctcccggc cgcagagctg     60
gccgcccagg gggagtcgca gagtttggaa gatctctcta acacctctcg gccaacttca    120
gaagtgtata agatcagctt tatctttcca aatggagaca agtatgatgg tgactgtaca    180
agaacatctt ctggaatcta cgagagaaat ggaataggta ttcataccac tcctaatggg    240
attgtctaca caggaagctg gaaagatgac aag atg aat ggt ttt gga aga ctt     294
                                     Met Asn Gly Phe Gly Arg Leu
                                     1                   5
gag cat ttt tca gga gca gta tat gaa gga caa ttt aag gat aat atg      342
Glu His Phe Ser Gly Ala Val Tyr Glu Gly Gln Phe Lys Asp Asn Met
        10                  15                  20
ttt cat gga ctg ggg act tac aca ttc cca aat ggg gca aag tat act      390
Phe His Gly Leu Gly Thr Tyr Thr Phe Pro Asn Gly Ala Lys Tyr Thr
    25                  30                  35
gga att tc                                                           398
Gly Ile
```

```
40

<210> 733
<211> 443
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 49..441

<400> 733
ggaagttctt gggagcgcca gttccgtctg tgtgttcgag tggacaaa atg gcg aag      57
                                                     Met Ala Lys
                                                     1
atc gcc aag act cac gaa gat att gaa gca cag att cga gaa att caa      105
Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg Glu Ile Gln
    5                   10                  15
ggc aag aag gca gct ctt gat gaa gct caa gga gtg ggc ctc gat tct      153
Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly Leu Asp Ser
20                  25                  30                  35
aca ggt tat tat gac cag gaa att tat ggt gga agt gac agc aga ttt      201
Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp Ser Arg Phe
                40                  45                  50
gct gga tac gtg aca tca att gct gca act gaa ctt gaa gat gat gac      249
Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu Asp Asp Asp
            55                  60                  65
gat gac tat tca tca tct acg agt ttg ctt ggt cag aag aag cca gga      297
Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys Lys Pro Gly
        70                  75                  80
tat cat gcc cct gtg gca ttg ctt aat gat ata cca cag tca aca gaa      345
Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln Ser Thr Glu
    85                  90                  95
cag tat gat cca ttt gct gag cac aga cct cca aag att gca gac cgg      393
Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile Ala Asp Arg
100                 105                 110                 115
gaa gat gaa tac aaa aag cat agg cgg acc atg ata att tcc cag agc      441
Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile Ser Gln Ser
                120                 125                 130
gt                                                                    443

<210> 734
<211> 373
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 128..373

<400> 734
gagaagccgc agtctcgaga gcgtcaacga ggtgtttcgg tagtctctgg ccatcctttc      60
tgcgcacccg gtgtcgctgg gctgcacccc gggcggggac gtccgccggg cacgggaggg      120
ggccaag atg ccg atc aat aaa tca gag aag cca gaa agc tgc gat aat      169
        Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn
        1               5                   10
gtg aag gtt gtt gtt agg tgc cgg ccc ctc aat gag aga gag aaa tca      217
Val Lys Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser
15                  20                  25                  30
atg tgc tac aaa cag gct gtc agt gtg gat gag atg agg gga act atc      265
Met Cys Tyr Lys Gln Ala Val Ser Val Asp Glu Met Arg Gly Thr Ile
                35                  40                  45
act gta cat aag act gat tct tcc aat gaa cct cca aag aca ttt act      313
```

Thr Val His Lys Thr Asp Ser Ser Asn Glu Pro Pro Lys Thr Phe Thr
50 55 60
ttt gat act gtt ttt gga cca gag agt aaa caa ctt gat gtt tat aac 361
Phe Asp Thr Val Phe Gly Pro Glu Ser Lys Gln Leu Asp Val Tyr Asn
65 70 75
tta act gca aga 373
Leu Thr Ala Arg
80

<210> 735
<211> 322
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 202..321

<400> 735
agagcggtgg cggcggctgc gcsggctgtg agtctctcgc cgccggagga agatgaggct 60
gaagattgga ttcatcttac gcagtttgct ggtggtggga agcttcctgg ggctagtggt 120
cctctggtct tccctgaccc cgcggccgga cgacccaagc ccgctgagca ggatgaggga 180
agacagagat gtcatgaccc c atg ccc aac cga ggc ggc aat gga cta gct 231
Met Pro Asn Arg Gly Gly Asn Gly Leu Ala
1 5 10
cct ggg gag gac aga ttc aaa cct gtg gta cca tgg cct cat gtt gaa 279
Pro Gly Glu Asp Arg Phe Lys Pro Val Val Pro Trp Pro His Val Glu
15 20 25
gga gta gaa gtg gac tta gag tct att aga aga ata aac aag g 322
Gly Val Glu Val Asp Leu Glu Ser Ile Arg Arg Ile Asn Lys
30 35 40

<210> 736
<211> 181
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 75..179

<400> 736
acttcgccat tttcctccgg aagtgcggat cccagcggcg gtcgtgtagc tgagcagscc 60
tggggcttgg ttct atg tcc ctg tgg cta tgt ttc cag tgt cct ctg ggt 110
Met Ser Leu Trp Leu Cys Phe Gln Cys Pro Leu Gly
1 5 10
gtt tcc aag agc aac aag aaa cga ata aat ctc tgt aat ggt ttc tgg 158
Val Ser Lys Ser Asn Lys Lys Arg Ile Asn Leu Cys Asn Gly Phe Trp
15 20 25
aat gaa aaa ata aaa aac agg ag 181
Asn Glu Lys Ile Lys Asn Arg
30 35

<210> 737
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 18..158

<400> 737

```
tgaatgactg gctattt atg ggc acc cat gtt ttt gct ata aat aaa cgt        50
                   Met Gly Thr His Val Phe Ala Ile Asn Lys Arg
                   1               5                   10
aca tat gta att tca aga gac cga gaa tta tca act gca aag ccc awr       98
Thr Tyr Val Ile Ser Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa
            15                  20                  25
tgt agc agt cta ctc acg gcc cct gta ctt tgc tac tgg agg gcc tgt      146
Cys Ser Ser Leu Leu Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys
        30                  35                  40
cct ctg caa acc ca                                                   160
Pro Leu Gln Thr
    45

<210> 738
<211> 234
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 66..233

<400> 738
gttgttagtt ttctttttag ctgaattacc cactcacatc cttattattt tatgccactg     60
atttc atg ttt tgt ttt cta ttt tca tgg tgg ctt aga gga ggt ctt cat    110
      Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His
      1               5                   10                  15
gta tta tta aac aca tgc tta tat gta cct tat ggg tat ttg tca ctt      158
Val Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu
                20                  25                  30
att tgt tta ctt tgt tta tgg tat ctt aat cta tac aaa ttc tca att      206
Ile Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile
            35                  40                  45
ttc ttt tct ttt ctt tct ttt ttt ttt t                                234
Phe Phe Ser Phe Leu Ser Phe Phe Phe
        50                  55

<210> 739
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 424..588

<400> 739
atcaaaagaa ctcttatata caggagccca ggcaccatac tgtcttttcg aggtaggagt     60
cgactcctgt gaggtatggt gctgggtgca gatgcagtgt ggctctggat agcaccttat    120
ggacagttgt gtccccaagg aaggatgaga atagctactg aagtcctaaa gagcaagcct    180
aactcaagcc attggcacac aggcattaga cagaaagctg gaagttgaaa tggtggagtc    240
caacttgcct ggaccagctt aatggttctg ctcctggtaa cgtttttatc catggatgac    300
ttgcttgggt atggagagtc ggcttgacta cactgtgtgg agcaagtttt aaagaagcaa    360
aggactcaga attcatgatt gaagaaatgc aggcagacct gttatcctaa actagggttt    420
tta atg acc aca aca agc aag cat gca gct tac tgc ttg aaa ggg tct      468
    Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser
    1               5                   10                  15
tgc ctc amc caa gct aga gtg cag tgg cct ttg aag cwt act aca gcc      516
Cys Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala
                20                  25                  30
tca aac ttc tgg gct caa gtg atc ctc agc ctc cca gtg gtc ttt gta      564
Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val
            35                  40                  45
```

```
gac tgc ctg atg gag tmt cat ggc a                                     589
Asp Cys Leu Met Glu Xaa His Gly
        50                  55

&lt;210&gt; 740
&lt;211&gt; 388
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 26..388

&lt;400&gt; 740
aaaaaacgct gttggaaatc tcgcg atg gag gga gga gga ggt ata ccc cta        52
                            Met Glu Gly Gly Gly Gly Ile Pro Leu
                            1               5
gaa aca ctt aaa gaa gaa agt cag tca aga cat gtt cta cct gca agt       100
Glu Thr Leu Lys Glu Glu Ser Gln Ser Arg His Val Leu Pro Ala Ser
10                  15                  20                  25
ttt gaa gtc aac agt ttg cag aaa agc aac tgg ggg ttc tta ctt act       148
Phe Glu Val Asn Ser Leu Gln Lys Ser Asn Trp Gly Phe Leu Leu Thr
                30                  35                  40
ggg ctt gtg ggt ggc acc ctg gtg gct gtg tac gct gta gcc acg ccg       196
Gly Leu Val Gly Gly Thr Leu Val Ala Val Tyr Ala Val Ala Thr Pro
            45                  50                  55
ttt gta acg cca gcc ctt cga aaa gtc tgt ttg cca ttt gta cct gca       244
Phe Val Thr Pro Ala Leu Arg Lys Val Cys Leu Pro Phe Val Pro Ala
        60                  65                  70
act atg aag cag att gaa aat gtt gtg aaa atg ttg cga tgc cga aga       292
Thr Met Lys Gln Ile Glu Asn Val Val Lys Met Leu Arg Cys Arg Arg
    75                  80                  85
gga tcc ctt gtg gac atc ggt agt ggg gac gga cgc att gtc ata gcg       340
Gly Ser Leu Val Asp Ile Gly Ser Gly Asp Gly Arg Ile Val Ile Ala
90                  95                  100                 105
gct gcg aag aaa ggg ttc ama gca gtt ggt tat gaa tta aac cca tgg       388
Ala Ala Lys Lys Gly Phe Xaa Ala Val Gly Tyr Glu Leu Asn Pro Trp
                110                 115                 120

&lt;210&gt; 741
&lt;211&gt; 478
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 15..476

&lt;400&gt; 741
agtgcgcctc taag atg gcg acg cct ttg gcg gta aat tcg gct gct agt        50
                Met Ala Thr Pro Leu Ala Val Asn Ser Ala Ala Ser
                1               5                   10
cta tgg ggt cct tac aaa gac att tgg cat aaa gtg gga aat gct ctt        98
Leu Trp Gly Pro Tyr Lys Asp Ile Trp His Lys Val Gly Asn Ala Leu
        15                  20                  25
tgg aga aga caa cct gaa gct gtt cam ctt ctt gat aag att ttg aag       146
Trp Arg Arg Gln Pro Glu Ala Val Xaa Leu Leu Asp Lys Ile Leu Lys
    30                  35                  40
aaa cac aaa cct gac ttc atc tca ttg ttc aaa aat ccg cca aaa aat       194
Lys His Lys Pro Asp Phe Ile Ser Leu Phe Lys Asn Pro Pro Lys Asn
45                  50                  55                  60
gtt caa cag cat gag aag gtt cag aaa gcc agt aca gag gga gtc gcc       242
Val Gln Gln His Glu Lys Val Gln Lys Ala Ser Thr Glu Gly Val Ala
```

```
                  65                  70                  75
att cag ggt caa cag gga act cga ctt ctt cct gaa cag ctc att aaa       290
Ile Gln Gly Gln Gln Gly Thr Arg Leu Leu Pro Glu Gln Leu Ile Lys
              80                  85                  90
gaa gcc ttt att ctc agt gac ctt ttt gat att gga gaa ttg gca gct       338
Glu Ala Phe Ile Leu Ser Asp Leu Phe Asp Ile Gly Glu Leu Ala Ala
          95                 100                 105
gtt gag ctt ctt ctt gct gga gag cat caa cag cca cat ttt cct ggc       386
Val Glu Leu Leu Leu Ala Gly Glu His Gln Gln Pro His Phe Pro Gly
    110                 115                 120
ctt acc aga gga tta gta gct gtt ctt ctg tac tgg gat gga aag cga       434
Leu Thr Arg Gly Leu Val Ala Val Leu Leu Tyr Trp Asp Gly Lys Arg
125                 130                 135                 140
tgc att gcg aat tcc ttg aaa gcc ttg ata cag tct aga cgg gg            478
Cys Ile Ala Asn Ser Leu Lys Ala Leu Ile Gln Ser Arg Arg
                145                 150

<210> 742
<211> 752
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 377..751

<400> 742
atttcctgcc gtaagtatac agtgcctccg ggtcgcggtc attttgagcc cctgtctgga      60
tgacttcttg cggctgttct acccctcccc ctccccgcgt cggcctgmct gctgtcgtcg     120
ggaggtgggt gaggtgacgc aaacagcccc gttgttgccc tccgcgtatc ccctcaccac     180
ctttgcggcc atccacgact ttcgcacctt ccgccatttt cctgcctgtg agggtggaca     240
gatcgcgctc gggtctcggc ctcctgagtg ccggtgactg cgggaggcga cggagtgctt     300
ctgggggtgt gagctgggga agttcgtggt cacggatgcg tgtggggttg ctgctcagtc     360
tgtaacggca ggaaag atg aat ggg agg gct gat ttt cga gag ccg aat gca     412
                  Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala
                  1               5                   10
gag gtt cca aga cca att ccc cac ata ggg cct gat tac att cca aca       460
Glu Val Pro Arg Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr
        15                  20                  25
gag gaa gaa agg aga gtc ttc gca gaa tgc aat gat gaa agc ttc tgg       508
Glu Glu Glu Arg Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp
    30                  35                  40
ttc aga tct gtg cct ttg gct gca aca agt atg ttg att act caa gga       556
Phe Arg Ser Val Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly
45                  50                  55                  60
tta att agt aaa gga ata ctt tca agt cat ccc aaa tat ggt tcc atc       604
Leu Ile Ser Lys Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile
                65                  70                  75
cct aaa ctt ata ctt gct tgt atc atg gga tac ttt gct gga aaa ctt       652
Pro Lys Leu Ile Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu
            80                  85                  90
tct tat gtg aaa act tgc caa gag aaa ttc aag aaa ctt gaa aat tcc       700
Ser Tyr Val Lys Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser
        95                 100                 105
ccc ctt gga gaa gct tta cga tca gga caa gca cga cga tct tca cca       748
Pro Leu Gly Glu Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro
    110                 115                 120
cct g                                                                 752
Pro
125

<210> 743
<211> 459
```

```
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 353..457

<221> misc_feature
<222> 438
<223> n=a, g, c or t


<400> 743
cctatcactg gagaatgggt ttggtgcttt gagctgtgtt tctacataaa aaagaaggaa      60
tcaaagtgat gctggtgtga caatataaca tttgaagctg ctccaaacaa ctttgactgt     120
aagaaaatgg ccaagagaat acaagaggct ctaaccaagg actctgactt cactaagcca     180
ctgaaacatt cctggcacta cctacctcct gccttttcgt tatgggagga aaccctattg     240
gttaggtcac tggtttaaaa cacgtccttt aaattgcaga ggaagaaaag gcttggaggt     300
gataaaggaa tayagttcat tcccttsmtt atggtgatgg tttcataggc at atg cat     358
                                                          Met His
                                                          1
atg tcc aaa ctc atc aac ttg tat aca tca rat atg tgc aat tta ctg       406
Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn Leu Leu
    5                   10                  15
tmt atc cac cty mtc tym ata agc tgt tta ant aat aat aar rta aca       454
Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys Xaa Thr
    20                  25                  30
tta cg                                                                459
Leu
35

<210> 744
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 79..411

<400> 744
atggggacgg ggctgttccc ggggaggctg tgatgggttg acaggtgcgt gacagtggga      60
gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc      111
                    Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala
                    1               5                   10
gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat      159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
            15                  20                  25
gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta      207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
        30                  35                  40
tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga      255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
    45                  50                  55
ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct      303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
60                  65                  70                  75
cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc      351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
                80                  85                  90
cat gat tac agt gct gca gca gct ccc agt cca gtg cta gga aac att      399
His Asp Tyr Ser Ala Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile
            95                  100                 105
```

```
ccc cca gga gat                                                 411
Pro Pro Gly Asp
        110

<210> 745
<211> 404
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..403

<400> 745
ctctggggcg gasggccacc atcttggaac gggaggcgga sagagtcgac tgggagcgac     60
cgagcgggcc gccgccgccg cc atg aac ccc gaa tat gac tac ctg ttt aag     112
                         Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys
                         1               5                   10
ctg ctt ttg att ggc gac tca ggc gtg ggc aag tca tgc ctg ctc ctg     160
Leu Leu Leu Ile Gly Asp Ser Gly Val Gly Lys Ser Cys Leu Leu Leu
                15                  20                  25
cgg ttt gct gat gac acg tac aca gag agc tac atc agc acc atc ggg     208
Arg Phe Ala Asp Asp Thr Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly
            30                  35                  40
gtg gac ttc aag atc cga acc atc gag ctg gat ggc aaa act atc aaa     256
Val Asp Phe Lys Ile Arg Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys
        45                  50                  55
ctt cag atc tgg gac aca gcg ggc cag gaa cgg ttc cgg acc atc act     304
Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr
    60                  65                  70
tcc agc tac tac cgg ggg gct cat ggc atc atc gtg gtg tat gac gtc     352
Ser Ser Tyr Tyr Arg Gly Ala His Gly Ile Ile Val Val Tyr Asp Val
75                  80                  85                  90
act gac cag gaa tcc tac gcc ary gtg aag cag tgg ctg cag gag att     400
Thr Asp Gln Glu Ser Tyr Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile
                95                  100                 105
gac c                                                           404
Asp

<210> 746
<211> 429
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 336..428

<221> misc_feature
<222> 393
<223> n=a, g, c or t


<400> 746
ggcttcttcc agtcacctcg gcccggatcg ggaagtgtca agcgggcgct cccccatctc     60
cgccgctatt accactgaac ccggaccccc tacccaggtc cagggccagc cgccatgacg    120
aacgtgtact ccttggatgg gattctggtg tttggtttgc tctttgtttg cacctgtgcc    180
tacttcaaga aagtacctcg tctcaaaacc tggctgctat cagagaagaa gggtgtttgg    240
ggtgtgtttt acaaagccgs tgtgattgga accaggctgc atgctgctgt ggcaattgct    300
tgtgttgtaa tgggctttta cgtcctgttt ataaa atg aat tcc aaa gca scc       353
                                       Met Asn Ser Lys Ala Xaa
                                       1               5
aag tca tca act gcc aac caa ggg gac ggg gat gaa gaa nct gtt ggg      401
```

```
Lys Ser Ser Thr Ala Asn Gln Gly Asp Gly Asp Glu Glu Xaa Val Gly
            10                  15                  20
mga mct gaa scc agt gta gga gag ttc a                              429
Arg Xaa Glu Xaa Ser Val Gly Glu Phe
        25                  30

<210> 747
<211> 179
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 35..178

<221> misc_feature
<222> 140
<223> n=a, g, c or t


<400> 747
gaaatataca ataccttatg ttgtatatta catt atg ttg tat agt acg ttg aaa      55
                                      Met Leu Tyr Ser Thr Leu Lys
                                      1               5
cat aca cta caa tac gtt atc att aat tgt ggt cac cat gct gtg caa       103
His Thr Leu Gln Tyr Val Ile Ile Asn Cys Gly His His Ala Val Gln
        10                  15                  20
aag atc tct aaa acg tat tcc tcc tgt ctg act gaa nyt ttg tat cct       151
Lys Ile Ser Lys Thr Tyr Ser Ser Cys Leu Thr Glu Xaa Leu Tyr Pro
    25                  30                  35
ttg cct aat atc tcc cca atc cct cca c                                 179
Leu Pro Asn Ile Ser Pro Ile Pro Pro
40                  45

<210> 748
<211> 383
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 101..382

<400> 748
ctatattagt tgtggagaag aacacacagc agttctcaca aagagwggag gtgtgtttac      60
ctttggcgct ggttcctgtg ggcaacttgg acacgactcc atg aat gat gag gtt       115
                                            Met Asn Asp Glu Val
                                            1               5
aac cct aga aga gtt cta gag ctg atg ggt agt gaa gta act caa att       163
Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser Glu Val Thr Gln Ile
                10                  15                  20
gct tgt ggc aga caa cat acc cta gsm ttc gtg cct tct tct gga ctc       211
Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val Pro Ser Ser Gly Leu
            25                  30                  35
atc tat gca ttt ggt tgt gga gca aga ggt caa tta gga act ggg cac       259
Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln Leu Gly Thr Gly His
        40                  45                  50
act tgt aat gtt aag tgc cca tct cct gtc aag ggt tac tgg gct gcc       307
Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys Gly Tyr Trp Ala Ala
    55                  60                  65
cac agt ggc cag ctt tca gcc cga gct gat cgc ttt aaa tat cat atc       355
His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg Phe Lys Tyr His Ile
70                  75                  80                  85
```

```
gtt aag cag atc ttc tct gga gga gac c                                383
Val Lys Gln Ile Phe Ser Gly Gly Asp
                90
```

<210> 749
<211> 446
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 381..446

<400> 749

```
aacaatcaca gctccgggca ttgggggaac cssagccggc tgcgccgggg gaatccgtgc      60
gggcgccttc cgtcccggtc ccatcctcgc cgcgctccag cacctctgaa gttttgcagc     120
gcccagaaag gaggcgagga aggcagggag tgtgtgagag gagggagcaa aaagctcacc     180
ctaaaacatt tatttcaagg agaaaagaaa aagggggggc gcaaaaatgg ctggggcaat     240
tatagaaaac atgagcacca agaagctgtg cattgttggt gggattctgc tcgtgttcca     300
aatcatcgcc tttctggtgg gaggcttgat tgctccaggg sccacaacgg cagtgtccta     360
catgtcggtg aaatgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt     413
                      Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
                      1               5                   10
tcg gtg cct tgg gga ccc aat cat tgt gac aag                           446
Ser Val Pro Trp Gly Pro Asn His Cys Asp Lys
            15                  20
```

<210> 750
<211> 410
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 129..410

<400> 750

```
ttttctcctc ctcctcaggg ctccagtcag gccgatccgc tccgctcacg gaaggaaaac      60
agaaataact tgctggcttg tctggagtca catggtgaca atttacagaa agtcatctct     120
gcagcttg atg ggc gac aac cct ttt caa cca aaa agt aat tca aaa atg     170
         Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met
         1               5                   10
gca gaa ctg ttt atg gaa tgt gaa gaa gag gag ctg gaa cca tgg cag     218
Ala Glu Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln
15                  20                  25                  30
aag aaa gta aaa gaa gtt gag gat gac gat gat gat gag cca atc ttt     266
Lys Lys Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe
                35                  40                  45
gtt ggc gag ata tca agt tca aaa cca gca att tca aat att ttg aac     314
Val Gly Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn
            50                  55                  60
aga gtt aac ccc agc tca tat tca agg gga cta aag aat ggt gca ctc     362
Arg Val Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu
        65                  70                  75
agt cga ggt att act gct gca ttc aag cct aca agt caa cac tac acg     410
Ser Arg Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr
    80                  85                  90
```

<210> 751
<211> 536
<212> DNA
<213> Homo sapiens

```
<220>
<221> CDS
<222> 334..534

<221> misc_feature
<222> 148
<223> n=a, g, c or t


<400> 751
cctccctccc accggaaaac tctgaggaca tgaatagtcg ccaggcttgg cggctcttgc      60
tctcccaagg cagaggagat cgttgggttt caaggccccg cgggcatttc tcgccggccc     120
tgcggagaga gttcttcact accacaancm arggagggat atgataggcg gccagtggat     180
ataactcctt tagaacaaag gaaattaact tttgataccc atgcattggt tcaggacttg     240
gaaactcatg gatttgacaa aacacaagca gaaacaattg tatcagcgtt aactgcttta     300
tcaaatgtca gcctggatac tatctataaa gag atg gtc act caa gct caa cag      354
                                     Met Val Thr Gln Ala Gln Gln
                                     1               5
gaa ata aca gta caa cag cta atg gct cat ttg gat gct atc agg aaa      402
Glu Ile Thr Val Gln Gln Leu Met Ala His Leu Asp Ala Ile Arg Lys
        10                  15                  20
gac atg gtc atc cta gag aaa agt gaa ttt gca aat ctg aga gca gag      450
Asp Met Val Ile Leu Glu Lys Ser Glu Phe Ala Asn Leu Arg Ala Glu
    25                  30                  35
aat gag aaa atg aaa att gaa tta gac caa gtt aag caa caa cta atg      498
Asn Glu Lys Met Lys Ile Glu Leu Asp Gln Val Lys Gln Gln Leu Met
40                  45                  50                  55
cat gaa acc agt yga atc aga gca gat aat aaa ctg ga                   536
His Glu Thr Ser Xaa Ile Arg Ala Asp Asn Lys Leu
                60                  65

<210> 752
<211> 139
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 25..138

<400> 752
cttggatctt tggtgttacc ttaa atg aaa ttt gga aat gtt agg atg tya       51
                           Met Lys Phe Gly Asn Val Arg Met Xaa
                           1               5
tct att caa ata ttt att gtg tcc atc tgg agc ttc ttc ctt ttc tat       99
Ser Ile Gln Ile Phe Ile Val Ser Ile Trp Ser Phe Phe Leu Phe Tyr
10                  15                  20                  25
ggc aag tat aca tat att aga ctg atc ttg tcc caa ggc c                139
Gly Lys Tyr Thr Tyr Ile Arg Leu Ile Leu Ser Gln Gly
                30                  35

<210> 753
<211> 193
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 87..191

<400> 753
tattacagag tttgcagact gaaagagagt ctagctaagg cttgctcctc atacccagga      60
tttgatctaa tccaacaagc ctttgt atg acc ttt gac ctc agt gtg ttc agt     113
```

```
                                  Met Thr Phe Asp Leu Ser Val Phe Ser
                                  1               5
act ttg tca gat cac ttt tac tca tca tca ttg tcc aat act gca agg      161
Thr Leu Ser Asp His Phe Tyr Ser Ser Ser Leu Ser Asn Thr Ala Arg
10                  15                  20                  25
aat ctg tat att tgt tta ttt cat atc aca ca                           193
Asn Leu Tyr Ile Cys Leu Phe His Ile Thr
                30                  35
```

<210> 754
<211> 395
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 310..393

<400> 754

```
cggcctcgca cttccggtgg ggagattccg gcctggagct cccagggccg agcagacctt    60
gggacctgtg agcgctgcat ccaattaacc atgggaaggg tcagcaccag ccaccagcca   120
cttaggtgag gactctgcct ggggctctgc tgatggttcc gaatcatgga gctgcagaga   180
gctcctccag cctggagacg ttcttggtga aagctgtggt ctaactccac cggctcttcc   240
tgcacattgt attcaagagg ggtgcctgcc cccgctgact caggagctcc ggtgctgcag   300
ccgccacga atg ggg agg tgg gcc ctc gat gtg gcc ttt ttg tgg aag gcg    351
          Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala
          1               5                   10
gtg ttg acc ctg ggg ctg gtg ctt ctc tac tac tgc ttc tcc at           395
Val Leu Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser
15                  20                  25
```

<210> 755
<211> 460
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 76..459

<400> 755

```
agaaggctgt gcgtgctcct cgctttctcc gcggtcttcc gagcggtcgc gtgaactgct    60
tcctgcaggc tggcc atg gcg ctt cac gtt ccc aag gct ccg ggc ttt gcc     111
                 Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala
                 1               5                   10
cag atg ctc aag gag gga gcg aaa cac ttt tca gga tta gaa gag gct      159
Gln Met Leu Lys Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala
        15                  20                  25
gtg tat aga aac ata caa gct tgc aag gag ctt gcc caa acc act cgt      207
Val Tyr Arg Asn Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg
    30                  35                  40
aca gca tat gga cca aat gga atg aac aaa atg gtt atc aac cac ttg      255
Thr Ala Tyr Gly Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu
45                  50                  55                  60
gag aag ttg ttt gtg aca aac gat gca gca act att tta aga gaa cta      303
Glu Lys Leu Phe Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu
                65                  70                  75
gaa gta cag cat cct gct gca aaa atg att gta atg gct tct cat atg      351
Glu Val Gln His Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met
        80                  85                  90
caa gag caa gaa gtt gga gat ggc aca aac ttt gtt ctg gta ttt gct      399
Gln Glu Gln Glu Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala
        95                  100                 105
```

```
gga gct ctc ctg gaa tta gct gaa gaa ctt ctg agg att ggc ctg tca      447
Gly Ala Leu Leu Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser
    110                 115                 120
gtt tca gag gtc a                                                     460
Val Ser Glu Val
125
```

<210> 756
<211> 142
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 42..140

<400> 756

```
aagcctgact tcagcgctcc cactctcggc cgacacccct c atg gcc aac cgt tac     56
                                              Met Ala Asn Arg Tyr
                                              1               5
acc atg gat ctg act gcc atc tac gag agc ctc ctg tcg ctg agc cct      104
Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu Leu Ser Leu Ser Pro
                10                  15                  20
gac gts acc ctc acc cac ttc gcc cac tgc aac ctc ca                   142
Asp Val Thr Leu Thr His Phe Ala His Cys Asn Leu
            25                  30
```

<210> 757
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 158..361

<400> 757

```
atcttgtagg cggggacacg ccgaggtaac ttccagggtg cgccttcgtt gtcttctcca     60
agctgtagtt ctacgtcccg acctccctat cataccacac tcttcagcga ccacgcaggc    120
actttcccgg tccccagtat accataattg aagaaaa atg atg gaa gag agt gga    175
                                         Met Met Glu Glu Ser Gly
                                         1               5
ata gag aca aca cca cct ggg act cct cca cca aat cct gca ggg ctg      223
Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro Pro Asn Pro Ala Gly Leu
            10                  15                  20
gct gct act gct atg tct tct acc cct gtt cca tta gcg gca acc agt      271
Ala Ala Thr Ala Met Ser Ser Thr Pro Val Pro Leu Ala Ala Thr Ser
        25                  30                  35
tct ttt tct tct cca aat gta tcc tcc atg gag tcc ttc cca cca ctc      319
Ser Phe Ser Ser Pro Asn Val Ser Ser Met Glu Ser Phe Pro Pro Leu
    40                  45                  50
gca tac tct act cct cag ccg ccc ctt cct cct gtg agg cct t            362
Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro Pro Val Arg Pro
55                  60                  65
```

<210> 758
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 219..368

```
<221> misc_feature
<222> 317
<223> n=a, g, c or t


<400> 758
gaagaaggct cttacagcat ggccgccggt actgcagctg ccttagcgtt tttgagtcag      60
gagagccgaa cgcgggccgg gggtgtcggg ggcctacggg tcccggcccc ggtcactatg     120
gacagttttt tcttcggctg tgagctctcc ggccacaccc gctccttcac ctttaaggta     180
gaggaagagg atgatgcgga sacgtgctgg cactaacc atg ctc tgc ctc acc gag     236
                                          Met Leu Cys Leu Thr Glu
                                          1               5
gga gcc aaa gac gag tgt aat gtg gta gaa gtt gtg gcc cgg aac cat       284
Gly Ala Lys Asp Glu Cys Asn Val Val Glu Val Val Ala Arg Asn His
            10                  15                  20
gac cat cag gag atc gca gtc cct gtg gcc aan ctc aag ctg tcc tgc       332
Asp His Gln Glu Ile Ala Val Pro Val Ala Xaa Leu Lys Leu Ser Cys
        25                  30                  35
caa ccc atg ctc agt ctg gat gac ttc cag ctc caa                       368
Gln Pro Met Leu Ser Leu Asp Asp Phe Gln Leu Gln
    40                  45                  50

<210> 759
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 36..452

<400> 759
agctcgctgc gcaggcgcag tgagttcgac acacc atg ccg act gtc agc gtg          53
                                       Met Pro Thr Val Ser Val
                                       1               5
aag cgt gat ctg ctc ttc caa gcc ctg ggc cgc acc tac act gac gaa       101
Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly Arg Thr Tyr Thr Asp Glu
            10                  15                  20
gaa ttt gat gaa cta tgt ttt gaa ttt ggt ctg gag ctt gat gaa att       149
Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly Leu Glu Leu Asp Glu Ile
        25                  30                  35
aca tct gag aag gaa ata ata agt aaa gaa caa ggt aat gta aag gca       197
Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu Gln Gly Asn Val Lys Ala
    40                  45                  50
gca gga gcc tct gat gtt gtt ctt tac aaa att gac gtc cct gcc aat       245
Ala Gly Ala Ser Asp Val Val Leu Tyr Lys Ile Asp Val Pro Ala Asn
55                  60                  65                  70
aga tat gat ctc ctg tgt ctg gaa gga ttg gtt cga gga ctt cag gtc       293
Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu Val Arg Gly Leu Gln Val
                75                  80                  85
ttc aaa gaa agg ata aag gct cca gtg tat aaa cgg gta atg cct gat       341
Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr Lys Arg Val Met Pro Asp
            90                  95                  100
gga aaa atc cag aaa ttg att atc aca gaa gag aca gct aag ata cgt       389
Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu Glu Thr Ala Lys Ile Arg
        105                 110                 115
cct ttt gcg gta gca gca gtt ctc cgt aat ata aag ttt act aaa gat       437
Pro Phe Ala Val Ala Ala Val Leu Arg Asn Ile Lys Phe Thr Lys Asp
    120                 125                 130
cga tat gac agc ttc                                                   452
Arg Tyr Asp Ser Phe
135
```

<210> 760
<211> 295
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 83..295

<400> 760
aagctgcggt tcgaaaatss tgacagcaca gggcttcctg ggctctgcag agcaaactgg 60
aaagagctgg gatccaggca ct atg ttc tct gaa gaa ctg tgg ctg gaa aat 112
Met Phe Ser Glu Glu Leu Trp Leu Glu Asn
1 5 10
gag aaa aag tgt gct gtg gtt cgg aag tct aag cag ggc agg aaa cgc 160
Glu Lys Lys Cys Ala Val Val Arg Lys Ser Lys Gln Gly Arg Lys Arg
15 20 25
caa gaa ctg ctg gcc gta gcc ttc ggg gtg aag gtc cac acg ttc cga 208
Gln Glu Leu Leu Ala Val Ala Phe Gly Val Lys Val His Thr Phe Arg
30 35 40
ggc cca cac tgg tgt gaa tat tgt gcc aat ttc atg tgg ggg ctc atc 256
Gly Pro His Trp Cys Glu Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile
45 50 55
gcc caa ggg gtc cgg tgc tca gac tgt gga ttg aac gta 295
Ala Gln Gly Val Arg Cys Ser Asp Cys Gly Leu Asn Val
60 65 70

<210> 761
<211> 212
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..210

<400> 761
ttggccattt tattcctttg gctttgattt gtgaactata tccaagactc attggagtaa 60
tagttaactg attgcagtgg atttcgaggt gtggcaacta gtggcaatgc tcatgcgaca 120
gtg atg gtg gtt ttc atg aca tat gta act tta ccc ttt ttt ttt tct 168
Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser
1 5 10 15
ttc atc tct tcc ctt ctt tca ttt ttt ttt ctt ttt cta ctc tc 212
Phe Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu
20 25

<210> 762
<211> 623
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 474..623

<400> 762
agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcacccagt gattgtattt 60
gatgactttt aagctttcat atgccgttat ttaatacctg tcacttccaa atgagagatg 120
taagggcaac ggccgttagc gttctgwttt ggatcaggct ctggagtgga cgcccctagc 180
ttaggggtcc ttctaggcag ccagaaacct gcggaaaatg gtagcgatgg cggctgggcc 240
gagtgggtgt ctggtgccgg cgtttgggct acggttgttg ttggcgactg tgcttcaagc 300
ggtgtctgct tttggggcag agttttcatc ggaggcatgc agagagttrg gcttttctag 360

```
caacttgctt tgcagctctt gtgatcttct cggacagttc aacctgcttc agctggatcc   420
tgattgcaga ggatgstgtc aggaggaagc acaatttgaa accaaaaagc tgt atg      476
                                                           Met
                                                           1
cag gag cta ttc ttg aag ttt gtg gat gaa aat tgg gaa ggt tcc ctc     524
Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser Leu
        5                   10                  15
aag tcc aag tat gtc cgt ggt tca gac cct gta tta aag ctt ttg gac     572
Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu Asp
    20                  25                  30
gac aat ggg aac att gct gaa gaa ctg agc att ctc aaa tgg aca cag     620
Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr Gln
    35                  40                  45
aca                                                                 623
Thr
50
```

<210> 763
<211> 261
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 58..261

<400> 763

```
gacatccacg gggcgcgagt gacacgcggg agggagagca gtgttctgct ggagccg       57
atg cca aaa acc atg cat ttc tta ttc aga ttc att gtt ttc ttt tat     105
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
1               5                   10                  15
ctg tgg ggc ctt ttt act gct cag aga caa aag aaa gag gag agc acc     153
Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
            20                  25                  30
gaa gaa gtg aaa ata gaa gtt ttg cat cgt cca gaa aac tgc tct aag     201
Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
        35                  40                  45
aca agc aag aag gga gac cta cta aat gcc cat tat gac ggc tac ctg     249
Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
    50                  55                  60
gct aaa gac ggc                                                     261
Ala Lys Asp Gly
65
```

<210> 764
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 4..159

<400> 764

```
agt atg ctt gag gaa ttg aaa gct ggc cag gag ttg gag gaa cag acc      48
    Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr
    1               5                   10                  15
att agc cac ggc ttt gca cgt ggt gtg agg agg ggt gtg gct att gtg      96
Ile Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val
                20                  25                  30
ggc aag ggt ctg gaa tgg cat ggg tgt tgg tgg atg tgc cac gga tac     144
Gly Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr
            35                  40                  45
```

```
agg att cta gcc ggg a                                                 160
Arg Ile Leu Ala Gly
        50

<210> 765
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 404..514

<400> 765
aagaaagaga gaggcaagcg aaattcctga atggatagac agatgctacg tcatcggagc      60
tgcatcctcc actccacaag aggctaggag ctggggggag agaggcagtc cagccgcagg     120
gccacccgaa cagtctctcc tcctcacaga agcctggagc tgggcatcca agaagaagca     180
gcctcatttg ttttctggtg tcatcgtagg tggccaccta tggcttttgg gcttctcacc     240
tggggcgggt gggttctgca ccaccctccc accctccttc ctccgtgtgg acgatagagc     300
cacatccagc accacggaca gctcccgggc gaccaaaaag aagaatgtac ttcatctggt     360
tgggctggat tccctctgat aagccttccc agttgactga aag atg agg cta ggc       415
                                                Met Arg Leu Gly
                                                1
tct agc aag ttg aag tca aac cag ctc ctt caa gaa gct ttg agc aga       463
Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu Ala Leu Ser Arg
5                   10                  15                  20
atg aag tgg gga gga ccc agc ttc cag ccc agg aag ccc act gta cct       511
Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys Pro Thr Val Pro
                25                  30                  35
gga gc                                                                516
Gly

<210> 766
<211> 626
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 68..238

<221> sig_peptide
<222> 68..106
<223> Von Heijne matrix
      score 15
      seq MLLLLLLLPLALG/DK

<221> misc_feature
<222> 529
<223> n=a, g, c or t


<400> 766
agtttctgag agaagaaccc tgaggaacag acgttccctg gcggccctgg cgccttcaaa      60
cccagac atg ctg ctg ctg ctg ctg ctg ctg ccc ctt gct ctg ggg gac       109
        Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp
                    -10                 -5                  1
aaa ggg gat gga ggg aga cag aca ata tgg gga tgg tta ctt gct gca       157
Lys Gly Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala
        5                   10                  15
agt gca gga gct ggt gac ggt gca gga ggg cct gtg tgt cca tgt gcc       205
Ser Ala Gly Ala Gly Asp Gly Ala Gly Gly Pro Val Cys Pro Cys Ala
        20                  25                  30
```

```
ctg ctc ctt ctc cta ccc cca gga tgg ctg gac tgactctgac ccagttcatg     258
Leu Leu Leu Leu Leu Pro Pro Gly Trp Leu Asp
    35                  40
gctactggtt ccgggcaggg aatgatataa gctggaaggc tccagtggcc acaaacaacc     318
cagcttgggc agtgcaggag gaaactcggg accgattcca mctycyttgg ggacccacag     378
accaaaaatt gcactctgag catcagagat gccagaatga gtgatgcggg gagatacttc     438
tttcgtatgg agaaaggaaa tataaaatgg aattataaat atgaccagct ctctgtgaac     498
gtgayagcct tgacccacag gcccaacats nktatccccg gtaccctgga gtctggctgc     558
ttccagaatc tgacctgctc tgtgccctgg gcctgtgagc aggggacgcc ccctatgatc     618
tcctggat                                                              626

<210> 767
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 60..344

<221> sig_peptide
<222> 60..113
<223> Von Heijne matrix
      score 10.3000001907349
      seq VLMLAALLLHCYA/DS

<400> 767
acagcaactt ccttgatccc tgccacgcac gactgaacac agacagcagc cgcctcgcc      59
atg aag ctg ctg atg gtc ctc atg ctg gcg gcc ctc ctc ctg cac tgc      107
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
            -15                 -10                 -5
tat gca gat tct ggc tgc aaa ctc ctg gag gac atg gtt gaa aag acc      155
Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
        1               5                   10
atc aat tcc gac ata tct ata cct gaa tac aaa gag ctt ctt caa gag      203
Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
15                  20                  25                  30
ttc ata gac agt gat gcc gct gca gag gct atg ggg aaa ttc aag cag      251
Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
                35                  40                  45
tgt ttc ctc aac cag tca cat aga act ctg aaa aac ttt gga ctg atg      299
Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
            50                  55                  60
atg cat aca gtg tac gac agc att tgg tgt aat atg aag agt aat          344
Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
        65                  70                  75
taactttacc caaggcgttt ggctcagagg gctacagact atggccagaa ctcatctgtt     404
gattgctaga aaccactttt ctttcttgtg ttgtctkttt atgwggaaam tgctagacaa     464
ctgttgaaa                                                             473

<210> 768
<211> 673
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 218..502

<221> sig_peptide
<222> 218..310
<223> Von Heijne matrix
      score 9.19999980926514
```

seq RLLLATVLQAVSA/FG

<400> 768
agtggggagt ttaggcaagt gcctgatttg ggtaatcgaa agcacccagt gattgtattt 60
gatgactttt aagctttcat atgccgttat ttaatacctg tcacttccaa atgagagatg 120
taagggcaac ggccgttagc gttctgwttt ggatcaggct ctggagtgga cgcccctagc 180
ttaggggtcc ttctaggcag ccagaaacct gcggaaa atg gta gcg atg gcg gct 235
Met Val Ala Met Ala Ala
-30
ggg ccg agt ggg tgt ctg gtg ccg gcg ttt ggg cta cgg ttg ttg ttg 283
Gly Pro Ser Gly Cys Leu Val Pro Ala Phe Gly Leu Arg Leu Leu Leu
-25 -20 -15 -10
gcg act gtg ctt caa gcg gtg tct gct ttt ggg gca gag ttt tca tcg 331
Ala Thr Val Leu Gln Ala Val Ser Ala Phe Gly Ala Glu Phe Ser Ser
-5 1 5
gag gca tgc aga gag tta ggc ttt tct agc aac ttg ctt tgc agc tct 379
Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser Asn Leu Leu Cys Ser Ser
10 15 20
tgt gat ctt ctc gga cag ttc aac ctg ctt cag ctg gat cct gat tgc 427
Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu Gln Leu Asp Pro Asp Cys
25 30 35
aga gga tgc tgt cag gag gaa gca caa ttt gaa acc aaa aag ctg tat 475
Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe Glu Thr Lys Lys Leu Tyr
40 45 50 55
gca gga gct att ctt gaa gtt tgt gga tgaaaattgg gaaggttccc 522
Ala Gly Ala Ile Leu Glu Val Cys Gly
60
tcaagtccaa gcttttgtta ggagtgataa acccaaactg ttcagaggac tgcaaatcaa 582
gtatgtccgt ggttcagacc ctgtattaaa gcttttggac gacaatggga acattgctga 642
agaactgagc attctcaaat ggacacagac a 673

<210> 769
<211> 539
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 190..492

<221> sig_peptide
<222> 190..285
<223> Von Heijne matrix
score 8.80000019073486
seq VPMLLLIVGGSFG/LR

<221> misc_feature
<222> 500..501
<223> n=a, g, c or t

<400> 769
acaagtatgt tacgatggct cgattgcttt tgcctagcgg aaaccattca ctaaggaccg 60
agcaccaaat aaccaaggaa aaggaagtga gttaaggacg tactcgtctt ggtgagagcg 120
tgagctgctg agatttggga gtctgcgcta ggcccgcttg gagttctgag ccgatggaag 180
agttcactc atg ttt gca ccc gcg gtg atg cgt gct ttt cgc aag aac aag 231
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys
-30 -25 -20
act ctc ggc tat gga gtc ccc atg ttg ttg ctg att gtt gga ggt tct 279
Thr Leu Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser
-15 -10 -5
ttt ggt ctt cgt gag ttt tct caa atc cga tat gat gct gtg aag agt 327
Phe Gly Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser

```
                1                   5                   10
aaa atg gat cct gag ctt gaa aaa aaa ctg aaa gag aat aaa ata tct      375
Lys Met Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser
15                  20                  25                  30
tta gag tcg gaa tat gag aaa atc aaa gac tcc aag ttt gat gac tgg      423
Leu Glu Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp
                35                  40                  45
aag aat att cga gga ccc agg cct tgg gaa gat cct gac ctc ctc caa      471
Lys Asn Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln
            50                  55                  60
gga aag aaa tcc aga aag cct taagacanng acaacttgac tctgctgatt         522
Gly Lys Lys Ser Arg Lys Pro
        65
ctttttcct ttttttt                                                    539
```

<210> 770
<211> 479
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 124..468

<221> sig_peptide
<222> 124..276
<223> Von Heijne matrix
score 8.10000038146973
seq VCLCGTFCFPCLG/CQ

<400> 770

```
aagttacctc tcccctttca cgtarttttc atttgtggtg agattctctc ccaggccaca      60
agacatttcc tgctcggaac cttgtttact aatttccact gcttttaagg ccctgcactg     120
aaa atg caa gct cag gcg ccg gtg gtc gtt gtg acc caa cct gga gtc       168
    Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val
        -50                 -45                 -40
ggt ccc ggt ccg gcc ccc cag aac tcc aac tgg cag aca ggc atg tgt       216
Gly Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys
    -35                 -30                 -25
gac tgt ttc agc gac tgc gga gtc tgt ctc tgt ggc aca ttt tgt ttc       264
Asp Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe
-20                 -15                 -10                 -5
ccg tgc ctt ggg tgt caa gtt gca gct gat atg aat gaa tgc tgt ctg       312
Pro Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu
                1                   5                   10
tgt gga aca agc gtc gca atg agg act ctc tac agg acc cga tat ggc       360
Cys Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly
        15                  20                  25
atc cct gga tct att tgt gat gac tat atg gca act ctt tgc tgt cct       408
Ile Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro
    30                  35                  40
cat tgt act ctt tgc caa atc aag aga gat atc aac aga agg aga gcc       456
His Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala
45                  50                  55                  60
atg cgt act ttc taaaaactga t                                          479
Met Arg Thr Phe
```

<210> 771
<211> 492
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> 25..402

<221> sig_peptide
<222> 25..96
<223> Von Heijne matrix
      score 7
      seq LLCCFRALSGSLS/MR

<221> misc_feature
<222> 371
<223> n=a, g, c or t


<400> 771
agsctggccc tccctctttc caaa atg gac aag tcc ctc ttg ctg gaa ctc       51
                           Met Asp Lys Ser Leu Leu Leu Glu Leu
                                          -20
ccc atc ctg ctc tgc tgc ttt agg gca tta tct gga tca ctt tca atg      99
Pro Ile Leu Leu Cys Cys Phe Arg Ala Leu Ser Gly Ser Leu Ser Met
-15                 -10                 -5                  1
aga aat gat gca gtc aat gaa ata gtt gct gtg aaa aac aat ttt cct     147
Arg Asn Asp Ala Val Asn Glu Ile Val Ala Val Lys Asn Asn Phe Pro
            5                   10                  15
gtg ata gaa att gtt cgg tgt agg atg tgc cac ctc cag ttc cca gga     195
Val Ile Glu Ile Val Arg Cys Arg Met Cys His Leu Gln Phe Pro Gly
        20                  25                  30
gaa aag tgc tcc aga gga aga gga ata tgc aca gca aca aca gaa gag     243
Glu Lys Cys Ser Arg Gly Arg Gly Ile Cys Thr Ala Thr Thr Glu Glu
    35                  40                  45
gcc tgc atg gtt gga agg atg ttc aaa agg gat ggt aat ccc tgg tta     291
Ala Cys Met Val Gly Arg Met Phe Lys Arg Asp Gly Asn Pro Trp Leu
50                  55                  60                  65
acc ttc atg ggc tgc cta aag aac tgt gct gat gtg aaa ggc ata agg     339
Thr Phe Met Gly Cys Leu Lys Asn Cys Ala Asp Val Lys Gly Ile Arg
                70                  75                  80
tgg agt gtc tat ttg gtg aac ttc agg tgc tnm agg agc cat gac ctg     387
Trp Ser Val Tyr Leu Val Asn Phe Arg Cys Xaa Arg Ser His Asp Leu
            85                  90                  95
tgc aat gaa gac ctt tagaagttaa tggttcttct gtgactccaa tttctgggtg     442
Cys Asn Glu Asp Leu
        100
aggttgttgc ctcagcctct tcacaatgac tttctaaaaa aatcacacac              492

<210> 772
<211> 396
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 7..312

<221> sig_peptide
<222> 7..54
<223> Von Heijne matrix
      score 6.80000019073486
      seq LWILPSLWLLLLG/GP

<400> 772
agcaag atg gat cta ctg tgg atc ctg ccc tcc ctg tgg ctt ctc ctg       48
       Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu
           -15                 -10                 -5
```

```
ctt ggg ggg cct gcc tgc ctg aag acc cag gaa cac ccc agc tgc cca       96
Leu Gly Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro
        1               5                   10
gga ccc agg gaa ctg gaa gcc agc aaa gtt gtc ctc ctg ccc agt tgt      144
Gly Pro Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys
15                  20                  25                  30
ccc gga gct cca gga agt cct ggg gag aag gga gcc cca ggt cct caa      192
Pro Gly Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln
                35                  40                  45
ggg cca cct gga cca cca ggc aag atg ggc ccc aag ggt gag cca gga      240
Gly Pro Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly
            50                  55                  60
gat cca gtg aac ctg ctc cgg tgc cag gaa ggc ccc aga aac tgc cgg      288
Asp Pro Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg
        65                  70                  75
gag ctg ttg agc agg gcg cca cct tgagcggctg gtamcatctg tgcctacctg     342
Glu Leu Leu Ser Arg Ala Pro Pro
    80                  85
agggcagggc ctcccagtct tttgtgacat ggacaccgag gggggcggct ggct          396
```

<210> 773
<211> 417
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..229

<221> sig_peptide
<222> 50..106
<223> Von Heijne matrix
score 6.59999990463257
seq SAVVLPSTPQASA/NP

<221> misc_feature
<222> 206,354
<223> n=a, g, c or t

<400> 773

```
acaggatcga tttacggycg cagagaaaaa ccaagatttc actttcaag atg gaa agt      58
                                                      Met Glu Ser
ccg tca grc tca gct gtg gtt tta cct agc act cct cag gcc tct gcg      106
Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln Ala Ser Ala
    -15                 -10                 -5
aat cca tca tct ccc tat aca aat agt tcc cga aaa caa cct atg agt      154
Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln Pro Met Ser
1               5                   10                  15
gca aca ctt aga gaa aga tta agg aaa aca aga ttt tca ttt aat tcc      202
Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser Phe Asn Ser
            20                  25                  30
tct nac aat gtg gtg aac gtc tta aag tagagagtga agaaaatgat            249
Ser Xaa Asn Val Val Asn Val Leu Lys
        35                  40
cagacctttt cagagaaccc agcatcttcc acagaggraa actgtttggr attcaaagaa    309
agtttaaamc atatagrcag tgatttgaag aaaatacaaa tttgnaaaat actttgaaga    369
atctcaatgt ctgtgaatct cagtcacttg attctggatc atgcagtg                 417
```

<210> 774
<211> 454
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 153..443

<221> sig_peptide
<222> 153..200
<223> Von Heijne matrix
score 6.40000009536743
seq WLWPLYFLPVSGA/LR

<221> misc_feature
<222> 359
<223> n=a, g, c or t

<400> 774
```
aggttgtcat ttcctcatcg tcaagctttg ttcctcgtgg gggctagaaa tctctttcca     60
gttccagatt gtgaagggtt cctgagtaag cagcgtgtct ccatccccct ctctaggggc    120
tcttggatgg accttgcact ctagaaggga ca atg gac ttc tgg ctt tgg cca      173
                                    Met Asp Phe Trp Leu Trp Pro
                                        -15                 -10
ctt tac ttc ctg cca gta tcr ggg gcc ctg agg atc ctc cca gaa gta      221
Leu Tyr Phe Leu Pro Val Ser Gly Ala Leu Arg Ile Leu Pro Glu Val
                -5                  1               5
aag gta gag ggg gag ctg ggc gga tca gtt acc atc aag tgc cca ctt      269
Lys Val Glu Gly Glu Leu Gly Gly Ser Val Thr Ile Lys Cys Pro Leu
        10                  15                  20
cct gaa atg cat gtg agg ata tat ctg tgc cgg gag atg gct gga tct      317
Pro Glu Met His Val Arg Ile Tyr Leu Cys Arg Glu Met Ala Gly Ser
    25                  30                  35
gga aca tgt ggt acc gtg gta tcc acc acc aac ttc atc aan gca gaa      365
Gly Thr Cys Gly Thr Val Val Ser Thr Thr Asn Phe Ile Xaa Ala Glu
40                  45                  50                  55
tac aag ggc cga gtt act ctg aga gca ata ccc acg caa gaa tct gtt      413
Tyr Lys Gly Arg Val Thr Leu Arg Ala Ile Pro Thr Gln Glu Ser Val
                60                  65                  70
cct agt gga ggt aac aca gct gac aga aag tgacagcgga g                 454
Pro Ser Gly Gly Asn Thr Ala Asp Arg Lys
            75                  80
```

<210> 775
<211> 531
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..253

<221> sig_peptide
<222> 8..109
<223> Von Heijne matrix
score 6.19999980926514
seq MAVLAPLIALVYS/XP

<400> 775
```
agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca      49
        Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala
                        -30                 -25
gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct      97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-20                 -15                 -10                 -5
```

```
ctc gtg tat tcg gys ccg cga ctt tca cga tgg ctc gcc caa cct tac      145
Leu Val Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
                1               5                   10
tac ctt ctg tcg scc ctg ctc tct gmt gcc ttc cta ctc gtg agg maa      193
Tyr Leu Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa
        15                  20                  25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa smc ggt aac      241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn
    30                  35                  40
ccg tcr wsa ytt tgactgggtg agcctcccgc gtgttagtac cccgcgacsk          293
Pro Ser Xaa Xaa
45
tgactgtscc tgcccttgca ggtgtatctg ggaaccctgg ggtttacctc tctgaggaca    353
cctgakgttc cgagcctgta gcggacttag agactattaw ktgcagggtc cgaaccatca    413
tcgagtctaa actttgtgtt taagatggga aaacggaaca tgttagtcgt agcccatgca    473
caacggccca acagcttttg actgttgagt ccaggtttct ttctgtttca ccattgag      531
```

```
<210> 776
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 220..363

<221> sig_peptide
<222> 220..270
<223> Von Heijne matrix
      score 6
      seq WLSCFLLPALVVS/VA

<221> misc_feature
<222> 201
<223> n=a, g, c or t


<400> 776
agagggtgcc cacctgtgtg ccagcgcctg tccggcgcct gcctgccgcc tccgtggcga     60
aggggacaca gaaatactca ctgagcctac actgggctca gcctgtgctt ggtcctgggg    120
tcacaaaggt gcatcagacg cagaccttgc cctcacatct cttctggcct ggtgggagag    180
gctcatctgc aaagagataa ngaggtccct gcggatgtg atg gcc cag cta tgg       234
                                           Met Ala Gln Leu Trp
                                                       -15
ctg tcc tgc ttc ctc ctt cct gcc ctc gtg gtg tct gtg gca gcc aac      282
Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val Ser Val Ala Ala Asn
        -10                 -5                  1
gtg gcc cck wag ttc cta gcc aac atg acg tca gtg atc ctg cct gag      330
Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser Val Ile Leu Pro Glu
5                   10                  15                  20
gac tgc ctg tgg gtg ccc agg cct tct ggt tgg tagcg                    368
Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp
                25                  30

<210> 777
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 8..322
```

```
<221> sig_peptide
<222> 8..109
<223> Von Heijne matrix
      score 5.90000009536743
      seq MAVLAPLIALVYS/VP

<221> misc_feature
<222> 233,352
<223> n=a, g, c or t


<400> 777
agtcgtt atg gtg ggg gag gcg ggg cga gac cta cga cgc cgg cga gca      49
        Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala
                        -30                 -25
gtg gcc gtt acg gcc gaa aag atg gcg gtc ttg gca cct cta att gct      97
Val Ala Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala
-20                 -15                 -10                 -5
ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac     145
Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
                1               5                   10
tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa     193
Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys
    15                  20                  25
ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gar nac ggt aac     241
Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn
    30                  35                  40
ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt     289
Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser
45                  50                  55                  60
gcc att gtg atg atg aag aac cgc aga tcc agc tgaatttgaa cttggacttc   342
Ala Ile Val Met Met Lys Asn Arg Arg Ser Ser
                65                  70
tatcccytmn gwgtctccta tttcaaagtg ccccatgaag agggacaaag aatgggatat   402
aggagtgcac agcccagcct gacctgtgac atctctgtgt ttcagtcact gtggagcaac   462
atatagg                                                             469

<210> 778
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 77..340

<221> sig_peptide
<222> 77..133
<223> Von Heijne matrix
      score 5.90000009536743
      seq AFLVCLAFSLATL/VQ

<400> 778
agctcckcct cggcctcccc ttcgggcgct ctcgcgctaa ctgtgctcct ccggggccct    60
ccgcctgctc ccagcc atg gtg gcc tgg cgc tcg gcg ttc ctt gtc tgc ctc   112
                  Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu
                                  -15                 -10
gct ttc tcc ttg gcc acc ctg gtc cag cga gga tct ggg gac ttt gat     160
Ala Phe Ser Leu Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp
        -5                  1               5
gat ttt aac ctg gag gat gca gtg aaa gaa act tcc tca gta aag cag     208
Asp Phe Asn Leu Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln
10                  15                  20                  25
```

```
cca tgg gac cac acc acc acc acc aca acc aat agg cca gga acc acc      256
Pro Trp Asp His Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr
                30                  35                  40
aga gct ccg gca aaa cct cca ggt agt gga ttg gac ttg gct gat gct      304
Arg Ala Pro Ala Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala
            45                  50                  55
ttg gat gat caa gat gat ggc cgc aga aac cgg gta taggaggaag           350
Leu Asp Asp Gln Asp Asp Gly Arg Arg Asn Arg Val
        60                  65
agagagatgg aaccatgtaa ccaccacgac caagaggcca gtaaccacca gagctccagc    410
aaatacttta ggaaatgatt ttgacttggc tgatgcctgg atgatcgaaa tgatcgag      468

<210> 779
<211> 479
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 73..429

<221> sig_peptide
<222> 73..231
<223> Von Heijne matrix
      score 5.80000019073486
      seq ILSLQVLLTTVTS/TV

<400> 779
gctctctcgc ggaastgggg aggaggcggt tgcggttagt ggaccgggac cggtaggggt     60
gctgttgcca tc atg gct gac ccc gac ccc cgg tac cct cgc tcc tcg atc    111
              Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile
                          -50                 -45
gag gac gac ttc aac tat ggc agc agc gtg gcc tcc gcc acc gtg cac      159
Glu Asp Asp Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His
-40                 -35                 -30                 -25
atc cga atg gcc ttt ctg aga aaa gtc tac agc att ctt tct ctg cag      207
Ile Arg Met Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln
                -20                 -15                 -10
gtt ctc tta act aca gtg act tca aca gtt ttt tta tac ttt gag tct      255
Val Leu Leu Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser
            -5                  1               5
gta cgg aca ttt gta cat gag agt cct gcc tta att ttg ctg ttt gcc      303
Val Arg Thr Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala
    10                  15                  20
ctc gga tct ctg ggt ttg att ttt gcg ttg ayt tta aac aga cat aag      351
Leu Gly Ser Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys
25                  30                  35                  40
tat ccc ctt aac ctg tac cta ctt ttt gga ttt acg ctg ttg gaa gct      399
Tyr Pro Leu Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala
                45                  50                  55
ctg act gtg gca gtt gtk gtt act gtt cta tgatgtatat attattctgc        449
Leu Thr Val Ala Val Val Val Thr Val Leu
            60                  65
aagctttcat actgactact acagtatttt                                     479

<210> 780
<211> 504
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 112..423
```

<221> sig_peptide
<222> 112..276
<223> Von Heijne matrix
score 5.59999990463257
seq ELCCLFCCPPCPG/KI

<400> 780
```
agtttcttcc gggtcattga cagaagcgtc aattcctggg agtagttcgt tggttttctt    60
tcccctcatc cttttgcctg ctcccggcga ggggtggctt tgatttcggc g atg agc    117
                                                        Met Ser
                                                        -55
tcc cag aaa ggc aac gtg gct cgt tcc aga cct cag aag cac cag aat     165
Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His Gln Asn
            -50                 -45                 -40
acg ttt agc ttc aaa aat gac aag ttc gat aaa agt gtg cag acc aag     213
Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln Thr Lys
        -35                 -30                 -25
agc atg aat aat ctt tca ttt agt gag cta tgt tgc ctc ttc tgc tgt     261
Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe Cys Cys
    -20                 -15                 -10
cca cct tgt cca ggg aag att gct tca aaa tta gcg ttt ttg cca cct     309
Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu Pro Pro
-5                  1               5                   10
gat cca act tac aca ctg atg tgt gat gaa agc gga agc gtt gga ctt     357
Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val Gly Leu
            15                  20                  25
tac atc tgt ctg aac gag cag act ggc agt att ctt cta gag aaa aag     405
Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu Lys Lys
        30                  35                  40
atg cta ttg agt gtt tca tgactagaac cagtaaaggc aacagaattg            453
Met Leu Leu Ser Val Ser
    45
cttgtatgtt tgtacgttgt tcacccaatg cgaaatacac tttactcttc t            504
```

<210> 781
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 102..479

<221> sig_peptide
<222> 102..287
<223> Von Heijne matrix
score 5.59999990463257
seq VIYLILLTAGAGL/LV

<221> misc_feature
<222> 521
<223> n=a, g, c or t

<400> 781
```
agctgcagtg gttcgatggg aaggatcttt ctccaagtgg ttcctcttga ggggagcatt    60
tctgctggct ccaggacttt ggccatctat aaagcttggc a atg aga aat aag aaa   116
                                              Met Arg Asn Lys Lys
                                                          -60
att ctc aag gag gac gag ctc ttg agt gag acc caa caa gct gct ttt     164
Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr Gln Gln Ala Ala Phe
        -55                 -50                 -45
```

```
cac caa att gca atg gag cct ttc gaa atc aat gtt cca aag ccc aag      212
His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn Val Pro Lys Pro Lys
    -40                 -35                 -30
agg aga aat ggg gtg aac ttc tcc cta gct gtg gtg gtc atc tac ctg      260
Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val Val Val Ile Tyr Leu
-25                 -20                 -15                 -10
atc ctg ctc acc gct ggc gct ggg ctg ctg gtg gtc caa gtt ctg aat      308
Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val Val Gln Val Leu Asn
                -5                  1                   5
ctg cag gcg cgg ctc cgg gtc ctg gag atg tat ttc ctc aat gac act      356
Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr Phe Leu Asn Asp Thr
        10                  15                  20
ctg gcg gct gag gac agc ccg tcc ttc tcc ttg ctg cag tca gca cac      404
Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His
    25                  30                  35
cct gga gaa cac ctg gct cag ggt gca tcg agg ctg cag tcc tgc agg      452
Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg Leu Gln Ser Cys Arg
40                  45                  50                  55
ccc aac tca cct ggg tcc gcg tca sca tgagcacttg ctgcagcggg            499
Pro Asn Ser Pro Gly Ser Ala Ser Xaa
                60
tagacaactt cactcagaak cnacggatgt tcagaatcaa aaggt                    544

&lt;210&gt; 782
&lt;211&gt; 455
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; 27..428

&lt;221&gt; sig_peptide
&lt;222&gt; 27..194
&lt;223&gt; Von Heijne matrix
      score 5.30000019073486
      seq LAKLLPLPAAITS/QL

&lt;400&gt; 782
aagagaggaa aaaaaatagc aggaag atg gcg ccc acc aag ccc agc ttt cag      53
                             Met Ala Pro Thr Lys Pro Ser Phe Gln
                                     -55                 -50
cag gat cct tcc agg cga gaa cgt tta caa gca ttg aga aag gag aaa      101
Gln Asp Pro Ser Arg Arg Glu Arg Leu Gln Ala Leu Arg Lys Glu Lys
        -45                 -40                 -35
tcc cga gat gct gct cgc tcc cgc cgg gga aaa gaa aac ttt gag ttc      149
Ser Arg Asp Ala Ala Arg Ser Arg Arg Gly Lys Glu Asn Phe Glu Phe
    -30                 -25                 -20
tat gaa ttg gcc aag ttg ttg cct ctt cct gca gcc att acc agc cag      197
Tyr Glu Leu Ala Lys Leu Leu Pro Leu Pro Ala Ala Ile Thr Ser Gln
-15                 -10                 -5                  1
ctc gac aag gca tcc atc att cga ctt aca att agc tat ctg aaa atg      245
Leu Asp Lys Ala Ser Ile Ile Arg Leu Thr Ile Ser Tyr Leu Lys Met
            5                   10                  15
agg gac ttt gct aac cag ggg gac cct ccg tgg aac ttg cga atg gaa      293
Arg Asp Phe Ala Asn Gln Gly Asp Pro Pro Trp Asn Leu Arg Met Glu
        20                  25                  30
ggc cct cca cct aac aca tca gta aaa gtt ata ggt gca cag cga agg      341
Gly Pro Pro Pro Asn Thr Ser Val Lys Val Ile Gly Ala Gln Arg Arg
    35                  40                  45
aga agc ccc agt gca cta gcc att gaa gta ttt gaa gca cat ttg gga      389
Arg Ser Pro Ser Ala Leu Ala Ile Glu Val Phe Glu Ala His Leu Gly
50                  55                  60                  65
```

```
agc cac att ttg cag tcc tgg atg gct ttg tat ttg cac taaatcagga       438
Ser His Ile Leu Gln Ser Trp Met Ala Leu Tyr Leu His
                70                  75
aggaaaattt ttgtaca                                                   455

<210> 783
<211> 453
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..168

<221> sig_peptide
<222> 85..144
<223> Von Heijne matrix
      score 5
      seq ALLSVCSTDVTTA/HA

<221> misc_feature
<222> 284
<223> n=a, g, c or t


<400> 783
ccccttgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg     60
agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg       111
                           Met Glu Glu Leu Gln Asp Gln Ala Leu
                           -20                 -15
ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg      159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr
    -10                 -5                  1               5
gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag              208
Val Leu Val
aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag    268
gagtaaagtg gacacntcag ctggtcccct gggtcgtcca cccgatgtcc cccattctcc    328
ccacttggcc tccccccacag gctctcggca aaggaccgtg ggaggcacct gtgacactgc   388
ccttttcctg tgcagctgtt tktcttcttc attcttttca ctcctcgtta ctcttttttt    448
tttca                                                                453

<210> 784
<211> 587
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 85..168

<221> sig_peptide
<222> 85..144
<223> Von Heijne matrix
      score 5
      seq ALLSVCSTDVTTA/HA

<400> 784
ccccttgtgg ccaagcctgg aacatcacat ctgtacgttg caatctgtgg atcagctacg     60
agactgagag aaaggaatga aagg atg gaa gaa tta caa gat cag gca ctg       111
                           Met Glu Glu Leu Gln Asp Gln Ala Leu
                           -20                 -15
ctg tct gtc tgt tcc acg gat gta acc aca gca cac gcg tgg ctc acg      159
Leu Ser Val Cys Ser Thr Asp Val Thr Thr Ala His Ala Trp Leu Thr
```

```
 -10                  -5                   1                5
gta cta gtg tgataaatgc ttgttacatg aaggcgtgaa cagggatgag             208
Val Leu Val
aagagacttc ctggagaaac aaaaggacta acaatcagga aggggaggtg atcggggcag    268
gagtaaagtg gacacctcag caaagccatt cgctgtgatc tctgattgtg cagtgtcatg    328
tcctgtcacc agagccccct cgtgtttgrk gttggccaat gccgccagca tgatctagca    388
ggccaaatcc taatctacca ttctctgaca ccagctggtc ccctgggtcg tccacccgat    448
gtcccccatt ctccccactt ggcctccccc acaggctctc ggcaaaggac cgtgggaggc    508
acctgtgaca ctgccctttt cctgtgcagc tgtttktctt cttcattctt ttcactcctc    568
gttactcttt ttttttttca                                                587
```

<210> 785
<211> 461
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 250..390

<221> sig_peptide
<222> 250..384
<223> Von Heijne matrix
score 4.80000019073486
seq ICCAAAAAAAAGS/RI

<221> misc_feature
<222> 218
<223> n=a, g, c or t

<400> 785

```
agaggcctcg cgaggcaggg ctagaagctg tggcctcacc cttgaggccc gggcacttcc     60
cgtctcctcc cttgctcccc ttcctcaccc caatccctac agcctcccgc gcasctgagc    120
tctaggattg tgggttttcc atcctccgaa gacatcacct ttgctcatct cccaggagag    180
tctcgtccaa aggagggggg tgctttctgc ttcagcanga tccaccccac cctgggatcc    240
gagggagca atg gtg ggg cga gtg agg gtc tgc cgt aaa tat ccc ccg acc    291
          Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr
          -45                 -40                 -35
acc ctc tgg gaa ggt gct aga ggc cac agg caa att tca gtc tcc cca      339
Thr Leu Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro
    -30                 -25                 -20
tgg aat atc tgc tgt gct gct gct gct gct gct gct gct ggg tca agg      387
Trp Asn Ile Cys Cys Ala Ala Ala Ala Ala Ala Ala Ala Gly Ser Arg
-15                 -10                 -5                  1
ata tgagcgagcc tcttcygaaa acagccggga agggagagga atccaagagg           440
Ile
aggagcaggt gggaaagaca a                                              461
```

<210> 786
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 53..463

<221> sig_peptide
<222> 53..208
<223> Von Heijne matrix
score 3.90000009536743
seq LCCGLSMFEVILT/RI

```
<400> 786
catttctgc tctgcgactc cttttgcaga gggggagcgc ctggaggtcc gg atg aaa      58
                                                         Met Lys
cgt ctg gaa gcc aag tat gcc ccg ctc cac ctg gtc cct ctg atc gag      106
Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu Ile Glu
-50                 -45                 -40                 -35
cgg ctg ggg acc cct cag caa atc gcc att gct cgc gag ggt gac ctc      154
Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly Asp Leu
                -30                 -25                 -20
ctg acc aag gag cgg ctg tgc tgt ggc ctg tcc atg ttc gag gtc atc      202
Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu Val Ile
            -15                 -10                 -5
ctg acc cgc att cgg agc tac ctg cag gac ccc atc tgg cgg ggc cca      250
Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg Gly Pro
        1               5                   10
ccg ccc acc aat ggc gtc atg cac gtc gat gag tgt gtg gag ttc cac      298
Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu Phe His
15                  20                  25                  30
cgg ctg tgg agc gcc atg cag ttc gtg tac tgc atc cct gtg gga acc      346
Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val Gly Thr
                35                  40                  45
aac gag ttc aca gct gag cag tgt ttc ggc gat ggc ttg aac tgg gct      394
Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn Trp Ala
            50                  55                  60
ggt tck ccr kca ttg tcc tgc tsg gcc agc agc gtc gct ttg acc tgt      442
Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu Thr Cys
        65                  70                  75
tcg act tct gtt acc acc tgc taaaagtgca gaggcaggac gggaag             489
Ser Thr Ser Val Thr Thr Cys
    80                  85

<210> 787
<211> 397
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 52..354

<221> sig_peptide
<222> 52..264
<223> Von Heijne matrix
      score 3.70000004768372
      seq LXDLSSLLTRGSG/NQ

<400> 787
ccctcacgcc cgccctcctt gccgcccagc cggtccaggc ctctggcgaa c atg gcg      57
                                                         Met Ala
                                                             -70
ctt gtc ccc tgc cag gtg ctg cgg atg gca atc ctg ctg tcy tac tgc      105
Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser Tyr Cys
                -65                 -60                 -55
tct atc ctg tgt aac tac aag gcc atc gaa atg ccc tca cac cag acc      153
Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His Gln Thr
            -50                 -45                 -40
tac gga ggg agc tgg aaa ttc ctg acg ttc att gat ctg gtt atc cag      201
Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val Ile Gln
        -35                 -30                 -25
gct gtc ttt ttt ggc atc tgt gtg ctg amt gat ctt tcc agt ctt ctg      249
Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser Leu Leu
    -20                 -15                 -10
```

```
act cga gga agt ggg aac cag gar caa gag agg cag ctc aag aag ctc      297
Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys Lys Leu
-5                  1               5                   10
atc tct ctc cgg gac tgg atg tta gct gtg ttg gct ttc ctg ttg ggg      345
Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu Leu Gly
            15                  20                  25
ttt ttg ttg tagcagtgtt ctggrtcatt tatgcctatg acagmgagat gat          397
Phe Leu Leu
        30
```

<210> 788
<211> 595
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 50..286

<221> sig_peptide
<222> 50..256
<223> Von Heijne matrix
score 3.70000004768372
seq ALTGSQLLGDTIP/RP

<400> 788

```
ctctctgtcc ccctccccct ccctgtcctt atctttccct tctgtctcc atg gcg act     58
                                                      Met Ala Thr
cac cac ctc ggc ttg cct gca tcc cag cct ctg cca ggg att ctg agc      106
His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly Ile Leu Ser
    -65                 -60                 -55
cgg gct cca tcc ctc cct cct cgg agc cct gct acc cgc agc cgt gtc      154
Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg Ser Arg Val
-50                 -45                 -40                 -35
tcc tcc ccc tgg ggt gag tcc agc agc agc ctc ctc ttt cct gac tgt      202
Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe Pro Asp Cys
                -30                 -25                 -20
cac att tct ttt cca gct ctg acc ggg agt cag ctc ctc ggg gat acc      250
His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu Gly Asp Thr
            -15                 -10                 -5
atc ccc cga cct cac ctt cca cct acc gca gcc tgc tagcctttcc           296
Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
        1               5                   10
gggagaaaag gcatccttac ctctggttga aggtctcggg gcctccccct ctgcatccgg    356
accctctccc catcccagcc tcccatgcca aggcccgcct tgtcagtcac ttccttttgt    416
catcggcttg gcaaacggga gagaaaacag agcttcatgg gaaacagcgg caacagtggt    476
cccatacacc tttccccaag ttggagctag gcctggggcc ccagcccatg gygccccggg    536
agctccctac ctgctccats tgcctggaga ggttgcgcga ccccatctsg ytggaatgt     595
```

<210> 789
<211> 359
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..344

<221> sig_peptide
<222> 21..125
<223> Von Heijne matrix
score 3.70000004768372
seq SPLLCHSLRKTSS/SQ

```
<400> 789
aggctcgggg agtcggcgcc atg acc cca tcg agg ctt ccc tgg ttg ctt agc      53
                      Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser
                      -35                 -30                 -25
tgg gtc tcg gcc acg gcg tgg aga gcg gca aga tca ccc ctt ctg tgt       101
Trp Val Ser Ala Thr Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys
                -20                 -15                 -10
cat tct ctg agg aaa aca agt tct tct caa gga gga aag tct gaa ctt       149
His Ser Leu Arg Lys Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu
            -5                  1               5
gtc aaa cag tcc ctt aag aag ccg aag tta cca gaa ggt cgt ttt gat       197
Val Lys Gln Ser Leu Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp
    10                  15                  20
gca cca gag gat tcc cat tta gag aaa gaa cca ctg gaa aaa ttt cca       245
Ala Pro Glu Asp Ser His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro
25                  30                  35                  40
gat gat gtk rat cca gtg acc aaa gaa aaa ggt gga ccc agg ggc cca       293
Asp Asp Val Xaa Pro Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro
                45                  50                  55
gaa cct acc cga tat gga gat tgg gaa cga aaa gga cgc tgt att gat       341
Glu Pro Thr Arg Tyr Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp
            60                  65                  70
ttt taagtcgcat attct                                                  359
Phe

<210> 790
<211> 836
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 118..360

<221> sig_peptide
<222> 118..270
<223> Von Heijne matrix
      score 3.59999990463257
      seq ICFVCGVFFSILG/TG

<221> misc_feature
<222> 7,359
<223> n=a, g, c or t


<400> 790
aggaagnsgg cgggaccgga cttccggctg gtctgtgggg tttcgggttc ggggtttcct      60
ggtgggcgtc aggggcaggc aacagagtgg cggccgctac ggccctggaa cggggcc        117
atg gag aag ctg cgg cga gtc ctg agc ggc cag gac gac gag gag cag       165
Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln
    -50                 -45                 -40
ggc ctg act gcg cag gtc ctg gat gcc tca tcc ctt agt ttc aac acc       213
Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr
-35                 -30                 -25                 -20
aga ttg aaa tgg ttt gcc atc tgc ttc gta tgt ggc gtt ttc ttt tct       261
Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser
                -15                 -10                 -5
att ctt gga act gga ttg ctg tgg ctt ccg ggc ggc ata aag ctt ttt       309
Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe
            1                   5                   10
gca gtg ttt tat acc ctc ggc aat ctt gct gcg tta sca gta cat gct       357
Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala
```

15 20 25
tnw taatgggacc tgtgaagcaa ctgaagaaaa tgtttgaagc aacaagattg 410
Xaa
30
cttgcaacaa ttgttatgct tttgtgtttc gtatttaccc tgtgtgctgc tctttggtgg 470
cataagaagg gactggctgt gttattctgc atattgcagt tcttgtcaat gacctggtat 530
agcctgtcrt acatcccata tgcaagggat gcagttatta aatgctgttc ttctctccta 590
agttgaaaat cagaaacttg tggaaaagag cacttgaatg ttggtactct atgtttggtg 650
aagtttgctt ttccccataa aacactccag gaacaactga cgtgacagtt gaagaccgtt 710
ttgtactaag tctcattttg tatactggta aaaactacat gcttgattaa accattaaat 770
gcttgtaact ttaaattcat tatgtgtcat taatatactt ttccaaagat aagattttta 830
atcact 836

<210> 791
<211> 551
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 6..329

<221> sig_peptide
<222> 6..284
<223> Von Heijne matrix
score 3.59999990463257
seq LLRLALRSPDVWL/GQ

<221> misc_feature
<222> 496,536
<223> n=a, g, c or t

<400> 791
tgtgt atg tgt gaa aat cag gaa gag cca gcg ggg agt gtg tgt tgc cat 50
Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His
-90 -85 -80
cgc gtc tcc gcc tgc agg ggc ggg acc cca gga gga ggg aga gga cag 98
Arg Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Gly Arg Gly Gln
-75 -70 -65
agc cac tgc aga gga cca gac tgg gaa aac aac gat atg gca gga gcc 146
Ser His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala
-60 -55 -50
agt ctt ggg gcc cgc ttc tac cgg cag atc aaa aga cat ccg ggg atc 194
Ser Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile
-45 -40 -35
atc ccg atg atc ggc tta atc tgc ctg ggc atg ggc agc gct gcg ctt 242
Ile Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu
-30 -25 -20 -15
tac ttg ctg cga ctc gcc ctt cgc agc ccc gac gtc tgg ctg gga cag 290
Tyr Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln
-10 -5 1
aaa gaa caa ccc gga gcc ctg gaa ccg cct gag ccc caa tgaccaatac 339
Lys Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln
5 10 15
aagttccttg cagtttccac tgactataag aagctgaaga aggaccggcc agacttctaa 399
gccaggctgg gctgccagtg ccatgcaagc cacagccagc cagcccatcc acttcttcca 459
ctcctccccg caggccccaa ggcatcactc cggccancct gtcccgctac tgcttacaca 519
ggccgggttc caccsanagg ggargctgct cc 551

<210> 792
<211> 437
<212> DNA

<213> Homo sapiens

<220>
<221> CDS
<222> 31..432

<221> sig_peptide
<222> 31..78
<223> Von Heijne matrix
score 3.5
seq AGLALLXRRVSSA/LK

<400> 792
```
ggaaacgcgt tttgccagtt atgcgaaaac atg gct gcg gcc ggt ttg gcc ctt      54
                                 Met Ala Ala Ala Gly Leu Ala Leu
                                         -15                 -10
ctt kgt agg aga gtt tca tcc gcc ctg aaa tct tcc cga tcg tta ata      102
Leu Xaa Arg Arg Val Ser Ser Ala Leu Lys Ser Ser Arg Ser Leu Ile
            -5                  1               5
act cct cag gtc cct gcc tgc aca ggg ttt ttt ctt agt ttg ttg cct      150
Thr Pro Gln Val Pro Ala Cys Thr Gly Phe Phe Leu Ser Leu Leu Pro
    10                  15                  20
aag agt aca cca aat gtg aca tcc ttt cac caa tat aga tta ctt cat      198
Lys Ser Thr Pro Asn Val Thr Ser Phe His Gln Tyr Arg Leu Leu His
25                  30                  35                  40
acc aca ttg tca agg aaa gga cta gaa gaa ttt ttt gat gac cca aaa      246
Thr Thr Leu Ser Arg Lys Gly Leu Glu Glu Phe Phe Asp Asp Pro Lys
                45                  50                  55
aac tgg ggg caa gaa aaa gta aaa tct gga gca gca tgg acc tgt cag      294
Asn Trp Gly Gln Glu Lys Val Lys Ser Gly Ala Ala Trp Thr Cys Gln
            60                  65                  70
caa cta agg aac aaa agt aat gaa gat tta cac aaa ctt tgg tat gtc      342
Gln Leu Arg Asn Lys Ser Asn Glu Asp Leu His Lys Leu Trp Tyr Val
        75                  80                  85
tta ctg aaa gaa aga aac atg ctt cta acc cta gag cag gag gcc aag      390
Leu Leu Lys Glu Arg Asn Met Leu Leu Thr Leu Glu Gln Glu Ala Lys
    90                  95                  100
cgg car aga ttg cca atg cca agt cca gag cgg tta gat agg tagta        437
Arg Gln Arg Leu Pro Met Pro Ser Pro Glu Arg Leu Asp Arg
105                 110                 115
```

<210> 793
<211> 350
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 130..321

<400> 793
```
ggaagtggac gaatttgaat cctgtgggcc gttgaatgtg gctgctcgcg gtcggcgtgc      60
cccgacgtac agcgggccgg gaaaagtggc actgaggctc tggaacttct gcccagctct      120
ccttgtaaa atg aat gaa agt aaa cct ggt gac tca cag aac ctt gct tgt     171
          Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys
          1               5                   10
gtt ttc tgt cga aaa cat gat gac tgt cct aat aaa tac gga gaa aag      219
Val Phe Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys
15                  20                  25                  30
aaa act aag gag aaa tgg aat ctc act gta cat tac tac tgt ttg ttg      267
Lys Thr Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu
                35                  40                  45
atg tca agt gga att tgg cag aga ggc aaa gaa gaa gaa gga gtt atg      315
```

```
Met Ser Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met
            50                  55                  60
gtt ttc taatagaaga tatcaggaag gaagtgaat                             350
Val Phe

<210> 794
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 37..273

<400> 794
gcgcatgtgc agaagggaaa cgtgaagaag gtgaag atg gcg gtg gcc agg gcc      54
                                        Met Ala Val Ala Arg Ala
                                        1               5
ggg gtc ttg gga gtc cag tgg ctg caa agg gca tcc cgg aac gtg atg     102
Gly Val Leu Gly Val Gln Trp Leu Gln Arg Ala Ser Arg Asn Val Met
            10                  15                  20
ccg ctg ggc gca cgg aca gcc tcc cac atg acc aag gac atg ttc ccg     150
Pro Leu Gly Ala Arg Thr Ala Ser His Met Thr Lys Asp Met Phe Pro
        25                  30                  35
ggg ccc tat cct agg acc cca gaa gaa cgg gcc gcc gcc gcc aag aag     198
Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg Ala Ala Ala Ala Lys Lys
    40                  45                  50
tat aat atg cgt gtg gaa gac tac gaa cct tac ccg gat gat ggc atg     246
Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro Tyr Pro Asp Asp Gly Met
55                  60                  65                  70
ggg tat ggc gac ctt ttc ctg twt gtc tgatttttat tatttaaaaa           293
Gly Tyr Gly Asp Leu Phe Leu Xaa Val
                75
aatggaaaaa caaaagtgca tttttcattc aataaatgtt ccatccttat ttagttttgt   353
tgaatcaagt cactttttac aagttttgtt tgatatgtat tttcatgctg ttaacacatt   413
tttctctgtc attatatt                                                 431

<210> 795
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 140..337

<400> 795
agagtgcatt ccggaacccg gggcgcggcg cactgcgcag gcggccggac tccgctcagt    60
ttccggtgcg gcgaacacca aagtccggga acttaagcat tttcggtttc tagggttgtt   120
acgaagctgc aggagcgag atg gag gtg gac gca ccg ggt gtt gat ggt cga    172
                     Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg
                     1               5                   10
gat ggt ctc cgg gag cgg cga ggc ttt agc gag gga ggg agg cag aac     220
Asp Gly Leu Arg Glu Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn
            15                  20                  25
ttc gat gtg agg cct cag tct ggg gca aat ggg ctt ccc aaa cac tcc     268
Phe Asp Val Arg Pro Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser
        30                  35                  40
tac tgg ttg gac ctc tgg ctt ttc atc ctt ttc gat gtg gtg gtg ttt     316
Tyr Trp Leu Asp Leu Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe
    45                  50                  55
ctc ttt gtg tat ttt ttg cca tgacttgttc gctgatatct aaattaagaa        367
Leu Phe Val Tyr Phe Leu Pro
```

60 65
gttggttctt gagtgaattc tgaaatggct acaaacttct tgaataaaga agacaggact 427
ctcaatagaa gaatttcaca tctccaaggg accttccttt cattttacac tttgttacta 487
atttgcagaa ctctattaat tgggtagga 516

<210> 796
<211> 442
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 40..174

<400> 796
cctggttttt ttgtttttttg tttggggtat ttttggtgt atg tat gtt tat gta 54
Met Tyr Val Tyr Val
1 5
tgt gtg tgg gta tgt gtg tat aca gtg gag agc aaa ttg gaa aac agt 102
Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser Lys Leu Glu Asn Ser
10 15 20
tct att tat cct cct ccc tcc cca gta gaa awa aaa aaa atc ttt aca 150
Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa Lys Lys Ile Phe Thr
25 30 35
ttt gtt act ttt ctt ttc ccc ccg taagacacag aattaatgga aagtgagtat 204
Phe Val Thr Phe Leu Phe Pro Pro
40 45
cttggatttc aaatctgaag agatttttac cattagtggt ttgattttaa tttgcttggt 264
taactatcat atttttcata cacttctctg gatttaaaat atcttgaggt attttgccac 324
tggcttcatg ctggagtaat gggtaacata tctttggtat ggttgcttag attaacttac 384
ctagtcagac ccagaagaac ttcttttact agcttgcttc ctaaatgctt ttttcctc 442

<210> 797
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 221..295

<400> 797
acaaacggcg gcgccggggc cggaggaaaa agctcgccac cctgaagggt cccttcccaa 60
gcccttaggg accgcagagg acttggggac cagcaagcaa cccccagggc acgagaagag 120
ctcttgctgt ctgccstgcc tcaccctgcm ccacgccagg cccggtggcc cccagctgca 180
tcaagtggag gcggaggagg aggcggagga gggtggcacc atg ggc ccg ggc ggt 235
Met Gly Pro Gly Gly
1 5
gcc ctc cat ggg ggg atg aag aca ctg ctg cca tgg aca gcc cgt gcc 283
Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro Trp Thr Ala Arg Ala
10 15 20
agc cgc agc ccc taagtcaggc tctccctcag ttaccagggt cttcgtcaga 335
Ser Arg Ser Pro
25
gcccttggag cctgagcctg gccgggccag gatgggagtg gagagttacc tgccctgtcc 395
cctgctcccc tcctaccact gtcca 420

<210> 798
<211> 413
<212> DNA
<213> Homo sapiens

<220>

```
<221> CDS
<222> 79..372

<221> misc_feature
<222> 364..365
<223> n=a, g, c or t


<400> 798
atggggacgg ggctgttccc ggggaggctg tgatgggttg acaggtgcgt gacagtggga    60
gctgctctcg gcacaagc atg tac ggc aaa ggc aag agt aac agc agc gcc     111
                    Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala
                    1               5                   10
gtc ccg tcc gac agc cag gcc cgg gag aag tta gca ctc tac gta tat     159
Val Pro Ser Asp Ser Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr
            15                  20                  25
gaa tat ctg ctc cat gta gga gct cag aaa tca gct caa aca ttt tta     207
Glu Tyr Leu Leu His Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu
        30                  35                  40
tca gag ata aga tgg gaa aaa aac atc aca ttg ggg gaa cca cca gga     255
Ser Glu Ile Arg Trp Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly
    45                  50                  55
ttc tta cat tct tgg tgg tgt gta ttt tgg gat ctc tac tgt gca gct     303
Phe Leu His Ser Trp Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala
60                  65                  70                  75
cca gag aga cgt gaa aca tgt gaa cac tca agt gaa gca aaa gcc ttc     351
Pro Glu Arg Arg Glu Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe
                80                  85                  90
cat gat tac gta nnt aac ata taattttaca aagttacact gtcagttttc        402
His Asp Tyr Val Xaa Asn Ile
            95
tgtttaacca c                                                        413

<210> 799
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 46..195

<400> 799
actgcagaga accagacaat accaggttgc ttataaaagg atgcc atg tgc ttg ctg    57
                                                  Met Cys Leu Leu
                                                  1
gag gtc cca ggt gca acc aaa ttg ctt gca gct agg agg acc ttg aag     105
Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg Arg Thr Leu Lys
5                   10                  15                  20
aga aat ggg atc agc ccg cca aac caa gaa ggg tta gca ctt ttg cta     153
Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu Ala Leu Leu Leu
                25                  30                  35
gga gag ctg acc acg cac aaa cag atg aga acc aaa acc gag             195
Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys Thr Glu
            40                  45                  50
tgaagaggat tgaagatgaa cccacatttt aaaagttctt gtctgctgga ggtggcatta   255
cctgtgacct cgcttcactt ctccatacat ggctgttata gcagaaaatc cagctttctg   315
aagcatattt cacgacatat gatgagactt atgtgatgtg agacctgaga aaactatgat   375
agamagaagc aactcaagtt gcaagg                                        401

<210> 800
<211> 465
<212> DNA
```

<213> Homo sapiens

<220>
<221> CDS
<222> 96..191

<400> 800
agagccgccc aagggatggc gatggcgtac ttggcttgga gactggcgcg gcgttcgtgt 60
ccgaggtcac tagtttcccg gtagttcagc tgcac atg aat aga aca gca atg 113
Met Asn Arg Thr Ala Met
1 5
aga gcc agt cag aag gac ttt gaa aat tca atr aat caa gtg aaa ctc 161
Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser Xaa Asn Gln Val Lys Leu
10 15 20
ttg aaa aag gat cca gga aac gar tgm agc taaaactcta cgcgctatat 211
Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
25 30
aagcaggcca ctgaaggacc ttgtaacatg cccaaaccag gtgtatttga cttgatcaac 271
aaggccaaat gggacgcatg gaatgccctt ggcagcctgc ccaaggaagc tgccaggcag 331
aactatgtgg atttggtgtc cagtttgagt ccttcattgg aatcctctag tcaggtggag 391
cctggaacag acaggaaatc aactgggttt gaaactctgg tggtgacctc cgaagatggc 451
atcacaaaga tcat 465

<210> 801
<211> 629
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 144..317

<221> misc_feature
<222> 583..584
<223> n=a, g, c or t

<400> 801
agtccatccc ctgtgcccgg gaaccgcggc tctgccccgc aaagggcacg cggactacaa 60
ctcccagagt ccactgcagc ggccaagggc tactgttccc agcgaggccc gsssggcggc 120
accgcgaagg gaggagtggc aac atg gcg tct tcg gga gct ggt gac cct ctg 173
Met Ala Ser Ser Gly Ala Gly Asp Pro Leu
1 5 10
gat tct aag cgt gga gag gcc ccg ttc gct cag cgt atc gac ccg act 221
Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr
15 20 25
cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag 269
Arg Glu Lys Leu Thr Pro Glu Gln Leu His Ser Met Arg Gln Ala Glu
30 35 40
ttg ccc agt ggc aga agg tcc tac cac ggc ggc gaa ccc gga aca tcg 317
Leu Pro Ser Gly Arg Arg Ser Tyr His Gly Gly Glu Pro Gly Thr Ser
45 50 55
tgaccggcct aggcatcggg gccctggtgt tggctattta tggttacacc ttctactcga 377
tttcccagga gcgtttccta gatgagctag aagacgaggc caaagctgcc cgagcccgag 437
ctctggcaag ggcgtcaggg tcctaatctg gatgggtatt gatcatgtcc aacctgctgg 497
agccccttca catggtggat gatgccccat gaccctgtga gaaattgaat cctgctcaca 557
acattgttgg ccttcttact aacctnngac ctgattgagc ccaagaaacc agggasttac 617
gcatttggcc aa 629

<210> 802
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 169..462

<400> 802
```
atataagtgg aggtcatttc ccctgccccc acccccagct tcctcagatc tgggcagagg      60
aaccaaaggg aaaagccacc ttcccaggca cagccataac atccacctca ctcaactgct     120
tgtcaagttc accaccaaca cagaggggc tcagataatc aagaaaca atg tcg agt       177
                                                    Met Ser Ser
                                                    1
gat gat aaa agt aaa tca aat gac ccc aag act gag ccc aag aac tgc       225
Asp Asp Lys Ser Lys Ser Asn Asp Pro Lys Thr Glu Pro Lys Asn Cys
    5                   10                  15
gat ccc aag tgt gaa caa aag tgt gag tcc aaa tgc cag ccc agc tgt       273
Asp Pro Lys Cys Glu Gln Lys Cys Glu Ser Lys Cys Gln Pro Ser Cys
20                  25                  30                  35
tta aag aag ctg ctg caa cgc tgt ttc gaa aag tgc cca tgg gaa aag       321
Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys Pro Trp Glu Lys
                40                  45                  50
tgt cca gca cca ccc aag tgc ctg ccc tgc ccc tcg cag tct cct tca       369
Cys Pro Ala Pro Pro Lys Cys Leu Pro Cys Pro Ser Gln Ser Pro Ser
            55                  60                  65
tcc tgc cct ccc cag ccc tgc acc aag ccc tgt cct cct aaa tgc cct       417
Ser Cys Pro Pro Gln Pro Cys Thr Lys Pro Cys Pro Pro Lys Cys Pro
        70                  75                  80
tca tcc tgc cca cat gct tgc cca mct ccc tgc cct ccc cca gag           462
Ser Ser Cys Pro His Ala Cys Pro Xaa Pro Cys Pro Pro Pro Glu
    85                  90                  95
tgaggcactg tgggc                                                      477
```

<210> 803
<211> 586
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 179..307

<400> 803
```
cggtagtsag aacccttccg gtgggctagg tactgagcgc gcgaggtgag gagttgtgca      60
gggtwtgggg aaaggaaggc tggcttggcg agagggcagg tttgcgggct ttcgcccccct    120
tttccaaaga ccaacaaaga gtccttcccc aactcccaac tcaacccctt ttggaact      178
atg tgt ggt ggt tgg gac cct gtg gcg cat cct tgt cgc tcg tgt cct       226
Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
1               5                   10                  15
tct cat gcc cgg cga cgc gtc ttt gtg gta acg ccc tgc tgc cat ctc       274
Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
            20                  25                  30
ttt tct tct cta tgc gag gat ttg gac tgg cag tgagaataag agacaacgat     327
Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
        35                  40
tcacgtctac tttctaggat gacttccatg tgctccatct cgcgcgtccc tgagcatgtt     387
gaatttccaa atcctaaata agccgcgcgg tgtagtttgt attatgttgc gtttctcttt     447
ctgcttttcc tcgccctttc tccatcatcc tttaggctct acagagtgaa ggtttaaatc     507
caaggtcatg gcaaaacatc tgaagttcat cgccaggact gtgatggtac aggaagggaa     567
cgtggaaagc gcatacagg                                                  586
```

<210> 804
<211> 559
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 78..548

<400> 804
```
acgtcattca cccgcgccac ccggaagccg cggttcctac cwaccgttct tattgctggc      60
ggcctgagga gcccatc atg gcg acg ccc cct aag cgg cgg gcg gtg gag        110
                   Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu
                   1               5                   10
gcc acg ggg gag aaa gtg ctg cgc tac gag acc ttc atc agt gac gtg       158
Ala Thr Gly Glu Lys Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val
            15                  20                  25
ctg cag cgg gac ttg cga aag gtg ctg gac cat cga gac aag gta tat       206
Leu Gln Arg Asp Leu Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr
        30                  35                  40
gag cag ctg gcc aaa tac ctt caa ctg aga aat gtc att gag cga ctc       254
Glu Gln Leu Ala Lys Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu
    45                  50                  55
cag gaa gct aag cac tcg gag tta tat atg cag gtg gat ttg ggc tgt       302
Gln Glu Ala Lys His Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys
60                  65                  70                  75
aac ttc ttc gtt gac aca gtg gtc cca gat act tca cgc atc tat gtg       350
Asn Phe Phe Val Asp Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val
                80                  85                  90
gcc ctg gga tat ggt ttt ttc ctg gag ttg aca ctg gca gaa gct ctc       398
Ala Leu Gly Tyr Gly Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu
            95                  100                 105
aag ttc att gat cgt aag agc tct ctc ctc aca gag ctc agc aac agc       446
Lys Phe Ile Asp Arg Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser
        110                 115                 120
ctc acc aag gac tcc atg aat atc aaa gcc cat atc cac atg ttg cta       494
Leu Thr Lys Asp Ser Met Asn Ile Lys Ala His Ile His Met Leu Leu
    125                 130                 135
gag ggg ctt aga gaa cta caa ggc ctg cag aat ttc cca gag aag cct       542
Glu Gly Leu Arg Glu Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro
140                 145                 150                 155
cac cat tgacttcttc c                                                  559
His His
```

<210> 805
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 122..478

<400> 805
```
aaacacatcc aagcttaaga cggtgaggtc agcttcacat tctcaggaac tctccttctt      60
tgggtctggc tgaagttgag gatctcttac tctctaggcc acggaattaa cccgagcagg     120
c atg gag gcc tct gct ctc acc tca tca gca gtg acc agt gtg gcc aaa     169
  Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
  1               5                   10                  15
gtg gtc agg gtg gcc tct ggc tct gcc gta gtt ttg ccc ctg gcc agg       217
Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
            20                  25                  30
att gct aca gtt gtg att gga gga gtt gtg gct gtg ccc atg gtg ctc       265
Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu
        35                  40                  45
agt gcc atg ggc ttc act gcg gcg gga atc gcc tcg tcc tcc ata gca       313
Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala
```

```
     50                  55                  60
gcc aag atg atg tcc gcg gcg gcc att gcc aat ggg ggt gga gtt gcc      361
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala
65                  70                  75                  80
tcg ggc agc ctt gtg gct act ctg cag tca ctg gga gca act gga ctc      409
Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu
                85                  90                  95
tcc gga ttg acc aag tkc atc ctg ggc tcc att ggg tct gcc att gcg      457
Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala
            100                 105                 110
gct gtc att gcg agg ttc tac tagctccctg cccctcgccc tgcagagaag         508
Ala Val Ile Ala Arg Phe Tyr
        115
agaaccatgc caggggagaa ggcacccagc catcctgacc cagcgaggrg caactatccc    568
aa                                                                   570

<210> 806
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 90..332

<400> 806
aaacacatcc aagcttaaga cggtgaggtc agcttcacat tctcaggaac tctccttctt     60
tgggggctca ccgtgtgggg gagcaaatc atg tat atc cag tgc tgt gag tgg      113
                                Met Tyr Ile Gln Cys Cys Glu Trp
                                1               5
ctc cag tca tgg agg agc aag gat gag ttc tgc ctg gaa gaa tct ggg      161
Leu Gln Ser Trp Arg Ser Lys Asp Glu Phe Cys Leu Glu Glu Ser Gly
    10                  15                  20
aag gct tcc tgg agg agg gaa caa tgg cat gga cct tgd dga gtc aga      209
Lys Ala Ser Trp Arg Arg Glu Gln Trp His Gly Pro Xaa Xaa Val Arg
25                  30                  35                  40
agc ttt caa ttc att cca ttc aag cat tgc tct cat gtg gca ttc aag      257
Ser Phe Gln Phe Ile Pro Phe Lys His Cys Ser His Val Ala Phe Lys
                45                  50                  55
cat tct ata gtg ctt gcc gtg act cag gcg cac agt gca aaa gga agc      305
His Ser Ile Val Leu Ala Val Thr Gln Ala His Ser Ala Lys Gly Ser
            60                  65                  70
aca tct ttc tct gcc atg agg act tat tagtgtctga agagcttttt            352
Thr Ser Phe Ser Ala Met Arg Thr Tyr
        75                  80
ctggactata ggagaaagtc atggtctccc tc                                  384

<210> 807
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 152..346

<221> misc_feature
<222> 302..303
<223> n=a, g, c or t


<400> 807
aaggttactt gactgggagt tctcagacct ccagtttcag ccctgccctc agcctccaat     60
```

```
ccgtaagaga cacccagccc cagcaattgg attgggcagc ccgtcttgac acrccastgt     120
gcygagtggc ttgaaggacg tgtttcaaca g atg gtt ggg gtt agt gtg tgt        172
                                   Met Val Gly Val Ser Val Cys
                                   1               5
cat cac att cga gtg ggg att aag aga agg aag gct gcc ttg ctg gag       220
His His Ile Arg Val Gly Ile Lys Arg Arg Lys Ala Ala Leu Leu Glu
        10                  15                  20
ctg tgt ggt ctt ctc caa gtg aga gtc gca ggc aat aga act act ttg       268
Leu Cys Gly Leu Leu Gln Val Arg Val Ala Gly Asn Arg Thr Thr Leu
    25                  30                  35
ctt ttg gag gaa aag mgg aat tca ttt tca gca nnc acr aga aaa gca       316
Leu Leu Glu Glu Lys Arg Asn Ser Phe Ser Ala Xaa Thr Arg Lys Ala
40                  45                  50                  55
gtt ttt ttt tca ggg gat ctt cac ttc tct tgaacaagga actcactcag         366
Val Phe Phe Ser Gly Asp Leu His Phe Ser
                60                  65
agact                                                                 371
```

<210> 808
<211> 435
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 98..430

<400> 808

```
cgacaggagc cctcaagctg atctggtcgg gaccggatac attattaacc ccagtgcagt      60
agggtcccca ggggcaacct gccccacagc gcccaag atg cct agc aga act gcc      115
                                         Met Pro Ser Arg Thr Ala
                                         1               5
cgc tat gcc cgc tac agc cca cgg cag cgg cgg cgg cgg atg ctg gct       163
Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg Arg Arg Arg Met Leu Ala
            10                  15                  20
gat cgc agc gtg cgt ttc cct aat gat gtc ctg ttc ttg gac cac atc       211
Asp Arg Ser Val Arg Phe Pro Asn Asp Val Leu Phe Leu Asp His Ile
        25                  30                  35
cgg cag ggt gac ctg gag cag gtg ggg cgc ttc atc cgg act cgg aaa       259
Arg Gln Gly Asp Leu Glu Gln Val Gly Arg Phe Ile Arg Thr Arg Lys
    40                  45                  50
gtc tcc ctg gcc acc atc cac ccc tca ggc ctg gcc gcc ttg cat gaa       307
Val Ser Leu Ala Thr Ile His Pro Ser Gly Leu Ala Ala Leu His Glu
55                  60                  65                  70
gcc gtg ctc tct gga aac ctg gaa tgc gtg aag ctg ctg gtc aaa tac       355
Ala Val Leu Ser Gly Asn Leu Glu Cys Val Lys Leu Leu Val Lys Tyr
                75                  80                  85
ggg gct gac att cac cag cga gat gag gcg ggc tgg aca ccc ctg cac       403
Gly Ala Asp Ile His Gln Arg Asp Glu Ala Gly Trp Thr Pro Leu His
            90                  95                  100
att gcc tgc agc gat ggg tac ctg aca tagcc                             435
Ile Ala Cys Ser Asp Gly Tyr Leu Thr
        105                 110
```

<210> 809
<211> 394
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 149..247

<221> misc_feature
<222> 375
<223> n=a, g, c or t

<400> 809
```
attcatttgg tgggcacttc ctgggtgcct gctctgggtc aggcctgtgg ggkggaccac      60
tgagggcagg aaacctggcc tgtccctcca ggaagcgaag tcaacactgg cacctgcaga     120
tgaagtggca gagcagcccc cagctttg atg gca tgg ggt ggt tgg ggg gca        172
                               Met Ala Trp Gly Gly Trp Gly Ala
                               1               5
cat tct gca tgc tca gaa gag aga gca act cgc cct gtg gaa gga gca       220
His Ser Ala Cys Ser Glu Glu Arg Ala Thr Arg Pro Val Glu Gly Ala
    10                  15                  20
tac agt ggg aga tgg gga cag gcc cag tgacgagcac catccggaag             267
Tyr Ser Gly Arg Trp Gly Gln Ala Gln
25                  30
tgaaggctga tgggtacgtg gacaacctcg cagagcagtg gacctgctgc tgcagcacgc     327
cgacaagtga tggcctcctg ggagagcccc gctcctccac ccctgccnct cctccacctg     387
cccccctg                                                              394
```

<210> 810
<211> 835
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 198..536

<221> misc_feature
<222> 511,749..750,790..791,807
<223> n=a, g, c or t

<400> 810
```
agacttggtt tgtgggacac acttggtttc agggaagggg aaagaggtca ccaagggcag      60
aggtgtccag gccggagcca ggggccccac tgttgggatg ctggctgcag tggggcgccc     120
caagcccagg tcccctctgt cttctctttc gactttgcag ctgtacttgt tttgctcctc     180
tacccgcagg agctgac atg gac cca aat cct cgg gcc gcc ctg gag cgc        230
                   Met Asp Pro Asn Pro Arg Ala Ala Leu Glu Arg
                   1               5                   10
cag cag ctc cgc ctt cgg gag cgg caa aaa ttc ttc gag gac att tta       278
Gln Gln Leu Arg Leu Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu
            15                  20                  25
cag cca gag aca gag ttt gtc ttt cct ctg tcc cat ctg cat ctc gag       326
Gln Pro Glu Thr Glu Phe Val Phe Pro Leu Ser His Leu His Leu Glu
        30                  35                  40
tcg cag aga ccc ccc ata ggt agt atc tca tcc atg gaa gtg aat gtg       374
Ser Gln Arg Pro Pro Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val
    45                  50                  55
gac aca ctg gag caa gta gaa ctt att gac ctt ggg gac ccg gat gca       422
Asp Thr Leu Glu Gln Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala
60                  65                  70                  75
gca gat gtg ttc ttg cct tgc gaa gat cct cca cca acc ccc cag tcg       470
Ala Asp Val Phe Leu Pro Cys Glu Asp Pro Pro Pro Thr Pro Gln Ser
                80                  85                  90
tct ggg gtg gac aac cat ttg gag gag ctg agc ctg ccg gnt gcc tac       518
Ser Gly Val Asp Asn His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr
            95                  100                 105
atc aga cag gac cac atc taggacctcc tcctcctcct cctccgactc              566
Ile Arg Gln Asp His Ile
        110
```

```
ctccaccaac ctgcataggc caaatccaag tgatgatgga gcagatacgc ccttggcaca     626
gtcggatgaa gaggaggaaa ggggtgatgg aggggcagag cctggagcct gcagctagca     686
gtgggcccct gcctacagac tgaccacgct ggctattctc cacatgagac cackagccca     746
mknnagagcc tgtcgggaga agaccagact ctttacttgc agtnnracca gaggtgggaa     806
ngatggtggg attgtgtacc tttctaaga                                      835
```

<210> 811
<211> 385
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> 21..194

<221> misc_feature
<222> 373
<223> n=a, g, c or t

<400> 811

```
aagtcacatg agccaccaaa atg gtg gtg ttc ggg tat gag gct ggg act aag      53
                      Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys
                      1               5                   10
cca agg gat tca ggt gtg gtg ccg gtg gga act gag gaa gcg ccc aag       101
Pro Arg Asp Ser Gly Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys
            15                  20                  25
gac aca aaa tat ata tca aat ggc gac att tgg aac aac agc tgg ttt       149
Asp Thr Lys Tyr Ile Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe
        30                  35                  40
ctc tgg aat att ctc aaa ctt cct gtt cag acg ctg ctt caa ggt           194
Leu Trp Asn Ile Leu Lys Leu Pro Val Gln Thr Leu Leu Gln Gly
    45                  50                  55
taaacatgat gctttgaaga catatgcatc attggctaca cttccatttt tgtctactgt     254
tgttactgac aagcttttg taattgatgc tttgtattca gataatataa gcaaggaaaa      314
ctgtgttttc agaagctcac tgattggcat agtttgtggw gttttctatc ccagttctnt     374
ggcttttact a                                                          385
```

<210> 812
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 812

```
Met Leu Leu Pro Leu Leu Leu Leu Leu Pro Met Cys Trp Ala Val Glu
                -10                 -5                  1
Val Lys Arg Pro Arg Gly Val Ser Leu Thr Asn His His Phe Tyr Asp
        5                   10                  15
Glu Ser Lys Pro Phe Thr Cys Leu Asp Gly Ser Ala Thr Ile Pro Phe
    20                  25                  30
Asp Gln Val Asn Asp Asp Tyr Cys Asp Cys Lys Asp Gly Ser Asp Glu
35                  40                  45                  50
Pro Gly Thr Ala Ala Cys Pro Asn Gly Ser Phe His Cys Thr Asn Thr
                55                  60                  65
Gly Tyr Lys Pro Leu Tyr Ile Pro Ser Asn
            70                  75
```

<210> 813
<211> 80

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 813
```
Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
    -15                 -10                 -5
Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
1               5                   10                  15
Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
            20                  25                  30
Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Val Ser Pro Ser Pro
        35                  40                  45
Leu Ser Pro Ala Leu Leu Thr Pro Leu Leu Lys Pro Ala Pro Thr Gly
    50                  55                  60
```

<210> 814
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 814
```
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
        -20                 -15                 -10
Leu Arg Gly Ala Arg Cys Gly Val Gln Met Thr Gln Phe Pro Leu Ser
    -5                  1               5                   10
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr Ser
            15                  20                  25
His Ile Ile Asn Ile Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
            30                  35                  40
Ala Pro Trp
        45
```

<210> 815
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 815
```
Met Ala Ala Ala Leu Trp Gly Phe Phe Pro Val Leu Leu Leu Leu Leu
            -20                 -15                 -10
Leu Ser Gly Asp Val Gln Ser Ser Glu Val Pro Gly Ala Ala Ala Glu
        -5              1                   5
Gly Ser Gly Gly Ser Gly Val Gly Ile Gly Xaa Arg Phe Lys Ile Glu
10                  15                  20                  25
Gly Leu
```

<210> 816
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 816
Met Asp Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Leu Trp
-20 -15 -10
Leu Xaa Gly Ala Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Val Leu
-5 1 5 10
Pro Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
15 20 25
Ser Ile Gly Ser Tyr Leu Asn Trp Tyr Gln His Lys Pro Gly His Ala
30 35 40
Pro Arg Leu Leu Ile Tyr Ala Ala Thr Thr Leu Ser Arg Gly Gly Pro
45 50 55
Ala Arg Phe Ser
60

<210> 817
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 817
Met Ala Ala Ser Arg Trp Ala Arg Lys Ala Val Val Leu Leu Cys Ala
-30 -25 -20
Ser Asp Leu Leu Leu Leu Leu Leu Leu Leu Pro Pro Pro Gly Ser Cys
-15 -10 -5
Ala Gly Arg Arg Ser Pro Xaa Thr Pro Asp Glu Ser Thr Pro Pro Pro
1 5 10 15
Arg Lys Lys Lys Lys Asp Ile Arg Asp Tyr Asn Asp Ala Asp Met Ala
20 25 30
Arg Leu Leu Glu Gln Gly Glu Gly
35 40

<210> 818
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 818
Met Glu Leu Gly Leu Cys Trp Val Leu Leu Leu Ala Leu Leu Glu Gly
-15 -10 -5
Val Gln Cys Asp Val Glu Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Phe
15 20 25
Ser Thr Tyr Glu Met His Trp Ile Arg Gln Ala Pro Gly Lys Gly Pro
30 35 40 45
Glu Trp Val Xaa Tyr Val Ser Gly Gly Gly Gly Thr Xaa Xaa Asn Ala
50 55 60
Xaa Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Asn Ser
65 70 75
Phe Val Tyr Leu Gln Met Asp Ser Leu Arg Val Glu Asp Thr Ala Leu
80 85 90

Tyr Tyr Cys Ala Arg Xaa Asp Tyr Asp Phe Trp Ser Gly Tyr Tyr
95 100 105

<210> 819
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 819
Met Ala Trp Thr Pro Leu Leu Leu Leu Leu Leu Ser His Cys Thr Gly
-15 -10 -5
Ser Leu Ser Gln Pro Val Leu Thr Gln Pro Arg Gly
1 5

<210> 820
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 820
Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Leu Leu Arg Gly
-15 -10 -5
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln
1 5 10
Pro Gly Thr Ser Leu Thr Leu Ser Cys Ala Gly Ser Gly Phe Ser Phe
15 20 25
Ser Asp Tyr Gly Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Val Ala Val Ile Ser His Asp Gly Asn Asn Lys Tyr Tyr Gly
50 55 60
Gly Ser Met Lys Gly Arg Val Thr Ile Ser Arg Asp Asn Ser Arg His
65 70 75
Thr Val Ser Leu Gln Met Ser Ser Leu Gly Pro Glu Asp Thr Ala Val
80 85 90
Tyr Tyr Cys Ala Lys Asp Arg Thr Gly Gly
95 100

<210> 821
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 821
Met Lys Leu Leu Trp Phe Phe Leu Leu Leu Leu Ala Ala Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Gln Leu Val Xaa Ser Gly Pro Gly Leu Val Lys
1 5 10
Pro Ser Gly Thr Leu Ser Leu Thr Cys Thr Val Xaa Gly Xaa Xaa Ile
15 20 25
Thr Asn Tyr Tyr Trp Ser Xaa Ile Arg Gln Ser Pro Gly Lys Gly Leu
30 35 40 45

```
Glu Trp Ile Gly Thr Ile Tyr Tyr Ser Gly Ser Ala Asp His Asn Pro
                50                  55                  60
Ser Leu Arg Ser Arg Ala Thr Ile Ser Leu Asp Thr Arg
            65                  70

<210> 822
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 822
Met Ala Ser Leu Gly Leu Leu Leu Leu Xaa Leu Leu Thr Ala Leu Pro
-20                 -15                 -10                 -5
Pro Leu Trp Ser Ser Ser Leu Pro Gly Leu Asp Thr Ala Glu Ser Lys
                1               5                   10
Ala Thr Xaa Ala Asp Leu Ile Leu Ser Ala Leu Glu Arg Ala Thr Gly
        15                  20                  25

<210> 823
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 823
Met Asp Val Gly Pro Ser Ser Leu Pro His Leu Gly Leu Lys Leu Leu
            -25                 -20                 -15
Leu Leu Leu Leu Leu Leu Pro Leu Arg Gly Gln Ala Asn Thr Gly Cys
        -10                 -5                  1
Tyr Gly Ile Pro Gly Met Pro Gly Leu Pro Gly Ala Pro Gly Lys Asp
5                   10                  15                  20
Gly Tyr Asp Gly Leu Pro Gly Pro Lys Gly Glu Pro Gly Ile Pro Ala
                25                  30                  35
Ile Pro Gly Ile Arg Gly Pro Lys Gly Gln Lys Gly Glu Pro Gly Leu
            40                  45                  50
Pro Gly His Pro Gly Lys Asn Gly Pro Met Gly Pro Pro Gly Met Pro
        55                  60                  65

<210> 824
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 824
Met Asp Cys Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Gly
                -15                 -10                 -5
Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
            1                   5                   10
Pro Gly Ala Ser Val Lys Val Ser Cys Gln Val Ser Gly Tyr Asn Val
    15                  20                  25
Val Glu Leu Ser Ile His Trp Val Arg Gln Ser Pro Gly Lys Gly Leu
30                  35                  40                  45
```

```
Glu Trp Met Gly Gly Phe Asp Leu Glu Ser Gly Glu Thr Ile Tyr Ala
                50                  55                  60
Gln Arg Phe Gln Gly Arg Ile Thr Met Thr Glu Asp Ser Ser Ser Asp
            65                  70                  75
Thr Ala Phe Met Glu Leu Ile Ser Leu Arg Pro Glu Asp Ala Ala Val
        80                  85                  90
Tyr Tyr Cys Ala Thr Ile Arg Leu Pro Val Val Leu Phe Phe Ala Ala
    95                  100                 105
Ser Gly Ala Arg Glu Pro Trp Ser Pro Ser Pro Gln Xaa Pro Arg
110                 115                 120
```

<210> 825
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 825

```
Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala Val
            -15                 -10                 -5
Leu Cys Lys Val Tyr Leu Gly Leu Phe Ser Gly Ser Ser Pro Asn Pro
        1               5                   10
Phe Ser Glu Glu Arg
15
```

<210> 826
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 826

```
Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu Leu
-25                 -20                 -15                 -10
Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp Trp Pro
                -5                  1               5
Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val Arg Lys Asp
        10                  15                  20
Ala Tyr Met
    25
```

<210> 827
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 827

```
Met Ala Trp Thr Pro Leu Phe Leu Phe Leu Leu Thr Cys Cys Pro Gly
                -15                 -10                 -5
Ser Asn Ser Gln Ala Val Xaa Thr Gln Glu Pro Leu Thr Asp Cys Val
            1                   5                   10
Pro Arg Xaa Thr Val Thr Leu Thr Cys Gly Ser Ser Ile Gly Ala Val
    15                  20                  25
```

Thr Asn Gly His Phe Pro Tyr Trp Phe Gln Gln Lys Pro Gly Gln Ala
30 35 40 45
Pro Arg Thr Leu Ile Ser Asp Thr Phe Asn Arg Gln Ser Ser Thr Pro
50 55 60
Ala Arg Phe Ser Gly Ser Leu Leu Gly Gly Lys Ala Val Leu Thr Leu
65 70 75
Ser Asp Ala Gln Pro Asp Asp Glu Ala Glu Tyr Tyr Cys Val Leu Ser
80 85 90
Tyr Ser Gly Gly Arg Pro Val Phe Gly Gly Gly Thr Lys Leu Thr Val
95 100 105
Leu Ser Gln
110

<210> 828
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 828
Met Gln Ala Cys Met Val Pro Gly Leu Ala Leu Cys Leu Leu Leu Gly
-20 -15 -10
Pro Leu Ala Gly Ala Lys Pro Val Gln
-5 1

<210> 829
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 829
Met Pro Ser Tyr Lys Val Cys Gly Val Phe Cys Leu Phe Val Cys Leu
-20 -15 -10
Phe Leu Ser Gln Ser Phe Ala Phe Val Leu Gln Ala Gly Val Gln Trp
-5 1 5
Arg Asp Leu Cys Ser Leu Gln Pro Gln Leu Pro Arg Phe Gly Pro Ser
10 15 20 25
Ser Cys Leu Ser Leu Pro Ser Gly Trp Asp Cys Arg Arg Pro Pro Pro
30 35 40
Arg Leu Ala Asn Ser Cys Val Phe Gly Gly Asp Gly Val Ser Pro
45 50 55

<210> 830
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 830
Met Gly Thr Gln Glu Gly Trp Xaa Leu Leu Leu Cys Leu Ala Leu Ser
-20 -15 -10
Gly Ala Ala Glu Thr Lys Pro His Pro Ala Glu Gly Gln Trp Arg Ala
-5 1 5 10

```
Val Xaa Val Val Leu Asp Xaa Phe Leu Val Lys Asp Xaa Ala His Arg
            15                  20                  25
Gly Ala Leu Ala Ser Ser Glu Asp Arg Ala Arg
        30                  35

<210> 831
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 831
Met Ser Met Leu Val Val Phe Leu Leu Leu Trp Gly Val Thr Trp Gly
    -15                 -10                 -5
Pro Val Thr Glu Ala Ala Ile Phe Tyr Glu Thr Gln Xaa Ser Leu Trp
1               5                   10                  15
Ala Glu Ser Glu His Xaa Leu Lys Thr Leu Gly Gln Cys Asp Ala Asp
            20                  25                  30
Val Pro Gly Pro Pro Gly Asp Ser Arg Leu Pro Ala Val Gln Glu Trp
        35                  40                  45
Gly Ala Gln Glu Pro Val His Leu Asp Ser Pro Ala Ile Lys His Gln
    50                  55                  60
Phe Leu Leu Thr Gly Asp Thr Gln Gly Arg Tyr Arg Cys Arg Ser Gly
65                  70                  75                  80
Leu Ser Thr Gly Trp Xaa Gln Leu Ser Lys Leu Leu Glu Leu Thr Gly
                85                  90                  95
Pro Lys Val Leu Ala Cys Ser Leu Ala Leu Asp Gly Ala Ser
            100                 105                 110

<210> 832
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 832
Met Leu Pro Ser Gln Leu Ile Gly Phe Leu Leu Leu Trp Val Pro Ala
                -15                 -10                 -5
Ser Arg Gly Glu Ile Val Leu Thr Gln Ser Pro Asp Phe Leu Ser Val
            1               5                   10
Thr Pro Lys Glu Lys Val Thr Ile Thr Cys Arg Ala Ser Xaa Ser Ile
    15                  20                  25
Gly Ser Ser Leu Tyr Trp Tyr Gln Gln Lys Pro His Gln Ser Pro Lys
30                  35                  40                  45
Leu Val Ile Lys Tyr Ala Ser Gln Ser Phe Ser Gly Val Ser Ser Arg
                50                  55                  60
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Asn Ser
            65                  70                  75
Leu Glu Pro Gly
        80

<210> 833
<211> 115
<212> PRT
<213> Homo sapiens

<220>
```

<221> SIGNAL
<222> -20..-1

<400> 833
Met Glu Lys Ile Pro Val Ser Ala Phe Leu Leu Leu Val Ala Leu Ser
-20 -15 -10 -5
Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala Lys Lys Asp
1 5 10
Thr Lys Asp Ser Arg Pro Lys Leu Pro Gln Thr Leu Ser Arg Gly Trp
15 20 25
Gly Asp Gln Leu Ile Trp Thr Gln Thr Tyr Glu Glu Ala Leu Tyr Lys
30 35 40
Ser Lys Thr Ser Asn Lys Pro Leu Met Ile Ile His His Leu Asp Glu
45 50 55 60
Cys Pro His Ser Gln Ala Leu Lys Lys Val Phe Ala Glu Asn Lys Glu
65 70 75
Ile Gln Lys Leu Ala Glu Gln Phe Val Leu Leu Asn Leu Val Tyr Glu
80 85 90
Thr Thr Asp
95

<210> 834
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 834
Met Arg Pro Gly Leu Ser Phe Leu Leu Ala Leu Leu Phe Phe Leu Gly
-20 -15 -10 -5
Gln Ala Ala Gly Asp Leu Gly Asp Val Gly Pro Pro Ile Pro Ser Pro
1 5 10
Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser Phe Ser Ser
15 20 25
Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu Gly Ser Gly Gly
30 35 40
Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly Ser Val Asp Asp Arg
45 50 55 60
Gly Thr Cys Gln Cys Ser Val Ser Leu Pro Asp Thr Thr Phe Pro Val
65 70 75
Asp Arg Val Glu Arg Leu Glu Phe Thr Ala His Val Leu Ser Gln Lys
80 85 90
Phe Glu Lys Glu Leu Ser Lys
95

<210> 835
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 835
Met Asp Leu Leu His Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
-25 -20 -15
Leu Val Ala Ala Pro Arg Trp Val Arg Ser Gln Val Gln Leu Xaa Glu
-10 -5 1 5
Ser Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Ile Cys

```
            10                  15                  20
Gly Val Ser Gly Asp Ser Val Thr Ile Ser Gly Trp Trp Ser Trp Val
        25                  30                  35
Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Ser Glu Ile Asp His
    40                  45                  50
Gly Gly Asn Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Xaa Ile
55                  60                  65                  70
Ser Leu Asp Lys Ser Lys Asn Lys Phe Ser Leu Arg Leu Thr Ser Val
                75                  80                  85
Thr Ala Ala Asp Thr Ala Met Tyr Xaa Cys Ala Arg Gly Gly Ala Xaa
            90                  95                  100
Ser Ser Ser Ala Phe Asp Val Trp Gly Leu Xaa Thr Met Val Ile Ile
        105                 110                 115
Ser Ser Ala
    120
```

<210> 836
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 836

```
Met Asp Ile Leu Cys Ser Thr Leu Leu Leu Leu Thr Val Pro Ser Trp
                -15                 -10                 -5
Val Leu Ser Gln Val Thr Leu Xaa Glu Ser Gly Pro Ala Leu Val Lys
            1               5                   10
Ala Thr Gln Thr Leu Arg Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu
    15                  20                  25
Ser Thr Asn Arg Met Arg Val Ser Trp Ile Arg Gln Pro Pro Gly Lys
30                  35                  40                  45
Ala Leu Glu Trp Leu Ala Arg Ile Asp Trp Asp Asp Tyr Lys Arg Tyr
                50                  55                  60
Ser Thr Ser Leu Lys Thr Arg Val Thr Ile Ser Lys Asp Thr Ser Lys
            65                  70                  75
Asn Gln Val Ile Leu Thr Met Thr Asn Val Asp Pro Ala Asp Thr Ala
        80                  85                  90
Thr Tyr Tyr Cys Ala Arg Leu Ser Thr Ala Ala Thr Pro Gln Phe Phe
    95                  100                 105
Asp Phe Trp Gly Gln Gly Val Leu Val Ser Val
110                 115                 120
```

<210> 837
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 837

```
Met Xaa His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            1               5                   10
Pro Ser Xaa Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Asp Ser Ile
    15                  20                  25
Ser Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
30                  35                  40                  45
```

```
Glu Trp Ile Gly Tyr Ile Tyr Tyr Ser Gly Ser Thr Asn Tyr Asn Pro
                50                  55                  60
Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
            65                  70                  75
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
        80                  85                  90
Tyr Cys Ala Arg Xaa Leu Xaa Tyr Tyr Asp Arg Ser Gly Tyr Phe Arg
    95                  100                 105
Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Trp Ser
110                 115                 120
```

<210> 838
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 838

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            1               5                   10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
    15                  20                  25
Asp Ser Gly Asn Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Ala Gly Lys
30                  35                  40                      45
Gly Leu Glu Trp Ile Gly Arg Ile Tyr Ser Thr Gly Ser Thr Asn Tyr
                50                  55                  60
Asn Pro Ser Leu Ser Ser Arg Val Gln Ile Ser Leu Asp Thr Ser Lys
            65                  70                  75
Asn Leu Leu Ser Leu Asn Leu Thr Ser Val Thr Ala Ala Asp Thr Ala
        80                  85                  90
Val Tyr Phe Cys Ala Arg Thr Phe Pro Phe Tyr Trp Tyr Leu Asp Leu
    95                  100                 105
Trp Gly Arg Gly Ile Leu Val Thr
110                 115
```

<210> 839
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 839

```
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Arg Leu Val Lys
            1               5                   10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
    15                  20                  25
Ser Ser Gly Gly Tyr Phe Trp Ser Trp Ile Arg Gln His Pro Gly Arg
30                  35                  40                      45
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Asn Trp Ser Thr Tyr Tyr
                50                  55                  60
Asn Pro Ser Leu Arg Ser Arg Val Thr Met Ser Met Asp Thr Ser Lys
            65                  70                  75
Asn Gln Phe Ser Leu Asn Leu Asn Ser Val Thr Ala Ala Asp Thr Xaa
```

```
        80                  85                  90
Met Tyr Tyr Cys Ala Arg Gly Arg Gly Arg Leu Gly Trp Phe Xaa Xaa
    95                  100                 105
Xaa Gly Xaa Gly Xaa Pro Gly His Arg Leu Ile Ser Arg Pro Gly
110                 115                 120

<210> 840
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 840
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
            1               5                   10
Pro Ser Glu Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Gly Ser Ile
    15                  20                  25
Arg Thr Gly Ser Tyr Tyr Trp Thr Trp Val Arg Gln Pro Pro Gly Lys
30                  35                  40                  45
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Tyr Thr Gly Asp Thr Tyr Tyr
                50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Ile Thr Met Ser Leu Asp Thr Xaa Xaa
            65                  70                  75
Asn Gln Phe Xaa Leu Ser Leu Thr Ser Val Thr Val Ala Asp Thr
        80                  85                  90

<210> 841
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 841
Met Lys Leu Ser Val Cys Leu Leu Leu Val Thr Leu Ala Leu Cys Cys
-15                 -10                 -5                  1
Tyr Gln Ala Asn Ala Glu Phe Cys Pro Ala Leu Val Ser Glu Leu Leu
            5                   10                  15
Asp Phe Phe Phe Ile Ser Glu Pro Leu Phe Lys Leu Ser Leu Ala Lys
        20                  25                  30
Phe Asp Ala Pro Arg
    35

<210> 842
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 842
Met Ser Pro Val Leu Leu Val Leu Ser Leu Ser Gln Cys Leu Leu Ser
    -15                 -10                 -5
Asp Pro Val Ile Pro Gly Leu
```

1 5

<210> 843
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 843
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Arg Leu Gln Glu Ser Gly Pro Arg Leu Val Lys
1 5 10
Pro Ser Glu Xaa Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser Val
15 20 25
Thr Asn Phe Phe Trp Asn Trp Ile Arg Lys Pro Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Leu Gly Tyr Met Ser Tyr Gly Val Ser Thr Asn Tyr His Pro
50 55 60
Ala Tyr Gln Ser Arg Val Ser Ile Ser Ile Asp Thr Trp
65 70

<210> 844
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 844
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Arg Leu Val Lys
1 5 10
Pro Ser Glu Ala Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Ser
15 20 25
Ser Asn Tyr Asp Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Ile Gly Tyr Ile Asp Asp Ser Lys Asn Arg Gly Ser Thr Thr
50 55 60
Tyr Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Thr Ser
65 70 75
Lys Xaa Gln Leu Ser Leu Arg Leu Thr Ser Val Thr Xaa Ala Asp Thr
80 85 90
Ala Val Tyr Tyr Cys Ala Arg Lys Ser Ser Met His Ser Ser Gly Trp
95 100 105
His Asn Arg Ser Leu Tyr Trp Tyr Phe Asp Pro
110 115 120

<210> 845
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 845
Met Asp Leu Leu His Lys Asn Met Lys Asp Leu Trp Phe Phe Leu Leu
-25 -20 -15
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Val Leu Gln Glu Ser
-10 -5 1 5
Gly Pro Gly Leu Val Lys Pro Ser Gly Thr Leu Ser Leu Thr Cys Ala
10 15 20
Val Ser Gly Gly Ser Ile Ile Ser Ser Asn Trp Trp Ser Trp Val Arg
25 30 35
Gln Thr Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile Tyr Glu Asp
40 45 50
Gly Ile Thr Asn Tyr Asn Pro Ser Leu Lys Ser Arg Val Ile Ile Ser
55 60 65 70
Val Asp Lys Ala Lys Asn Gln Phe Ser Leu Lys Met Arg Ser Val Thr
75 80 85
Ala Ser Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Ser Ser Val
90 95 100
Arg Thr Asp Tyr Trp Gly
105

<210> 846
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 846
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Ser Gly Pro Val Asp
1 5 10
Xaa Xaa Gln Thr Leu Xaa Leu Thr Cys Thr Xaa Ser Gly Val Ser Ile
15 20 25
Ser Ser Ser Asp Asn Cys Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
30 35 40 45
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr His Ser Gly Gly Thr Tyr Tyr
50 55 60
Asn Pro Thr Leu Lys Ser Arg Val Thr Ile Ser Xaa Asp Arg Ile Arg
65 70 75
Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Xaa Asp Thr Ala
80 85 90
Val Tyr Xaa Cys Gly Arg Ala Gln Gly Arg Met Gly Ile Gly Thr Thr
95 100 105
Ile Phe Asp Leu Trp Gly Gly Gly Gln Trp Ser Pro Ser Leu Gln Pro
110 115 120 125

<210> 847
<211> 140
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 847
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
-15 -10 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
1 5 10

```
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Xaa Phe
    15                  20                  25
Thr Xaa Xaa Ala Xaa His Trp Val Arg Gln Ala Pro Gly Gln Arg Leu
30                  35                  40                  45
Glu Trp Met Gly Trp Ile Asn Ala Ala Xaa Gly Xaa Thr Xaa Tyr Ser
                50                  55                  60
Gln Xaa Phe Gln Xaa Arg Val Thr Xaa Thr Arg Asp Thr Ser Ala Ser
            65                  70                  75
Thr Val Ser Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
        80                  85                  90
Tyr Phe Cys Ala Arg Asp Trp Glu Ile Ala Val Val Pro Thr Ala Ile
    95                  100                 105
Asn Ser Tyr Gly Phe Asp Pro Gly Ala Arg Glu Pro
110                 115                 120
```

<210> 848
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 848

```
Met Glu Ala Arg Val Glu Arg Ala Val Gln Lys Arg Gln Val Leu Phe
    -25                 -20                 -15
Leu Cys Val Phe Leu Gly Met Ser Trp Ala Gly Ala Glu Pro Leu Arg
-10                 -5                  1               5
Tyr Phe Val Ala Glu Glu Thr Glu Arg Gly Thr Xaa Leu Thr Asn Leu
            10                  15                  20
Ala Lys Asp Leu
        25
```

<210> 849
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 849

```
Met Asp Trp Thr Trp Ser Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
                -15                 -10                 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys
            1               5                   10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25
Thr Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45
Glu Trp Met Gly Trp Ile Ser Ala Xaa Asn Gly Asn Thr Asn Tyr Ala
                50                  55                  60
Gln Xaa Val Gln Gly Arg Val Thr Met Thr Thr Asp Thr Ser Thr Arg
            65                  70                  75
Thr Ala Tyr Met Glu Leu Arg Ser Leu Arg Ser Asp Asp Thr Ala Ile
        80                  85                  90
Tyr Tyr Cys Ala Arg Glu Ile Xaa Val Xaa Xaa Cys Asp Gly Gln Leu
    95                  100                 105
Gly Pro Gly Asn Leu Val
110                 115
```

<210> 850
<211> 140
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 850
Met Asp Val Leu His Lys His Met Lys His Leu Trp Phe Phe Leu Leu
-25 -20 -15
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Glu Gln Leu Arg Gln
-10 -5 1 5
Trp Gly Ala Xaa Leu Leu Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
10 15 20
Ser Val Tyr Gly Gly Ser Phe Asn Gly Tyr Tyr Trp Ser Trp Ile Arg
25 30 35
Gln Ser Pro Gly Lys Gly Leu Glu Trp Ile Gly Gly Ile Asn His Ser
40 45 50
Gly Ser Thr Leu Ser Asn Pro Ser Leu Lys Ser Arg Val Asp Leu Ser
55 60 65 70
Val Asp Ala Ser Lys Asp Gln Val Ser Leu Arg Leu Lys Leu Val Thr
75 80 85
Ala Ala Asp Thr Ala Val Tyr Phe Cys Ala Arg Pro His Tyr Asp Met
90 95 100
Ser Thr Asp Ser Ser Phe Asp Gly Phe Asp Leu Trp
105 110

<210> 851
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 851
Met Met Leu Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser
-15 -10 -5 1
Gln Gly Leu Leu Trp Phe His Thr Asn Phe Lys Val Phe Val Val Ser
5 10 15
Ile Cys Val Lys Thr Ile Ile Gly Ile Ser Gly Gly
20 25

<210> 852
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 852
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
-15 -10 -5
Ala Leu Ser Gln Val Gln Leu Val Gln Ser Gly Gly Glu Val Lys Lys
1 5 10
Pro Gly Ala Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe
15 20 25
Ile Gly Tyr Tyr Val His Trp Ile Arg Gln Thr Pro Gly Arg Xaa Leu

```
30                  35                  40                  45
Glu Trp Met Gly Trp Val Asn Pro Xaa Thr Gly Asp Asn Gly
                50                  55

<210> 853
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 853
Met Phe Phe Gln Phe Trp Lys Ser Ser Ala Tyr Leu Ile Phe Val Ser
        -35                 -30                 -25
Ile Cys Lys Gly Phe Leu Pro Val Tyr Leu Leu Leu Val Leu Ser Leu
    -20                 -15                 -10
Ser Leu Ser Leu Cys Cys Ser Leu Leu Leu Ser Leu
-5                  1                   5

<210> 854
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 854
Met Asp Trp Thr Trp Arg Ile Leu Phe Leu Val Ala Ala Ala Thr Gly
                -15                 -10                 -5
Val His Ser Gln Val His Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            1                   5                   10
Pro Gly Thr Pro Val Asn Ile Ser Cys Lys Ala Phe Gly Tyr Thr Phe
    15                  20                  25
Pro Ala Phe Ala Ile His Trp Val Arg Gln Ala Pro Gly Gln Ser Leu
30                  35                  40                  45
Glu Trp Met Gly Trp Val Asn Ile Gly His Gly Asn Thr Lys Tyr Ser
                50                  55                  60
Gln Lys Phe Gln Gly Arg Leu Ala Ile Ser Arg Asp Thr Ser Ala Asn
            65                  70                  75
Ile Val Tyr Xaa Glu Leu Ser Gly Leu Arg Ser Glu Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Ala Arg Asp Asn Leu Phe Phe Gly Ser Met Gly Phe Asp
    95                  100                 105

<210> 855
<211> 152
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 855
Met Ala Trp Thr Val Leu Leu Leu Gly Leu Leu Ser His Cys Thr Gly
    -15                 -10                 -5
Ser Val Thr Ser Tyr Val Leu Thr Gln Pro Pro Ser Val Ser Val Ala
1               5                   10                  15
Pro Gly Lys Thr Ala Ser Ile Thr Cys Gly Gly Asp Asn Ile Glu Ser
```

20 25 30
Gln Val Val His Trp His Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu
35 40 45
Val Ile Tyr Asp Asp Thr Asp Arg Pro Ser Gly Ile Pro Asp Arg Phe
50 55 60
Ser Gly Ser Asn Ser Gly His Thr Ala Thr Leu Thr Ile Ser Arg Val
65 70 75 80
Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg Ser
85 90 95
Ser Gly Gln Gly Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Arg
100 105 110
Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu
115 120 125
Glu Leu Gln Ala Asn Lys Ala Thr
130 135

<210> 856
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 856
Met Arg Leu Leu Phe Leu Leu Leu Phe Val Cys Phe Ser Arg Gln Gly
-15 -10 -5 1
Leu Ala Leu Ser Leu Arg Leu Glu Cys Ser Gly Met Ile Met Ala Tyr
5 10 15
Cys Ser Ile Ser Leu Pro Gly Ser Ser Ser Pro Leu Thr Ser Ala Ser
20 25 30

<210> 857
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 857
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ser Ala Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys
1 5 10
Pro Ser Gly Arg Leu Ser Leu Ala Cys Asp Val Val Glu Leu Ser Pro
15 20 25
Pro Ala Pro Arg Gly Gly Ser Ala Val His Leu Arg Asn Leu Ser Ser
30 35 40 45
Trp Glu Pro His Leu Gln Pro Val Ser Gly
50 55

<210> 858
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 858
Met Thr Tyr Phe Pro Leu Gly Arg Tyr Pro Val Met Gly Leu Leu Asp
-30 -25 -20
Gln Met Val Val Val Phe Leu Leu Leu Leu Val Ser Thr Leu Ser Ser
-15 -10 -5
Val Val Val Leu Leu Val Cys Ile Pro Thr Ser Ser Val Lys Leu Phe
1 5 10 15
Pro Phe His His Ile His Thr Asn Trp
20 25

<210> 859
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 859
Met Glu Phe Gly Leu Ser Trp Val Leu Leu Val Ala Met Leu Arg Gly
-15 -10 -5
Leu Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Thr Ala
1 5 10

<210> 860
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 860
Met Tyr Leu Ser Leu Leu Ile Leu Leu Leu Glu Asn Val Ser Gly Phe
-15 -10 -5 1
Pro Phe Pro Leu Ile Phe Gln Leu His Ala Ser Pro Gly His Lys Ile
5 10 15
Leu Pro Asp Cys Met Ile Tyr Ser Ile Thr Val Ser Leu Met Phe Pro
20 25 30
Val Val Asp Tyr Ile Ser Thr Gln Gly
35 40

<210> 861
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 861
Met Met Arg Ala Phe Tyr Leu Ala Ile Leu Phe Cys Leu Ser Leu Ser
-25 -20 -15
Leu Trp Phe Xaa Cys Leu Leu Phe Leu Leu Phe Ala Trp Pro Gly
-10 -5 1

<210> 862
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 862
```
Met Ala Trp Thr Pro Leu Leu Phe Leu Thr Leu Leu Leu His Cys Thr
-20                 -15                 -10                 -5
Gly Ser Leu Ala Gln Leu Val Leu Thr Gln Ser Pro Ser Ala Ser Ala
                1               5                   10
Ser Leu Gly Ala Ser Val Lys Leu Thr Cys Thr Leu Ser Ser Gly His
        15                  20                  25
Ser Asn Tyr Gly Ile Ala Trp Tyr Gln Gln Gln Pro Glu Lys Gly Pro
    30                  35                  40
Arg Phe Leu Met Lys Val Asn Ser Asp Gly Ser His Met Lys Ala Asp
45                  50                  55                  60
Gly Ile Pro Asp Arg Phe Ser Gly Ser Ser Ser Gly Ala Glu Arg Tyr
                65                  70                  75
Leu Ser Ile Ser Ser Leu
            80
```

<210> 863
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 863
```
Met Pro Leu Ala Leu Phe Phe Leu Leu Ser Val Ala Leu Ala Ile Gln
                -10                 -5                  1
Gly Gln
```

<210> 864
<211> 129
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 864
```
Met Asp Trp Thr Trp Arg Xaa Phe Cys Leu Leu Ala Val Ala Pro Gly
                -15                 -10                 -5
Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            1                   5                   10
Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe
    15                  20                  25
Thr Ser His Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45
Glu Trp Met Gly Ile Ile Tyr Pro Asp Ser Asp Thr Thr Lys Tyr Xaa
                50                  55                  60
Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
            65                  70                  75
Thr Val Tyr Met Glu Leu Ser Ser Leu Thr Ser Asp Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Ala Arg Glu Ala Tyr Ser Gly Ser Tyr Arg Phe Asp Tyr
    95                  100                 105
Trp
110
```

<210> 865
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 865
```
Met Asp Leu Met Cys Lys Lys Met Arg His Leu Trp Phe Leu Leu Leu
    -25                 -20                 -15
Leu Val Ala Ala Pro Arg Trp Val Leu Ser Gln Leu Gln Leu Gln Glu
-10                 -5                  1               5
Ser Gly Pro Gly Leu Val Lys Ala Ser Glu Thr Leu Ser Leu Ala Cys
            10                  15                  20
Ser Val Ser Gly Asp Ser Ile Ser Ser Gly Asn Tyr Tyr Trp Gly Trp
        25                  30                  35
Ile Arg Gln Pro Pro Gly Lys Gly Leu Gln Trp Leu Gly Ser Leu Trp
    40                  45                  50
Asn Arg Gly Gly Pro Gln Tyr Asn Xaa Ser Leu Lys Asn Arg Val Thr
55                  60                  65                  70
Val Ser Val Asp Thr Ser Thr Asn His Phe Phe Leu Arg Leu Asn Ser
                75                  80                  85
Val Asn Xaa Gly His Gly Asn Leu Leu Leu Cys Ala
            90                  95
```

<210> 866
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 866
```
Met Arg Xaa Xaa Leu Xaa Leu Ser Val Leu Leu Gly Xaa Xaa Xaa Xaa
    -15                 -10                 -5
Lys Xaa Asp Phe Val Gly His Gln Val Leu Arg Ile Ser Val Ala Asp
1               5                   10                  15
```

<210> 867
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 867
```
Met Ala Glu Ser Arg Glu Glu Gly Glu Ser Cys Val Glu Ser His Cys
    -35                 -30                 -25
Val Leu Phe Phe Thr Leu Phe Phe Leu Leu Phe Phe Cys Phe Val Phe
-20                 -15                 -10                 -5
Cys Leu Arg Gly Gln Gly
                1
```

<210> 868
<211> 110
<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 868
```
Met Glu Leu Gly Leu Ser Trp Leu Phe Leu Val Ala Phe Leu Lys Gly
                -15                 -10                 -5
Val Gln Cys Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln
            1               5                   10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
    15                  20                  25
Ser Ser Tyr Ala Met Leu Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
Glu Trp Val Ser Gly Ile Ser Ala Gly Ala Asp Asp Thr Tyr Asp Ala
                50                  55                  60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Lys
            65                  70                  75
Ile Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Arg
        80                  85                  90
```

<210> 869
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 869
```
Met Ala Val Ser Val Leu Arg Leu Thr Val Val Leu Gly Leu Leu Val
            -20                 -15                 -10
Leu Phe Leu Thr Cys Tyr Ala Asp Asp Lys Pro Asp Lys Pro Asp Asp
        -5                  1               5
Lys Pro Asp Asp Ser Gly Lys Asp Pro Lys Pro Asp Phe Pro Lys Phe
10                  15                  20                  25
Leu Ser Leu Leu Gly Thr Glu Ile Ile Glu Asn Ala
                30                  35
```

<210> 870
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 870
```
Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
                -20                 -15                 -10
Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
            -5                  1               5
Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
    10                  15                  20
His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
25                  30                  35                  40
Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
                45                  50                  55
Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
            60                  65                  70
```

```
Gln His Glu Ile Asn Leu Ile Ala Tyr Arg
        75                  80

<210> 871
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 871
Met Val Val Ala Asp Arg Asn Arg Ala Ser Ser Ser Ser Tyr Leu Cys
        -25                 -20                 -15
Leu Leu Leu Phe Ser Leu Ser Leu Phe Leu Cys His Glu Thr Val Cys
    -10                 -5                  1               5
Asp Arg Ala Thr Cys
                10

<210> 872
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 872
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                -15                 -10                 -5
Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
            1               5                   10
Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe
    15                  20                  25
Ser Xaa Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
30                  35                  40                  45
Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Xaa Tyr Ala
                50                  55                  60
Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Xaa Ser Thr Xaa
            65                  70                  75
Thr Xaa Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Xaa
        80                  85                  90
Tyr Tyr Cys Ala Arg Gly Gln Ala Pro Gly Arg Val Val Val Pro Leu
    95                  100                 105
Phe Leu Trp Gly Gln Gly Thr Trp Ser Pro Ser Pro Gln Pro
110                 115                 120

<210> 873
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 873
Met Thr Tyr Ser Tyr Ser Phe Phe Arg Pro Glu Leu Ile Val Asn His
-45                 -40                 -35                 -30
Leu Asn Tyr Val His Ser Glu Ala Asn Arg Arg Thr Lys Thr Lys Thr
                -25                 -20                 -15
```

Leu Leu Ser Leu Leu Ser Phe Leu Asp Glu Thr Ser Gly Leu Ser Thr
-10 -5 1
His Leu Pro Cys Leu Ser Leu Ser Lys Glu Cys Gly Val Leu His Leu
5 10 15
Asp Ile His Gly Lys Lys Glu Asp Met Arg Asp Glu Val Leu Leu Ala
20 25 30 35
Leu Asn Xaa Cys Thr His Arg
40

<210> 874
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 874
Met Lys Ser Phe Ser Arg Ile Leu Phe Leu Val Phe Leu Leu Ala Gly
-15 -10 -5
Leu Arg Ser Lys Ala Ala Pro Ser Ala Pro Leu Pro Leu Gly Cys Gly
1 5 10
Phe Pro Asp Met Ala His Pro Ser Glu Thr Ser Pro Leu Lys Gly Ala
15 20 25
Ser Glu Asn Ser Lys Arg Asp Arg Leu Asn Pro Glu Phe Pro Gly Thr
30 35 40 45
Pro Tyr Pro Glu Pro Ser Lys Leu Pro His Thr Val Ser Leu Glu
50 55 60

<210> 875
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 875
Met Arg Val Pro Ile Phe Pro His Pro His Gln Leu Ser Leu Leu Phe
-40 -35 -30
Ile His Leu Phe Ile Tyr Leu Phe Arg Glu Arg Val Ser Leu Cys His
-25 -20 -15 -10
Leu Gly Trp Ser Ala Val Val Gln Ser Gln Pro Thr Thr Thr Leu Thr
-5 1 5
Ser Arg Ala
10

<210> 876
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 876
Met Trp Lys Glu Ser Ser His Gly Cys Asn Asn Leu Gly Ser Ser Tyr
-35 -30 -25
Leu Asp Asp Thr Gly Val Gly Ser Phe Leu Phe Val Leu Phe Cys Phe
-20 -15 -10

Gly Gly Ser Arg Ala Leu Leu Leu Pro Gly Ser Gly
-5 1 5

<210> 877
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 877
Met His Thr Phe Leu Cys Leu Leu Phe Tyr Leu Ile Val Ser Cys Gly
-15 -10 -5
Ala Val Phe Leu Thr Val Pro Ser Pro Gln
1 5 10

<210> 878
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 878
Met Ala Trp His Pro Thr Pro Pro Pro Leu Xaa Xaa Pro Pro Pro Leu
-35 -30 -25
Xaa Arg Xaa Ser Leu Pro Ala Cys Ala Asp Ser Ile Ile Leu Xaa Leu
-20 -15 -10
Xaa Phe Pro Gly Ile Leu Gly Gln Ala His Leu Xaa Ser Glu Gln Trp
-5 1 5
Thr Gln Tyr Leu
10

<210> 879
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 879
Met Pro Ile Leu Pro Gln Asp Ile Leu His Leu Leu Ile Leu Leu Ser
-20 -15 -10
Gly Thr Cys Phe Thr Trp Ile Leu Leu Trp Leu Pro Leu Ser Pro Leu
-5 1 5 10
Leu Gly Leu Lys Cys
15

<210> 880
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 880
Met Lys Ala Leu Gly Ala Val Leu Leu Ala Leu Leu Leu Cys Gly Arg
-20 -15 -10 -5
Pro Gly Arg Gly Gln Thr Gln Gln Glu Glu Glu Glu Glu Asp Glu Asp
1 5 10
His Gly Pro Asp Asp Tyr Asp Glu Glu Asp Glu Asp Glu Val Glu Glu
15 20 25
Glu Glu Thr Asn Arg Leu Pro Gly Gly Arg Ser Arg Val Leu Leu Arg
30 35 40
Cys Tyr Thr Xaa Xaa Ser Leu Pro Arg Asp Glu Arg Cys Asn Leu Thr
45 50 55 60
Gln Asn Cys Ser His
65

<210> 881
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 881
Met Lys Glu Tyr Val Leu Leu Leu Phe Leu Ala Leu Cys Ser Ala Lys
-15 -10 -5 1
Pro Phe Phe Ser Pro Ser His Ile Ala Leu Lys Asn Met Met Leu Lys
5 10 15
Asp Met Glu Asp Thr Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp Asp
20 25 30
Asp Asp Glu Asp Asn Ser Leu Phe Pro Thr Arg Glu Pro Arg Ser His
35 40 45
Phe Phe Pro Phe Asp Leu Phe Pro Met Cys Pro Phe Gly Cys Gln Cys
50 55 60 65
Tyr Ser Arg Val Val His Cys Ser
70

<210> 882
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 882
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
-15 -10 -5
Ala Met Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Arg Leu Val Lys
1 5 10
Pro Ser Gly Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Met
15 20 25
Ala Thr Ser Asp Trp Trp Ser Trp Phe Arg Gln Thr Pro Glu Lys Gly
30 35 40 45
Leu Glu Trp Ile Gly Glu Ile Phe Gln Thr Gly Pro Thr Asn Tyr Asn
50 55 60
Pro Ser Leu Lys Ser Arg Val Ser Met Ser Val Asp Met Ser Lys
65 70 75

<210> 883
<211> 129
<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 883
Met Asp Leu Thr Cys Lys Lys Met Lys His Leu Trp Phe Phe Leu Leu
    -25                 -20                 -15
Leu Val Ala Ala Pro Arg Trp Ala Leu Ser Gln Leu Gln Leu Gln Glu
-10                 -5                  1                   5
Ser Gly Pro Gly Leu Val Lys Pro Ser Glu Thr Leu Ser Leu Thr Cys
            10                  15                  20
Thr Val Ser Gly Glu Ser Ile Thr Thr Asn Ser Phe Cys Trp Ala Trp
        25                  30                  35
Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu Gly Thr Val Cys
    40                  45                  50
Tyr Gly Gly Thr Thr Tyr Xaa Asn Xaa Ser Leu Lys Ser Arg Val Lys
55                  60                  65                  70
Leu Ser Leu Asp Thr Ser Thr Asn Gln Phe Ser Leu Lys Val Thr Ser
                75                  80                  85
Met Thr Ala Gly Asp Ala Ala Val His Tyr Cys Ala Gly Leu Arg Val
            90                  95                  100
Ser

<210> 884
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 884
Met Ala Asn Gly Thr Asn Ala Ser Ala Pro Tyr Tyr Ser Tyr Glu Tyr
            -60                 -55                 -50
Tyr Leu Asp Tyr Leu Asp Leu Ile Pro Val Asp Glu Lys Lys Leu Lys
        -45                 -40                 -35
Ala His Lys His Ser Ile Val Ile Ala Phe Trp Val Ser Leu Ala Ala
    -30                 -25                 -20
Phe Val Val Leu Leu Phe Leu Ile Leu Leu Tyr Met Ser Trp Ser Ala
-15                 -10                 -5                  1
Ser Pro

<210> 885
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 885
Met Asp Trp Thr Trp Arg Phe Leu Phe Val Val Ala Ala Ala Thr Gly
                -15                 -10                 -5
Val Gln Ser Gln Xaa Xaa Leu Xaa Gln Ser Gly Ala Glu Val Lys Lys
            1                   5                   10
Pro Gly Ser Ser Val Lys Val Ser Cys Xaa Ala Ser Gly Gly Ile Xaa
    15                  20                  25
Ser Xaa Tyr Ser Phe Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Phe
30                  35                  40                  45

Glu Trp Leu Gly Arg Ile Ile Pro Ile Leu Gly Ile Thr Asn Tyr Ala
                50                  55                  60
Glu Lys Phe Arg Gly Arg Leu Thr Ile Thr Val Asp Lys Ser Thr Arg
            65                  70                  75
Val Val Tyr Met Glu Gln Ser Ser Leu Thr Ser Ala Asp Thr Ala Val
        80                  85                  90
Tyr Tyr Cys Ala Lys Pro Thr Met Thr Ser Glu Leu Arg Val Tyr Tyr
    95                  100                 105
Gln Xaa Thr Leu Trp
110

<210> 886
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 886
Met Trp Asn Arg Tyr Phe Val Phe Tyr Leu Leu Leu Leu Ser Ala Phe
        -20                 -15                 -10
Thr Ser Gln Thr Val Ser Gly Gln Arg Lys Lys Gly Pro Arg
    -5                  1               5

<210> 887
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 887
Met Lys His Leu Gly Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
                -15                 -10                 -5
Val Leu Ser Gln Leu Gln Leu Gln Glu Ser Gly Ser Gly Leu Glu Lys
            1                   5                   10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
    15                  20                  25
Ser Ser Asp Asp Leu Ser Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys
30                  35                  40                  45
Gly Leu Glu Trp Ile Gly Tyr Ile Tyr Gln Asn Glu Arg Thr Leu Tyr
                50                  55                  60
Asn Pro Ser Leu Lys Ser Arg Ala Ala Ile Ser Val Asp Arg Ser Lys
            65                  70                  75
Asn Gln Phe Ser Leu Lys Leu Thr Ser Val Thr Ala Ala Asp Met Ala
        80                  85                  90
Val Tyr Tyr Cys Ala Thr Ser Val Met Xaa Ser Phe Gly Gly Val Leu
    95                  100                 105
Val Pro Asn Leu Phe Leu Thr Thr Gly Ala Arg Glu Ser Arg
110                 115                 120

<210> 888
<211> 155
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 888
Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Gly Pro Arg Trp
-15 -10 -5
Val Leu Ser Gln Val Gln Leu Xaa Glu Ser Gly Pro Arg Leu Val Lys
1 5 10
Pro Ser Gln Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ala Ser Val
15 20 25
Ser Ser Arg Gly Tyr Tyr Trp Thr Trp Ile Arg Gln Leu Pro Gly Lys
30 35 40 45
Gly Leu Glu Trp Ile Gly Tyr Ile Xaa Tyr Thr Gly Ser Thr Phe Tyr
50 55 60
Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Ile Asp Thr Ser Lys
65 70 75
Asn Gln Phe Ser Leu Asn Leu Arg Ser Val Thr Thr Ala Asp Thr Ala
80 85 90
Val Tyr Tyr Cys Ala Arg Asp His Phe Asp Leu Leu Phe Asp Pro Trp
95 100 105
Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
110 115 120 125
Ser Val Phe Pro Leu Ala Xaa Ser Ser Lys Ser
130 135

<210> 889
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 889
Met Ala Cys Arg Glu Arg Pro Arg Pro Leu Leu Trp Arg Ser Arg Gly
-40 -35 -30
Arg Phe Phe Asn Trp Gly Lys Leu Phe Phe Cys Phe Val Leu Xaa Leu
-25 -20 -15 -10
Phe Cys Phe Val Phe Glu Ala Glu Ser Arg Ser Val Ala Gln Ala Gly
-5 1 5
Val Gln Trp Arg Tyr Phe Gly Ser Leu Gln Ala Leu Pro Pro Trp
10 15 20

<210> 890
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 890
Met His Glu Phe Ile Ser Gly Phe Phe Ile Leu Phe His Trp Ser Leu
-20 -15 -10
Cys Leu Cys Leu Cys Gln Tyr His Ala
-5 1

<210> 891
<211> 44
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -42..-1

<400> 891
Met Ala Tyr Ala Ile Ser Pro Phe His Ser Ser Trp Asn Pro Leu Phe
-40 -35 -30
Thr Ser His Lys Ala Ser Ala Ser His Ser His Leu Gly Leu Leu Val
-25 -20 -15
Cys Leu Phe Ala Val Thr Ser Ile Leu Cys Ser Ser
-10 -5 1

<210> 892
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 892
Met Ser Pro Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu
-15 -10 -5 1
Pro Gly Ser Ala Xaa Ala Xaa Ser Ala Ser Leu Gly Gln Phe Ser Met
5 10 15
Cys Gly Arg Cys Pro Thr Cys Pro Gly Asn Gly Pro Leu Arg Thr Pro
20 25 30
Ala Ala Thr Xaa Xaa Xaa Val Pro Gly His Val Asp
35 40 45

<210> 893
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 893
Met Ala Thr Ala Met Asp Trp Leu Pro Trp Ser Leu Leu Leu Phe Ser
-20 -15 -10
Leu Met Cys Glu Thr Ser Ala Phe Tyr Val Pro Gly Val Ala Pro Ile
-5 1 5
Asn Phe His Gln Asn Asp Pro Val Glu Ile Lys Ala Val Lys Leu Thr
10 15 20 25
Ser Ser Arg Thr Gln Leu Pro Tyr Glu Tyr Tyr Ser Leu Pro Phe Cys
30 35 40
Gln Pro Ser Lys Ile Thr Tyr Lys Ala Glu Asn Leu Gly Glu Val Leu
45 50 55
Arg Gly Asp Arg Ile Val Asn Thr Pro Phe Gln Val Leu Met Asn Ser
60 65 70
Glu Lys Lys Cys Glu Val Leu Cys Ser Gln Ser Asn Lys Pro Val Thr
75 80 85
Leu Thr Val Glu Gln Ser Arg Leu Val Ala Glu Arg Ile Thr Glu Asp
90 95 100 105
Tyr Tyr Val His Leu Ile Ala Asp Asn Leu Pro Val Ala Thr Gly Trp
110 115 120
Ser Ser Thr Pro Thr Glu Thr Ala Met Thr
125 130

<210> 894
<211> 28

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 894
```
Met Pro Ser Pro Cys Leu Ile Ser Leu Leu Gln Cys Ala His Val Ser
            -15                 -10                 -5
Leu Gly Leu Gln Tyr Pro Cys Xaa Leu Leu Leu Pro
        1               5                   10
```

<210> 895
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 895
```
Met Asn Leu Ser Leu Val Leu Ala Ala Phe Cys Leu Gly Ile Ala Ser
        -15                 -10                 -5
Ala Val Pro Lys Phe Asp Gln Asn Leu Asp Thr Lys Trp Tyr Gln Trp
    1               5                   10                  15
Lys Ala Thr His Arg Arg Leu Tyr Gly Ala Asn Glu Glu Gly Trp Arg
                20                  25                  30
Arg Ala Ala Trp Glu
            35
```

<210> 896
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 896
```
Met Glu Phe Gly Leu Asn Trp Val Phe Leu Val Ala Ile Phe Thr Gly
                -15                 -10                 -5
Val His Cys Glu Val Gln Leu Val Glu Ser Gly Gly Asp Leu Val Gln
            1               5                   10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Thr Ala Ser Gly Phe Thr Phe
    15                  20                  25
Gly Asp Tyr Ala Met Thr Trp Phe Arg Gln Ala Ser Gly Lys Arg Leu
30                  35                  40                  45
Glu Trp Leu Gly Phe Ile Arg Asn Arg Gly Ser Gly Gly Ser Ala Glu
                50                  55                  60
Tyr Gly Ala Ser Val
            65
```

<210> 897
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 897
Met Lys Asn Cys Leu Leu Ile Leu Leu Met Leu Leu Leu Phe Ala Ile
-15 -10 -5
His Ile Asn Arg Met Asn Val Arg Asn Val Gly Asn Thr Leu Val Val
1 5 10 15
Val Gln Ile Leu Phe Ser Ile Arg Val Phe Ile Leu Glu Arg Asn Pro
20 25 30
Leu Asn Val

<210> 898
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 898
Met Glu Leu Gly Leu Ser Trp Ile Phe Leu Leu Ala Ile Leu Lys Gly
-15 -10 -5
Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Asp Asp Tyr Ala Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Glu Trp Val Ser Gly Ile Thr Trp Asn Ser Gly Xaa Ile Gly Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
65 70 75
Ser Leu Tyr Leu Gln Met Asn Ser Leu Arg Thr Glu Asp Thr Ala Phe
80 85 90
Tyr Phe Cys Ala Lys Ala Arg Gly Leu Phe Ser Asp Thr Trp Pro Tyr
95 100 105
Xaa His Tyr Ala Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
110 115 120 125
Ser Ser Ala Ser Thr
130

<210> 899
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 899
Met Leu Leu Val Phe Phe Val Leu Trp Thr Cys Ser Leu Ala Leu Leu
-10 -5 1
Ala Ser Ser Pro Ile Ala Ala Xaa Pro
5 10

<210> 900
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -19..-1

<400> 900
Met Asp Trp Thr Trp Arg Ile Leu Leu Leu Val Ala Ala Ala Thr Asp
-15 -10 -5
Ala Ser Ser Gln Met Gln Leu Leu Gln Ser Gly Pro Glu Val Lys Lys
1 5 10
Thr Gly Ser Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Asp Thr Leu
15 20 25
Ala Tyr His Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Ala Leu
30 35 40 45
Glu Trp Met Gly Trp Ile Thr Pro Phe Ser Gly Asp Thr Asn Phe Ala
50 55 60
Gln Arg Phe Gln Asp Arg Leu Thr Phe Thr Arg Asp Arg Ser Met Ser
65 70 75
Thr Val Tyr Met Thr Leu Thr Ser Leu Ile Ser Glu Asp Thr Ala Met
80 85 90
Tyr Tyr Cys Ala Thr Asp Gly Arg Arg Thr Asn Arg Leu Phe Glu
95 100 105

<210> 901
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 901
Met Ala Gly Gln Leu Leu Gly Cys Leu Leu Trp Leu Leu Thr His Ile
-15 -10 -5
Lys Ala Gln Asp Ser Val Arg Asp Ala Tyr Trp Lys Thr Gly Ser Cys
1 5 10
Pro Pro Pro Phe Leu His Val Ser Thr Phe Xaa Xaa Lys Leu Thr Phe
15 20 25 30
Ser Thr Lys Gly Asn Leu Leu His Ser Ile Pro Leu Ser Ser Pro Leu
35 40 45
Ala Cys Val Leu
50

<210> 902
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -91..-1

<400> 902
Met Lys Glu Ala Val Pro Pro Gly Cys Thr Lys Ser Pro Ser His Phe
-90 -85 -80
Ser Glu Gly Phe Asp Arg Trp Ala Leu Glu Glu Thr Pro Pro Glu Asn
-75 -70 -65 -60
Leu Ile Gly Ala Leu Leu Ala Ile Phe Gly His Leu Val Val Ser Ile
-55 -50 -45
Ala Leu Asn Leu Gln Lys Tyr Cys His Ile Arg Leu Ala Gly Ser Lys
-40 -35 -30
Asp Pro Arg Ala Tyr Phe Lys Thr Lys Thr Trp Trp Leu Gly Leu Phe
-25 -20 -15
Leu Met Leu Leu Gly Glu Leu Gly Val Phe Ala Ser Tyr Ala Phe Ala
-10 -5 1 5

```
Pro Leu Ser Leu Ile Val Pro Leu Ser
                10

<210> 903
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 903
Met Ala Phe Leu Trp Leu Leu Ser Cys Trp Ala Leu Leu Gly Thr Thr
            -15                 -10                 -5
Phe Gly Cys Gly Val Pro Ala Ile His Pro Gly Cys Gln Leu Ser Pro
        1               5                   10
Arg Leu Pro Pro Thr Leu Leu Pro Thr Glu Arg Gly
15                  20                  25

<210> 904
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 904
Met Ala Pro Phe Gln Asn Phe Leu Trp Leu Phe Phe Val Leu Asn Leu
-20                 -15                 -10                 -5
Gly Ser Phe Ala Phe Ser Ser Xaa Pro Asn Ser Leu Phe Tyr Thr Ile
                1               5                   10
His Phe Gly Pro Asn Phe Phe Thr Leu Leu Tyr Lys Gln Gly Ala Glu
        15                  20                  25
Met Cys Val Tyr Val Phe Asn Phe Leu Tyr Pro Phe Ala Leu Gly Tyr
    30                  35                  40
Phe Phe Ser Tyr Asp Ile Leu Asp Leu Pro Val Xaa Val Arg Pro Pro
45                  50                  55                  60
Ser Gly

<210> 905
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 905
Met Asp Phe Thr Gln Cys His Ser Leu Leu Leu Arg Val Glu Tyr Ser
-35                 -30                 -25                 -20
Pro Val Ser Val Cys Phe Leu Leu Leu Ser Val Ala Phe Asn Gln Leu
                -15                 -10                 -5
Val Phe Ala Leu Tyr Pro Ile Gln Ala Thr Xaa Cys Phe Ser Xaa Val
            1               5                   10
Ser Leu Pro Phe Pro Ala
    15

<210> 906
<211> 23
```

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 906
Met Leu Leu Leu Leu Leu Ala Cys Gly Val Pro Ser Leu Trp Pro Phe
-15 -10 -5 1
Ala Leu Ala Leu Leu Lys Thr
5

<210> 907
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 907
Met Phe Ile Glu Asn Ile Gly Leu Lys Phe Ser Phe Leu Leu Leu His
-20 -15 -10
Leu Cys Gln Val Leu Leu Ser Arg Arg Ala Gly Thr Ile Pro Thr Glu
-5 1 5
Thr Ile Pro Lys Lys Leu Arg Arg Arg Asp Gly
10 15 20

<210> 908
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 908
Met Gln Asn Arg Thr Gly Leu Ile Leu Cys Ala Xaa Ala Leu Leu Met
-20 -15 -10
Gly Phe Leu Met Val Cys Leu Gly Ala Phe Phe Ile Ser Trp Gly Ser
-5 1 5
Ile Phe Asp Cys Gln Gly Ser Leu Ile Ala Ala Tyr Leu Leu Leu Pro
10 15 20
Leu Gly Phe Val Ile Leu Leu Ser Gly Ile Phe Trp Ser Asn Tyr Arg
25 30 35 40
Gln Val Thr Glu Ser Lys Gly Val Leu Arg His Met Leu Arg Gln His
45 50 55
Leu Ala His Gly Ala Leu Pro Val Ala Thr Val Asp Ser Ala Ala Leu
60 65 70
Leu Lys Ile Met Cys Lys Gln Leu Leu
75 80

<210> 909
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 909
Met Lys Val Glu Gly Glu Glu Lys Leu Tyr Arg Leu Leu Arg Ser Gly
-40 -35 -30
Asp Leu Phe Lys Phe His Gln Pro His Phe Tyr Glu Leu Ser Gly Leu
-25 -20 -15
Thr Cys Thr Ser Ser Leu Leu Ser Phe Ala Leu Gly Arg Ser Ile Pro
-10 -5 1
Gly Ser Phe Pro
5

<210> 910
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 910
Met Glu Ser Arg Thr Leu Leu Leu Leu Phe Ser Gly Ala Val Ala Leu
-15 -10 -5
Ile Gln Thr Trp Ala Gly Glu Cys Gly Val Gly Arg Glu Lys Ala Ser
1 5 10
Ala Gly Arg Ser Glu Gly Pro Ala Arg Arg Ser Lys Ser Ala His Ile
15 20 25
Xaa Asn Tyr Arg Leu Gln Leu Gln Ser Arg Gln Gly
30 35 40

<210> 911
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 911
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
-15 -10 -5
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
1 5 10 15
Asp Lys Leu

<210> 912
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 912
Met Pro Trp Thr Ile Leu Leu Phe Ala Ala Gly Ser Leu Ala Ile Pro
-10 -5 1
Ala Pro Ser Ile Arg Val Val Pro Pro Tyr Pro Ser Ser Gln Glu Asp
5 10 15
Pro Ile His Ile Ala Cys Met Ala Ala Gly Asn Phe Pro Gly Ala Asn
20 25 30
Phe Thr Leu Tyr

35

<210> 913
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64..-1

<400> 913
```
Met Ala Glu Gly Glu Arg Val Cys Ala Ser Val Val Pro Ser Ala Leu
                -60                 -55                 -50
Arg Thr Leu Lys Arg Arg Ser Asn Leu Ser Arg Ile Pro Ala Gly Gln
            -45                 -40                 -35
Glu Lys Glu Gly Lys Ser Arg His Val Ala Pro Pro Phe Arg Phe Phe
        -30                 -25                 -20
Pro Phe Ser Gly Phe Leu Phe Phe Gly Phe Leu Phe Pro Val Phe Ser
    -15                 -10                 -5
Phe Pro Ser
1
```

<210> 914
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 914
```
Met Phe Cys Leu Ala Ala Ile Leu Ala Ser Ala Ser Ala Gln Arg Phe
            -10                 -5                  1
Pro Ser Ala Phe Ser Pro Ser Pro Phe Xaa Trp Leu Xaa Gln Cys Xaa
    5                   10                  15
Thr Ala Thr Ser Leu Gly Phe Xaa Thr Val Cys Xaa Asn Ser Ile Ile
20                  25                  30                  35
Ser Leu Trp Tyr Leu Xaa Gly Val Pro Pro Glu Val Xaa Glu Leu Pro
                40                  45                  50
Phe Phe Pro Tyr Cys Ser Met
            55
```

<210> 915
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 915
```
Met Val Asp Gly Thr Leu Leu Leu Leu Leu Ser Glu Ala Leu Ala Leu
        -15                 -10                 -5
Thr Gln Thr Trp Ala Gly Ser His Ser Xaa Lys Tyr Phe His Thr Ser
    1               5                   10                  15
Val Ser Arg Xaa Gly Arg Gly Glu Pro Arg Phe Ile Ser Val Gly Tyr
                20                  25                  30
Val Asp Asp Thr Arg Ser Glu Tyr Trp Asp Arg Glu Thr Arg Ser Ala
            35                  40                  45
Arg Asp Thr Ala Gln Ile Phe Arg Val Asn Leu Arg Thr Leu Arg Gly
```

```
        50                  55                  60
Tyr Tyr Asn Gln Ser Glu Ala Gly Ser Xaa Thr Leu Gln
    65                  70                  75

<210> 916
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 916
Met Asn Phe Arg Gly Pro Gln Thr Phe Ser Leu Ser His Ser Leu Val
        -25                 -20                 -15
Leu Ser Leu Ile Ser Leu Ser Ile Ala Trp Ser Met Val Glu Met Xaa
    -10                 -5                  1               5
Thr Ser Ala Ser Tyr Lys Gln Lys Phe Ala Leu Arg Ile Leu Val Val
                10                  15                  20
Gln Leu Pro Thr Trp Val Glu Cys Pro Val Asn His Arg Cys Ala Leu
            25                  30                  35
Gly Arg Lys Asn Cys Ser Ile Arg Thr Gln Pro
        40                  45

<210> 917
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 917
Met Thr Gly Ile Ser Ile Cys Ser Cys Ile Cys Leu Phe Leu Pro Ser
-20                 -15                 -10                 -5
Leu Ile His Ser Phe Pro Pro Pro Cys
                1                   5

<210> 918
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 918
Met Asp Leu Leu Cys Lys Asn Met Lys His Leu Trp Phe Phe Leu Leu
    -25                 -20                 -15
Leu Val Ala Ala Pro Arg Trp Val Gln Leu Gln Glu Ser Gly Pro Arg
-10                 -5                  1                   5
Leu Val Arg Pro Pro Glu Thr Leu Lys Pro Ser Glu Thr Leu Ser Leu
            10                  15                  20
Thr Cys Thr Ile Ser Gly Asp Ser Met Ser Ser Ala Ser Tyr Tyr Trp
        25                  30                  35
Ala Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Phe Ile Gly Arg
    40                  45                  50
Ala Leu Tyr Ser Gly Thr Thr Asp Tyr Asn Pro Ser Leu Ser Ser Arg
55                  60                  65                  70
Ile Thr
```

<210> 919
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 919
```
Met Ser Ser Glu Lys Ser Gly Leu Pro Asp Ser Val Pro His Thr Ser
-45                 -40                 -35                 -30
Pro Pro Pro Tyr Asn Ala Pro Gln Pro Pro Ala Glu Pro Pro Ala Pro
                -25                 -20                 -15
Pro Leu Ser Leu Ser Leu Cys Leu Ser Leu Cys His Thr His Thr His
            -10                 -5                  1
Thr His Thr His
    5
```

<210> 920
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 920
```
Met Thr Pro Ala Leu Arg Cys Ala Phe Ala Leu Ala Ile Ala Gly Leu
            -25                 -20                 -15
Val Ser Leu Leu Met Gln Pro Glu Gly Ala Leu Gly Glu Glu Ala Ala
        -10                 -5                  1
Ser Ala Ala Ala Gln Gly Arg Gln Leu Ala Glu Leu Arg Leu
5                   10                  15
```

<210> 921
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 921
```
Met Ser Gly Leu Phe Pro Val Pro Val Arg Val Asn Val Asp Ile Ala
            -35                 -30                 -25
Gln Asn Ile Thr Cys Ser Ser Phe Ser Leu Leu Leu Ile Phe Leu Ser
        -20                 -15                 -10
Phe Pro Tyr Thr Leu Cys Ile Leu Tyr Arg Val Lys Ser Tyr Thr Pro
    -5                  1                   5                   10
Thr Glu Ser Ile Thr Ala Phe Asn Leu Thr Ile Gly Xaa Phe Pro Tyr
                15                  20                  25
Leu Xaa Xaa Ser Thr Pro
            30
```

<210> 922
<211> 39
<212> PRT
<213> Homo sapiens

```
<220>
<221> SIGNAL
<222> -33..-1

<400> 922
Met Cys Arg Ala Ala Cys Ile Ile Arg Met Ala Val Arg Ile Ser Phe
            -30                 -25                 -20
Phe Leu Ser Tyr His Ala Leu Ser Leu Cys Leu Cys Thr Cys Ala Phe
        -15                 -10                 -5
Ala Phe Leu Ser Leu Leu Gly
    1               5

<210> 923
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 923
Met Lys Phe Leu Leu Leu Xaa Ala Leu Gly Phe Leu Xaa Gln Val Asn
        -15                 -10                 -5
Pro Xaa Pro Ile Xaa Gly Gly Ser Lys Met Cys Glu Xaa His Pro Arg
    1               5                   10                  15
Ile Leu Gln Asp Met Leu Pro Leu Gly Gly Asp Ser Ile Val His Val
                20                  25                  30
Gln Arg Xaa Gln Lys Met Leu His Gln Leu Leu
            35                  40

<210> 924
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 924
Met Val Pro Trp Val Arg Thr Met Gly Gln Lys Leu Lys Gln Arg Leu
        -40                 -35                 -30
Arg Leu Asp Val Gly Arg Glu Ile Cys Arg Gln Tyr Pro Leu Phe Cys
    -25                 -20                 -15
Phe Leu Leu Leu Cys Leu Ser Ala Ala Ser Leu Leu Leu Asn Arg Tyr
-10                 -5                  1               5
Ile His Ile Leu Met Ile Phe Trp Ser Phe Val Ala Gly Val Val Thr
            10                  15                  20
Phe Tyr Cys Ser Leu Gly Pro Asp Ser Leu Leu Pro Asn Ile Phe Phe
        25                  30                  35
Thr Ile Lys Tyr Lys Pro Lys Gln Leu Gly Leu Gln Glu Leu Phe Pro
    40                  45                  50
Gln Gly His Ser Cys Ala Val Cys Gly
55                  60

<210> 925
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
```

<222> -34..-1

<400> 925
Met Ala Trp Gly Ser Pro Gly Lys Ile Phe Leu Met Gly Phe Leu Gly
-30 -25 -20
Gly Glu Leu Val Phe Leu Leu Cys Leu Phe Xaa Leu Phe Phe Phe Ser
-15 -10 -5
Phe Leu Lys Arg Ser Phe Ala Leu Glu Cys Asn
1 5

<210> 926
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 926
Met Phe Phe Ser Ile Leu Leu Leu Leu Ala Pro Pro Leu Pro Ser Ala
-15 -10 -5
Val Ser Leu Leu Pro Phe Phe Phe Tyr Cys Val Gln
1 5 10

<210> 927
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 927
Met Val Asp Phe Ile Leu Arg Ser Leu Leu Leu Val Cys Ser Trp Leu
-20 -15 -10
Ser Ile Ser Leu His Ala His Thr Thr Ala Phe Cys Thr Tyr Ser Lys
-5 1 5 10
Lys Ile His Thr Val Met Ser Phe Phe Cys
15 20

<210> 928
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 928
Met Arg Ser Leu Leu Tyr Phe Leu Cys Val Ser Ser Tyr Val Thr Ser
-15 -10 -5
Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10

<210> 929
<211> 68
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -15..-1

<400> 929
Met Pro Phe Ile Ser Phe Leu Cys Leu Ile Ala Leu Ala Gly Thr Ser
-15 -10 -5 1
Ser Thr Met Leu Arg Ser Ala Leu Ala Gly Thr Ser Ser Thr Met Xaa
5 10 15
Xaa Arg Ser Gly Xaa Ser Gly Xaa Pro Xaa Leu Val Xaa Val Leu Arg
20 25 30
Gly Asn Ala Phe Ser Phe Phe Pro Phe Ser Leu Met Xaa Ala Met Gly
35 40 45
Cys His Arg Trp
50

<210> 930
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 930
Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser Ser Ser
-15 -10 -5
Arg Ile Leu Leu Val Lys
1 5

<210> 931
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 931
Met Cys Leu Cys Pro Cys Trp Asp Val Phe Thr Val Phe Val Cys Val
-40 -35 -30
Ser Val Cys Val Ser Val Ser Val Pro Val Gly Met Tyr Leu Val Cys
-25 -20 -15
Val Cys Val Cys Val Cys Val Cys Xaa Cys Xaa Arg
-10 -5 1

<210> 932
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 932
Met Leu Ile Ala Lys Gln Ala Gln Pro Gln Gly Leu Thr Ala Ile Cys
-30 -25 -20
Phe Pro Leu Thr Pro Leu Phe Ser Leu Leu Met Leu Thr Gln Ser Pro
-15 -10 -5
Leu Ala Gly Gln Glu Gly Arg Glu Gly Gly Lys Glu Arg Tyr Leu Leu
1 5 10

Val Ile
15

<210> 933
<211> 62
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 933
Met Leu Arg Thr Trp Ser Ser Leu Pro Trp Thr Arg Phe Arg Val Cys
-25 -20 -15
Leu Leu Ser Leu Ser Leu Phe Leu Trp Ala Asn Arg Leu Glu Asp Ser
-10 -5 1 5
Arg Ser Cys Gln Pro Asn Pro Met Ser Leu Thr Thr Leu Pro Gly His
10 15 20
Arg Leu Lys Glu Ala Val Trp Leu Pro Ala Pro Ser Leu Gly
25 30 35

<210> 934
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 934
Met Ala Pro Phe Leu Arg Gln Val Asp Xaa Trp Gly Ala Gln Ala Gly
-25 -20 -15
Leu Val Val Xaa Trp Leu Leu Pro Xaa Gln Cys Ser Cys Glu Arg Ser
-10 -5 1
Glu Gln Tyr Leu Ser Thr Cys Leu Pro Gln His Ser Ser Ile Lys Gln
5 10 15
Ser Cys Ile Lys His Pro Ala Gly Pro Ile Pro Ala Gly His Leu Gln
20 25 30 35
Gly Lys Ala Thr Ala Ala Pro Leu
40

<210> 935
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 935
Met Glu Phe Gly Leu Lys Trp Leu Phe Leu Val Ala Ile Leu Lys Gly
-15 -10 -5
Val Arg Cys Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Gln
1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Val Gly Ser Gly Phe Val Phe
15 20 25
Asp Lys Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Gln Trp Val Ala Gly Ile Gly Gly Gly
50

<210> 936
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 936
Met Ala Leu Ala Met Leu Val Leu Val Val Ser Pro Trp Ser Ala Ala
-15 -10 -5
Arg Gly Val Leu Arg Asn Tyr Trp Glu Arg Leu Leu Arg Lys Leu Pro
1 5 10 15
Gln Ser Arg Pro Gly Phe Pro Ser Pro Pro Trp Gly Pro Ala Leu Ala
20 25 30
Val Gln Gly Pro Ala Met Phe Thr Glu Pro Ala Asn Asp Thr Ser Gly
35 40 45
Ser Lys Glu Asn Ser Ser Leu Leu Asp Ser Ile Phe Trp Met Ala Ala
50 55 60
Pro Lys Asn Arg Arg Thr Ile Glu Val Asn Arg Cys Arg Arg Arg Asn
65 70 75 80
Pro Gln Lys Leu Ile Lys Val Lys Asn Asn Ile Asp Val Cys Pro Glu
85 90 95
Cys Gly His Leu Lys Gln Lys Xaa Val Leu Cys Ala Thr Ala Met Lys
100 105 110

<210> 937
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 937
Met Phe Phe Tyr Ser His Phe Leu Leu Leu Phe Pro Leu Ser Leu Leu
-20 -15 -10 -5
Phe Thr Leu Gly Phe Leu Phe Val Phe Phe Phe Phe Phe Phe
1 5 10

<210> 938
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 938
Met Lys Gln Ser Lys Arg Xaa Met Val Lys Arg Arg Arg Ser Pro Ala
-45 -40 -35
Leu Gly Glu Glu Arg Phe Ser Pro Ser Ser Ile Leu His Pro Arg Leu
-30 -25 -20 -15
Pro Leu Val Leu Leu Gly Thr Arg Val Pro Leu Ser Gly Gly Gly Pro
-10 -5 1
Gly Glu Pro Asp Gln Gly Arg Ser Ala Pro Ser Trp Lys Ser Leu Ala
5 10 15
Ser Thr His Xaa His Ser Arg Pro Ala Ala Gly Ala Thr Pro Ala Arg
20 25 30

Pro Ala Thr Gln Ser Gln Leu Gly Pro Phe Ala Pro Pro Leu Pro Gly
35 40 45 50
Val Arg Pro Ala Pro
55

<210> 939
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 939
Met Leu Leu Glu Ser Leu Cys Val Leu Ser Leu Leu Val Ser Phe Lys
-15 -10 -5
Ser Ala Cys Leu Thr Arg Glu Pro Ala Phe Asp Ser Gln Ala Arg Pro
1 5 10

<210> 940
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 940
Met Val Phe Gly Tyr Trp Lys Gln Pro Leu Ile Thr Leu Ala Lys Lys
-45 -40 -35
Ser Val Lys Cys Ala Arg Glu Cys Leu Arg Cys Ser Leu Arg Pro Leu
-30 -25 -20 -15
Val Leu Leu Tyr Leu Ser Phe Ala Ala Leu Gly Val Val Ala Leu Arg
-10 -5 1
Ser Val Glu Ser Pro Leu Ala Glu Thr His Ser Cys Trp Leu Ser Leu
5 10 15
Gly Met Cys Val Leu Gln Cys Glu Gln Gln Trp Val Pro Thr Pro Val
20 25 30
Ser Phe Leu Cys Gly Leu Ser Gly Ser Ser Thr Ile Ile Val
35 40 45

<210> 941
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 941
Met Cys Val Val Cys Ser Val His Gly Val Cys Cys Val Tyr Val Val
-20 -15 -10
Cys Leu Val Ser Cys Val Leu Cys Val Val Cys Pro Val Cys Trp Val
-5 1 5
Met Cys Cys Val Trp Cys Ile Cys Val Cys Val Trp Cys Val Cys Cys
10 15 20
Met Cys Cys Val Leu Ser Cys Val Val Ser His Gly Leu Cys Gly Val
25 30 35 40
Ser Trp

<210> 942
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 942
Met Glu Leu Gly Leu Ser Trp Val Phe Leu Val Ala Val Leu Glu Val
-15 -10 -5
Val Gln Cys Glu Ile Gln Leu Ile Asp Ala Gly Gly Gly His Val Gln
1 5 10
Ala Gly Gly Ser Leu Arg Leu Ser Cys Val Ala Ser Asp Phe Leu Phe
15 20 25
Arg Ser Tyr Trp Met Thr Trp Val Arg His Pro
30 35 40

<210> 943
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 943
Met Ser Ile Leu Leu Arg Val Leu Gly Ile Lys Gly Cys Trp Ile Leu
-35 -30 -25
Ser Asn Pro Phe Ser Ala Cys Ile Glu Met Ile Leu Leu Phe Leu Phe
-20 -15 -10
Leu Ile Leu Phe Ile Trp His Ile Arg
-5 1

<210> 944
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 944
Met Ala Glu Lys Ala Gly Ser Thr Phe Ser His Leu Leu Val Pro Ile
-25 -20 -15 -10
Leu Leu Leu Ile Gly Trp Ile Val Gly Cys Thr
-5 1

<210> 945
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 945
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys Leu Ala Ala
-15 -10 -5

Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp Phe Ile Lys
            1               5                   10
Pro Leu
    15

<210> 946
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 946
Met Leu Thr Ser Leu Pro Phe Leu Leu Pro Thr Ile Ser Phe Leu Leu
    -25                 -20                 -15
Leu Leu Tyr Phe Phe Xaa Ile Ala Val Thr His Pro Ser Val Leu Ile
-10                 -5                  1               5
Asn Phe Ser Phe Ser Phe Pro Arg
            10

<210> 947
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 947
Met Arg Lys Asp Val Arg Phe Leu Leu Phe Phe Thr Cys Gly Leu Pro
-20                 -15                 -10                 -5
Ala Leu His Gly Asp Ser Arg Val Glu Cys Ser Lys Ala His Pro Pro
                1               5                   10
Ala Met Tyr Tyr
        15

<210> 948
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 948
Met Leu Phe Trp Leu Pro Ser Pro Ser Glu Thr Thr Ser Ala Trp Thr
        -25                 -20                 -15
Leu Leu Ser Ile Ser Leu Ser Val Phe Trp Ser Glu Pro Phe Asn Lys
    -10                 -5                  1               5
Ser Leu Gly Ser Ser Lys Leu Pro Cys His Phe Phe Ser Ile Lys Arg
                10                  15                  20

<210> 949
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -47..-1

<400> 949
Met Pro Val Cys Phe Tyr Ser Leu Ile Cys Phe Phe Ile Tyr Phe Cys
-45 -40 -35
Leu Leu Ser Pro Arg Glu Thr Ile Glu Glu Val Ala Leu Phe Gln Phe
-30 -25 -20
Ser Leu Leu Xaa Leu Gly Glu Gly Leu Thr Phe Leu Cys Leu Cys Gln
-15 -10 -5 1
Val Met Thr Asn Xaa Met Gln Leu Leu Phe Leu Ser Gly Val Val Cys
5 10 15
Gly

<210> 950
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 950
Met Ala Pro Leu Leu Leu Ser Leu Ser Cys Ser Phe Ser Cys His Val
-10 -5 1
Thr Leu Leu Pro Arg
5

<210> 951
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 951
Met Val Pro Ala Ala Gly Ala Leu Leu Trp Val Leu Leu Leu Asn Leu
-20 -15 -10 -5
Gly Pro Arg Ala Ala Gly Ala Gln Gly Leu Thr Gln Thr Pro Thr Glu
1 5 10
Met Gln Arg Val Ser Leu Arg Phe Gly Gly Pro Met Thr Arg Arg
15 20 25

<210> 952
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 952
Met Val Phe Trp Glu Ile Ser Val Gln Ile Ile Leu Ile Ser Glu Leu
-20 -15 -10
Leu Leu Leu Arg Ser Val Thr Ser His Asn Thr Met Met Arg Ala Leu
-5 1 5
Ser Ser Gln Met Leu Ser Gln Ser Phe Pro Arg Pro Ser Phe Gly Phe
10 15 20
Ile Ser Lys Ile His Pro Ser His Pro Pro
25 30

<210> 953
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 953
```
Met Phe Phe Leu Asn Ile Ala Met Phe Ile Val Val Met Val Gln Ile
    -50                 -45                 -40
Cys Gly Arg Asn Gly Lys Arg Ser Asn Arg Thr Leu Arg Glu Glu Val
-35                 -30                 -25                 -20
Leu Arg Asn Leu Arg Ser Val Val Ser Leu Thr Phe Leu Leu Gly Met
                -15                 -10                 -5
Thr Trp Gly Phe Ala Phe Phe Ala Trp Gly Pro Leu Asn Ile Pro Phe
            1               5                   10
Met Tyr Leu Phe Ser Ile Phe Asn Ser Leu
    15                  20
```

<210> 954
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 954
```
Met Asn Lys His Phe Leu Phe Leu Phe Leu Leu Xaa Xaa Leu Ile Val
        -15                 -10                 -5
Ala Val Thr Ser Leu Gln Cys Ile Thr Cys His Leu Arg Thr Arg Thr
    1               5                   10                  15
Asp Arg Cys Arg Arg Gly Phe Gly Xaa Cys Thr Ala Gln Lys Gly Glu
                20                  25                  30
Ala Cys Met Leu Leu Arg Ile His Gln Arg
            35                  40
```

<210> 955
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 955
```
Met Tyr Ile Lys Met Glu Ser Val Thr Leu Ser Pro Ala Pro Val Phe
-35                 -30                 -25                 -20
Pro Val Pro Ala Gln Leu Leu Leu Leu Thr Ser His Phe Leu Gly Glu
                -15                 -10                 -5
Ser Leu Gly Gly Gly Thr Leu Leu Val Pro Leu Leu Pro Pro Gly
            1               5                   10
```

<210> 956
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 956
Met Xaa Xaa Ala Leu Leu Arg Ser Arg Met Ile Gln Gly Arg Ile Leu
-25 -20 -15
Leu Leu Thr Ile Cys Ala Ala Gly Ile Xaa Gly Thr Arg Gln Phe Gly
-10 -5 1 5
Tyr Asn Leu Ser Ile Ile Asn Asp
10

<210> 957
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 957
Met Met Gly Xaa Leu Cys Pro Arg Ser Leu Pro Ile Pro Pro Met Ile
-45 -40 -35
Leu Ser Trp Trp Lys Met Gln Trp Lys Pro Leu Ala Leu Glu Asn Phe
-30 -25 -20
Ser Gly Ser Cys Leu Phe Ser Xaa Ala Trp Leu Xaa Cys Xaa Cys His
-15 -10 -5 1
Gly Asp Asp Asp Leu Ser
5

<210> 958
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 958
Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Gly Asn Ser Val
-15 -10 -5 1
Glu Thr Val Arg Gly Gly Gly Arg Thr Trp Ala Trp Gly Arg Lys Thr
5 10 15
Gln Lys Leu Leu Ala His Leu Arg Gly Ile Leu Gly Ala Trp Xaa Arg
20 25 30

<210> 959
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 959
Met Leu Val Leu Val His Ser Ser Leu Ser Lys Thr Leu Ser Gln Lys
-10 -5 1
Lys Lys Lys Phe Thr Xaa Pro Thr Arg
5 10

<210> 960
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 960
Met Ser Phe Ser Ser Ala Leu Ile Leu Val Ile Ser Cys Leu Leu Leu
-15 -10 -5
Ala Phe Glu Cys Val Cys Ser Cys Phe Ser Gly Ser Phe Asn Cys Asp
1 5 10
Val Arg Val Ser Ile Ser Asp Leu Ser Cys Phe Leu Leu Trp Gly Lys
15 20 25

<210> 961
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 961
Met Gly Phe Trp Cys Gly Cys Pro Phe Cys Leu Xaa Val Phe Leu Leu
-20 -15 -10
Thr Asp Arg Thr Leu Ser Cys Arg Ser Val Gly Val
-5 1 5

<210> 962
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 962
Met Val Leu Leu Ser Leu Ser Leu Trp Gly Ile Ser Thr Leu Ser Ser
-15 -10 -5 1
Thr Thr Ile Glu Leu Ile Tyr Thr Pro Ile Gly
5 10

<210> 963
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 963
Met Ala Ser Leu Leu Ser Gly Phe Thr Ser Phe Cys Leu Leu His Val
-25 -20 -15 -10
His Ser Phe Leu Pro Pro Val Phe Ser Thr Gln Asn
-5 1

<210> 964

<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 964
Met Glu Thr Ala Leu Xaa Xaa Thr Pro Gln Lys Arg Gln Val Met Phe
-30 -25 -20 -15
Leu Ala Ile Leu Leu Xaa Xaa Trp Glu Ala Gly Ser Glu Ala Val Arg
-10 -5 1
Tyr Ser Ile Pro Glu Glu Thr Glu Ser Gly
5 10

<210> 965
<211> 66
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 965
Met Met Leu Asp Phe Ala Leu Ser Pro Arg Leu Glu Arg Ser Gly Leu
-35 -30 -25 -20
Ile Met Ala Cys Cys Thr Leu Asp Leu Leu Gly Ser Ser Ser Pro Pro
-15 -10 -5
Thr Ser Ala Ser Gln Val Ala Gly Thr Gly His Val Pro Pro His Pro
1 5 10
Ala Ser Phe Phe Tyr Phe Xaa Val Xaa Gln Val Tyr Tyr Val Ser Gln
15 20 25
Leu Ile
30

<210> 966
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 966
Met Arg Thr Pro Gln Leu Ala Leu Leu Gln Val Phe Phe Leu Val Phe
-20 -15 -10
Pro Asp Gly Val Arg Pro Gln Pro Ser Ser Ser Pro Ser Gly Ala Val
-5 1 5 10
Pro Thr Ser Leu Glu Leu Gln Arg Gly Thr Asp Gly Gly Thr Leu Gln
15 20 25
Ser Pro Ser Glu Ala Thr Ala Thr Arg Pro Ala Val Pro Gly Leu Arg
30 35 40

<210> 967
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -21..-1

<400> 967
Met Pro Arg Pro Arg Ala Cys Ala Ser Trp Pro Leu Leu Ala Ala Val
    -20                 -15                 -10
Ser Gly Leu Arg Gly Leu Glu Trp Pro Pro Ser Trp Arg Arg Val Val
-5                  1                   5                   10
Ala Ala Val Gly Val Cys Arg Val Arg Asp Trp Gly Pro Arg
            15                  20                  25

<210> 968
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 968
Met Asn Gly Ile Phe Leu Leu Leu Ile Ser Val Leu Thr Val Ile Trp
        -15                 -10                 -5
Phe Trp Lys Thr His Pro Gly
    1               5

<210> 969
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 969
Met Val Phe Leu Val Xaa Leu Leu Cys Ile Ile Xaa Leu Tyr Leu Ile
            -15                 -10                 -5
Arg Gly Ser Glu Trp Xaa Leu Pro Pro Asn Trp
        1                   5

<210> 970
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 970
Met Met Thr Leu Ala Leu Phe Phe Leu Leu Arg Ile Ala Leu Ala Ser
            -15                 -10                 -5
Trp Ala Leu Phe Trp Ile His Met Asn Phe Arg Arg Ala Phe Phe His
        1                   5                   10
Leu Arg Trp Phe Asp Ile Asn Ser Thr Glu Ser Val Asn Cys Phe Gly
15                  20                  25                  30
Gln Tyr Gly Leu Ala
                35

<210> 971
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 971
Met Ser Ile Arg Ser Asn Trp Ser Ser Val Glu Ser Lys Ser Arg Ile
-25 -20 -15
Ser Leu Leu Val Phe Cys Leu Asn Asp Leu Ser Asn Ala Val Xaa Xaa
-10 -5 1
Gly Ile Glu Xaa Pro
5

<210> 972
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 972
Met Ala Trp Ile Pro Leu Phe Leu Gly Val Leu Ala Tyr Cys Thr Gly
-15 -10 -5
Ser Val Ala Ser Tyr Glu Leu Thr His Pro Pro Ser Val Ser Val Ser
1 5 10 15
Pro Gly Gln Thr Ala Ser Ile Thr Cys Ser Gly Asp Lys Leu Gly Asp
20 25 30
Lys Tyr Ala Cys Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Val Leu
35 40 45
Val Ile Tyr Gln Asp Ser Lys Arg Pro Ser Gly Ile Pro Glu Arg Phe
50 55 60
Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Thr
65 70 75 80
Gln Ala Met Asp Glu Ala Asp Tyr Tyr Cys Gln Ala Trp Asp Ser Ser
85 90 95
Thr Val Val Phe Gly Gly Gly Thr
100

<210> 973
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 973
Met Val Cys Val Ile Phe Lys Glu Leu Met Glu Phe Glu Phe Pro Gly
-25 -20 -15
Phe Cys Phe Xaa Leu Cys Phe Gly Arg Ser Ser Leu Cys Cys Arg Xaa
-10 -5 1

<210> 974
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 974
Met Glu Ser Ser Gly Thr Pro Ser Val Thr Leu Ile Val Gly Ser Gly
-30 -25 -20 -15
Leu Ser Cys Leu Ala Leu Xaa Thr Leu Ala Val Val Tyr Ala Ala Leu
-10 -5 1
Trp Arg Tyr Ile Arg Ser Glu Arg Ser Ile Ile Leu Ile Asn Phe Cys
5 10 15
Leu Ser Ile Ile Ser Ser Asn Ile Leu Ile Leu Val Gly Gln Thr Gln
20 25 30
Thr His Asn Lys Glu Tyr Leu His Asn His His Cys Ile Phe
35 40 45

<210> 975
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 975
Met Gly Val Cys Cys Ala Gln Asn Cys Ser Val Ser Gly Xaa Xaa Arg
-30 -25 -20
Asn Ala Leu Xaa Phe Leu Ala Ser Ser Phe Cys Phe Gly Glu Ala Asp
-15 -10 -5 1
Ser Gly Ser Arg Cys Cys Leu Lys Ile Ile Leu Gly Phe Tyr Leu Ile
5 10 15
Arg Tyr Ser Leu Ile Thr Tyr Gln Val Arg
20 25

<210> 976
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 976
Met Lys Ile Leu Tyr Leu Phe Phe Phe Leu Lys Trp Ser His Pro Gly
-15 -10 -5
Trp Ser Ala Thr Xaa Trp Ser Trp His Thr Ala Thr Ser Ala Ser Leu
1 5 10
Ile Gln Val Ile Leu Pro Pro Trp
15 20

<210> 977
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 977
Met Thr Pro Cys Phe Leu Gln Met Asp Asn Leu Thr Pro Leu Phe Leu
-25 -20 -15
Ser Gly Cys Phe Leu Phe Leu Ser Xaa Cys Xaa Ile Tyr Leu Ala Arg
-10 -5 1 5

Ile Leu

<210> 978
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 978
```
Met Gly Ser Ala Gly Arg Leu His Tyr Leu Xaa Met Thr Ala Glu Asn
-40                 -35                 -30                 -25
Pro Thr Pro Gly Asp Leu Ala Pro Xaa Pro Leu Ile Thr Cys Lys Leu
                -20                 -15                 -10
Cys Leu Cys Glu Gln Ser Xaa Gly Gln Asp Asp His Thr Pro Gly Met
            -5                   1               5
```

<210> 979
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 979
```
Met Asn His Leu Pro Pro Asn His Tyr Arg Xaa His Val Phe Thr Cys
                -45                 -40                 -35
His Val Asp Gln Tyr Leu Thr Val Glu Thr Ala Gly Gly Met Glu Lys
            -30                 -25                 -20
Glu Ala Val Ser Val Thr Val Leu Leu Ser Ala Ala Pro Cys Leu Leu
        -15                 -10                 -5
Ser Cys Phe Leu Gly Ser Ser Val Ser Gly Leu Ala Phe Trp Val Ser
     1               5                  10                  15
Gln Gln Lys Thr Lys Gly Pro Glu Arg Cys Lys Asn Thr His His Xaa
                20                  25                  30
Ala Xaa Asn Asn Phe Pro Ala Arg
            35
```

<210> 980
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 980
```
Met Asn Lys Ile Lys Glu Asn Thr His Thr His Thr His Thr His Thr
-40                 -35                 -30                 -25
His Lys Asn Asn Thr Lys Leu Val Ser Asn Leu Phe Leu Phe Met Leu
                -20                 -15                 -10
Pro Leu Trp Cys Ser Ile Gly Thr Cys Thr
            -5                   1
```

<210> 981
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 981
Met His Asp Ser Ser Gly Lys Asn Asn Phe Arg Lys Ile Pro Val Val
-40 -35 -30
Asn Leu Ile Tyr Leu Tyr Val Asp Ile His Ile His Lys Leu Phe Leu
-25 -20 -15
Tyr Ser Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu
-10 -5 1 5
Arg Arg Leu

<210> 982
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 982
Met Gly Arg Leu His Arg Pro Arg Ser Ser Thr Ser Tyr Arg Asn Leu
-30 -25 -20
Pro His Leu Phe Leu Phe Phe Leu Phe Val Gly Pro Phe Ser Cys Leu
-15 -10 -5
Gly Ser Tyr Ser Arg
1

<210> 983
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 983
Met Gln Ser Gln Ala Ala Arg Glu His Lys Pro Gly Xaa Ser Arg Leu
-25 -20 -15
Leu Leu Leu Leu Leu Leu Xaa Leu Pro Leu Pro Pro Pro Xaa Leu Arg
-10 -5 1 5
Thr Arg Xaa Phe Ser Xaa Thr Thr Leu Thr Ala Gly
10 15

<210> 984
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 984
Met Arg Leu Trp Ser Leu Ala Cys Leu Ser Pro Pro Ala Val Gln Leu
-15 -10 -5 1
Gly Ser Gln Gln Ala Thr Asp Trp Trp
5 10

<210> 985
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 985
```
Met Ser Pro Leu Phe Ile Leu Ile Val Leu Ile Trp Ile Phe Ser Phe
-25                 -20                 -15                 -10
Phe Phe Phe Ile Thr Leu Val Arg Gly Ser Ile Asn Leu Phe Phe Phe
                -5                  1               5
```

<210> 986
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 986
```
Met Asn Leu Gly Gly His Ser Asp His Ser Thr Phe Leu Phe Phe Leu
        -20                 -15                 -10
Phe Phe Ser Val Phe Cys Phe Phe Phe
    -5                  1
```

<210> 987
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 987
```
Met Leu Asp Phe Ala Ile Phe Ala Val Thr Phe Leu Leu Ala Leu Val
    -20                 -15                 -10
Gly Ala Val Leu Tyr Leu Tyr Pro Ala Ser Arg Gln Ala Ala Gly Ile
-5                  1               5                   10
Pro Gly Ile Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu Pro Asp Ile
            15                  20                  25
Val Asn Ser Gly Ser Leu His Glu Xaa Leu Val Asn Leu His Glu Arg
        30                  35                  40
Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg Arg Leu Val Val Ser
    45                  50                  55
Leu Gly Thr Val Asp Val Leu Lys Gln His Arg
60                  65                  70
```

<210> 988
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 988

```
Met Ala His Cys Ser Leu Glu Leu Leu Gly Ser Ser Ser Pro Pro Ile
            -15                 -10                 -5
Ser Ala Ser Gln Ser Thr Gly Ile Thr Ser Val Ser
        1               5                   10

<210> 989
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 989
Met Pro Ser Gln Leu Leu Leu Leu Ser Leu Ser Leu Phe Leu Phe Phe
        -15                 -10                 -5
Trp Arg Gln Ser Leu Val Leu Trp Pro Arg Leu Glu Cys Ser Cys Val
    1               5                   10                  15
Ile Ala Ala His Cys Ser Leu Thr Ser Gln Ala Arg
                20                  25

<210> 990
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 990
Met Tyr Thr Asn Lys Tyr Thr Leu Ile Tyr Asn Ile Leu Ile Tyr Asn
    -45                 -40                 -35
Ile Cys Xaa Xaa Tyr Met Trp Leu Ile Leu Ile Tyr Met Tyr Leu His
-30                 -25                 -20                 -15
Ile Cys Leu Phe Cys Cys Xaa Phe Ile Ser Ser Cys Asn Ser Val Phe
                -10                 -5                  1
Pro Cys Val Ile Xaa Phe Leu Leu Pro Glu Glu Leu Leu Xaa Val Xaa
        5                   10                  15
Leu Xaa Xaa Xaa Phe Xaa Val Arg Trp Ser Leu Xaa Xaa Ser Ser Arg
    20                  25                  30
Leu Glu Cys
35

<210> 991
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 991
Met Leu Leu Thr His Asn Glu Asp Tyr Met Pro Gly Asn Xaa Xaa Xaa
    -30                 -25                 -20
Xaa Xaa Leu Trp Ser Leu Ile Gln Ala Val His Ile Cys Leu Gly Arg
-15                 -10                 -5                  1
Lys Lys Lys

<210> 992
<211> 89
```

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 992
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Ile Lys Gly
-15 -10 -5
Val Gln Cys Gln Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys
1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe
15 20 25
Ser Asp Tyr Xaa Xaa Thr Xaa Ile Arg Xaa Ala Xaa Gly Lys Gly Leu
30 35 40 45
Xaa Trp Ile Xaa Xaa Ile Thr Thr Ser Gly Asn Thr Ala Xaa Tyr Ala
50 55 60
Xaa Ser Val Lys Xaa Arg Phe Thr Ile
65 70

<210> 993
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 993
Met Lys Arg Phe Phe Leu Phe Val Cys Leu Xaa Phe Asp Glu Ser Cys
-15 -10 -5
Ser Val Thr Arg Leu Gly Cys Cys Gly Ala Ile Ser Ala His Cys Xaa
1 5 10 15
Leu Arg Leu Pro Gly Ser Ser Xaa Xaa Pro Ala Ser Thr Ser Arg Val
20 25 30
Xaa Gly Ile Thr Gly Met Arg
35

<210> 994
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 994
Met Ser Cys His Ser Leu Leu Ala Cys Lys Val Phe Thr Glu Lys Ser
-35 -30 -25
Pro Thr Lys His Ile Arg Glu His His Cys Met Leu Phe Val Ser Phe
-20 -15 -10
Leu Leu Leu Leu Leu Gly Ser Arg
-5 1

<210> 995
<211> 50
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -26..-1

<400> 995
Met Thr Ser Ser Val His Leu Leu Val Phe Lys Asp His Leu Leu Ser
    -25                 -20                 -15
Met Leu Ser Cys Cys Gln Gly Ala Cys Cys Pro Ser Thr Pro His Glu
-10                 -5                  1               5
Gly Thr Arg Ser Thr Val Ser Trp Ile Pro Pro Thr Tyr Lys Ala Ala
            10                  15                  20
Thr Gln

<210> 996
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 996
Met Val Arg Ala Ser Ile Leu Leu Ser Met Phe Cys Val Ser His Thr
                -15                 -10                 -5
Val Gln Thr Ala Thr Tyr Thr
            1

<210> 997
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 997
Met Glu Lys Thr Ala Leu Ser Ser Phe Thr Trp Trp Ala Pro Ala Cys
        -15                 -10                 -5
Cys Ala Pro Arg Thr Tyr Val Val Ser Ala Thr Thr Leu Ser Ala Val
    1               5                   10                  15
Gln Gly His Cys Pro Leu Gln Ser Arg Thr Ser Thr Lys Gly Lys Leu
                20                  25                  30
Trp Pro Phe Gly
            35

<210> 998
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 998
Met Ile Phe Thr Phe Gln Gln Ile Gly Gly Lys Leu Leu Leu Ser Gly
            -20                 -15                 -10
Leu Thr Gln Glu Cys Leu Gly Ala Leu Pro Glu Ala Asn Val Phe Cys
        -5                  1               5
Arg Gly Gly Cys Thr Ala Thr Val Leu Lys His Gly Lys Ala Ser Pro
10                  15                  20                  25
Glu Ser

<210> 999
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 999
```
Met Asn Cys Val Arg Gln Ala Asn Ile Arg Met Gln Cys Lys Ile Tyr
    -30                 -25                 -20
Asp Ser Leu Leu Ala Leu Ser Pro Asp Leu Gln Ala Ala Arg Gly Leu
-15                 -10                 -5                  1
Met Cys Ala Ala Ser Val Met Ser Phe Leu Ala Phe Met Met
            5                   10                  15
```

<210> 1000
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1000
```
Met Ile Trp Leu Ser Phe Cys Leu Leu Leu Val Tyr Arg Asn Ala Cys
-40                 -35                 -30                 -25
Asp Phe Cys Thr Leu Thr Leu Tyr Pro Gly Thr Leu Leu Lys Leu Leu
                -20                 -15                 -10
Ile Ser Leu Arg Ser Phe Trp Ala Glu Thr Thr Gly
            -5                  1
```

<210> 1001
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1001
```
Met Phe Ser Ser Pro Gly Leu Arg Thr Leu Phe Val Leu Val Gly Ser
-25                 -20                 -15                 -10
Leu His Leu Phe Leu Ser Val Leu Ala Ser Lys Ser Arg Asn Ser Lys
                -5                  1                   5
Lys Gln Arg Leu Phe Leu Leu Val Pro Leu Tyr
        10                  15
```

<210> 1002
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1002
```
Met Leu Thr Asp Gly Ile Leu Met Arg Val Asn Val Cys Ser Leu Pro
```

-20 -15 -10
Ala Pro Gly Leu Cys Ser Gly Gln Pro Gly Val Arg Ala Trp Pro Gly
-5 1 5
Val Thr Gln Leu Thr Gln Xaa Glu Glu Cys Pro Trp Phe Ser Ala Leu
10 15 20 25
Glu Gly Leu

<210> 1003
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1003
Met Phe Asn Trp Asn Pro Trp Leu Thr Thr Leu Ile Thr Gly Xaa Ala
-30 -25 -20
Gly Pro Leu Leu Ile Leu Leu Leu Ser Leu Ile Phe Gly Pro Cys Ile
-15 -10 -5
Leu Asn Ser Phe Leu Asn Xaa Ile Lys Gln Arg Ile Ala Ser Gly Lys
1 5 10 15
Arg

<210> 1004
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1004
Met Ala Gly Ser Arg Gln Arg Gly Leu Arg Ala Arg Val Arg Pro Leu
-25 -20 -15
Phe Cys Ala Leu Leu Leu Ser Leu Xaa Xaa Xaa Xaa Pro Xaa Xaa Arg
-10 -5 1
Arg Xaa Arg Arg Pro Arg Gly Arg Val Ala Thr Ser Pro Phe Arg Val
5 10 15
Xaa Ile Gln Leu Gln Gly Ala Ala Pro Gly Ala Glu Arg Arg Asp Arg
20 25 30 35
Ala Leu Leu Gly Pro Arg Gly Glu Cys Tyr Ser Lys Phe Arg Ser Asn
40 45 50
Ser Ser Ser Thr Ile Phe Lys Lys Xaa Lys Arg Leu Ser Val Xaa Xaa
55 60 65
Asp Xaa Ser Gly Pro Gly
70

<210> 1005
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1005
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
-15 -10 -5
Val His Cys Asp Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln

1 5 10
Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Leu Thr Leu
15 20 25
Ser Asn Asp Trp Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30 35 40 45
Val Trp Val Ser His Ile Asp Ser Ser Xaa Thr Ile Thr Asn Tyr Ala
50 55 60
Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Trp
65 70 75

<210> 1006
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1006
Met Gly Leu Phe Leu Gly Phe Leu Ala Cys Ser Val Ala Tyr Gln Cys
-15 -10 -5 1
His Ser Ala Phe Val Thr Val Ala Ser Gln Tyr Thr Leu Lys Ser Glu
5 10 15
Thr Leu Met Pro Ala Ala
20

<210> 1007
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 1007
Met Trp Glu Asp Ser Arg Asn Lys Arg Gly Gly Arg Trp Leu Val Ser
-45 -40 -35
Leu Ala Lys Gln Gln Arg His Ile Glu Leu Asp Arg Leu Trp Leu Glu
-30 -25 -20
Thr Phe Ser Val Phe Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala Thr
-15 -10 -5
Gly Ile Leu Ala Phe Val Phe Lys Asp Trp Ile Arg Asp Gln Leu Asn
1 5 10 15
Leu Phe Ile Asn Asn Asn Val Lys Ala Tyr Arg Asp Asp Ile Asp Leu
20 25 30
Gln Xaa Leu Ile Asp Phe Ala Gln Glu Tyr Trp Ser Cys Cys Gly Xaa
35 40 45
Glu Ala Pro Ile Xaa Gly Thr Gly
50 55

<210> 1008
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1008
Met Phe Leu Ser Leu Ser Thr Ala Phe Trp Val Val Tyr Ala Met Ile

```
                -10                  -5                 1
Ile Tyr Ser Ala Leu Ser Ala Gly Phe Ile Ile Phe Phe Leu Val Val
        5                   10                  15
Phe Asn
    20

<210> 1009
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1009
Met Tyr Ile Val Met Asp Leu Pro Leu Trp Leu Ser His Glu Val Gln
                -30                 -25                 -20
Ser Tyr Ile Pro Ser Phe Phe Leu Phe Phe Cys Phe Glu Thr Gly Ser
            -15                 -10                 -5
His Ser Val Thr His Gly
        1

<210> 1010
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1010
Met Val Ala His Asp Tyr Gln Asn Ile Ile Ser Leu Phe Phe Leu Ala
        -25                 -20                 -15
Phe Ser Phe Ser Phe Phe Pro Ser Ser Phe Ser Ser Phe Phe Leu Xaa
    -10                 -5                  1               5
Phe Leu Ser Phe Phe Ser Ser Phe Phe Leu Ser Leu Leu Ser Phe Pro
                10                  15                  20
Ser Phe Leu Pro Pro Gly
            25

<210> 1011
<211> 136
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1011
Met Ala Ala Leu Arg Ala Leu Cys Gly Phe Arg Gly Val Ala Ala Gln
-15                 -10                 -5                  1
Val Leu Arg Xaa Gly Ala Gly Val Arg Leu Pro Ile Gln Pro Ser Arg
            5                   10                  15
Gly Val Arg Gln Trp Gln Pro Asp Val Glu Trp Ala Gln Gln Phe Gly
        20                  25                  30
Gly Ala Val Met Tyr Pro Ser Lys Glu Thr Ala His Trp Lys Pro Pro
    35                  40                  45
Pro Trp Asn Asp Val Asp Pro Pro Lys Asp Thr Ile Val Lys Asn Ile
50                  55                  60                  65
Thr Leu Asn Phe Gly Pro Gln His Pro Ala Ala His Gly Val Leu Arg
```

```
                70                  75                  80
Leu Val Met Glu Leu Ser Gly Glu Met Val Arg Lys Cys Asp Pro His
            85                  90                  95
Ile Gly Leu Leu His Arg Gly Thr Glu Lys Leu Ile Glu Tyr Lys Xaa
        100                 105                 110
Tyr Leu Gln Ala Leu Pro Tyr Phe
    115                 120

<210> 1012
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1012
Met Leu Ile Trp Ser Ser Ser Ser Phe Pro Ala Pro Pro Leu Phe Leu
            -25                 -20                 -15
Val Phe Leu His Leu Phe Leu Xaa Val Tyr Leu Gly Leu Val Met Pro
        -10                 -5                  1
Thr Gln Gln Tyr Leu Leu Leu Gln Ser Pro Leu Met Phe Thr Asp Lys
5                   10                  15                  20
Ala Gln

<210> 1013
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 1013
Met Cys Arg Met Cys Arg Phe Val Thr Trp Ile Asn Val Cys His Gly
    -45                 -40                 -35
Asp Leu Leu His Arg Ser Ser Arg Arg Leu Gly Val Lys Pro Ser Thr
-30                 -25                 -20                 -15
His Trp Leu Phe Phe Leu Met Leu Ser Leu Cys Thr Pro Pro Asp Arg
                -10                 -5                  1
Pro Trp Cys Val Leu Phe Pro Pro Leu
        5                   10

<210> 1014
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1014
Met Xaa Thr Gln Glu Ala Gly Leu Ile Phe Phe Ser Pro Pro Phe Ser
    -30                 -25                 -20
Leu Ser Leu Ser Leu Ser Leu Pro Leu Ser Leu Xaa Leu Leu Xaa Xaa
-15                 -10                 -5                  1
Pro His Ser Arg Thr Pro Gln Arg
        5

<210> 1015
```

<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1015
```
Met Glu Phe Leu Leu Leu Trp Ser Leu Xaa Ser Asn Gly Lys Arg Gly
            -10                 -5                  1
Gln Ala Trp Arg Leu Met Pro Val Val Pro Ala Val Trp Glu Pro Glu
    5                   10                  15
Ala Gly Gly Leu Leu Gln Leu Gly Gly Ser Arg
20                  25                  30
```

<210> 1016
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1016
```
Met Met Val Thr Tyr Arg Trp Gly Phe Gly Val Asp Val Xaa Phe Val
        -35                 -30                 -25
Ala Val Asp Ala Ile Pro Phe Cys Leu Leu Val Phe Phe Leu Ile Val
    -20                 -15                 -10
Arg Thr Leu Ser Cys Arg Ser Val Gly Val Cys Trp Arg Ser Thr Pro
-5                  1               5                   10
Asp Pro Val Cys Leu Gly Ile Thr Ser Arg Gly Cys Arg Thr Glu Ile
            15                  20                  25
Leu Gln Asn Ser Lys Cys Cys Ser Leu Ile Leu Pro Leu Glu Ala Ser
        30                  35                  40
Ser Gln Arg Gly Thr Glu Cys Met
    45                  50
```

<210> 1017
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1017
```
Met Leu Tyr Pro Leu Pro Glu Ile Phe Leu Pro Phe Ser Leu Ser Pro
                -15                 -10                 -5
Ala Asn Ala Gln Ser Lys Phe Ser Leu Tyr Phe Phe Pro Leu Val Lys
            1                   5                   10
Pro Gly
    15
```

<210> 1018
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -27..-1

<400> 1018
Met Ser Leu Glu Pro Ala Ser Xaa Leu Leu Gly Val Arg Arg Arg Leu
        -25                 -20                 -15
Leu Cys Leu Xaa Phe Xaa Arg Leu Leu Leu Gly Thr Ser Leu Leu Lys
    -10                 -5                  1               5
Phe Val Xaa Ser Xaa Ser Pro Pro Xaa Pro Xaa Thr Leu Thr Ser Ser
                10                  15                  20

<210> 1019
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1019
Met Leu Ile Leu Tyr Leu Ala Thr Leu Leu Asn Leu Ser Val Leu Ile
                -20                 -15                 -10
Leu Cys Val Cys Val Cys Val Cys Val Tyr Asp Leu Tyr Ile Xaa Arg
            -5                  1                   5
Gly

<210> 1020
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1020
Met Ala Pro Leu Gly Thr Thr Val Leu Leu Trp Ser Leu Leu Arg Ser
    -15                 -10                 -5
Ser Pro Gly Val Glu Arg Val Cys Phe Arg Ala Arg Ile Gln Pro Trp
1               5                   10                  15
His Gly Gly Leu Leu Gln Pro Leu Pro Cys Ser Phe Glu Met Gly Leu
            20                  25                  30
Pro Arg Arg Arg Phe Ser Ser Glu Ala Ala Glu Ser Gly Ser Pro Glu
        35                  40                  45
Thr Lys Lys Pro Thr Phe Met Asp Glu Glu Val Gln Ser Ile Leu Thr
    50                  55                  60
Lys Met Thr Gly Leu Asn Leu Gln Lys Thr Phe Lys Pro Ala Ile Gln
65                  70                  75                  80
Glu Leu Lys Pro Pro Thr Tyr Lys Leu Met Xaa Gln Ala Gln Leu Glu
                85                  90                  95
Glu Ala Thr Arg Gln
            100

<210> 1021
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1021

```
Met Leu Leu Thr Phe Ser Ser Ser Ser Arg His Arg Arg Leu Tyr Arg
                -30                 -25                 -20
Arg Arg Arg His His Leu Leu Phe Val Val Leu Leu Pro Pro Pro Pro
            -15                 -10                 -5
Gly Ser Val Xaa Leu Cys Ser Xaa Xaa Xaa Xaa Xaa Val Leu Xaa Xaa
        1               5                   10
Xaa Lys Phe Arg Xaa Gly Leu His Gly Ala Met Leu Pro Gly Leu Phe
15                  20                  25                  30
Arg Gly Arg Pro Arg Ala Ala Leu Arg Leu Arg Val Ser Pro Xaa Cys
                35                  40                  45
Pro Gly Trp Lys Val Ala Arg Ser Arg Leu Thr Ala Thr Ser Ala Ser
            50                  55                  60
Arg Xaa Arg
        65
```

<210> 1022
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1022

```
Met Leu Leu Leu Leu Gln Leu Asn Leu Lys Thr Leu Ser Ser Ser Thr
            -10                 -5                  1
Ile Ala Leu Lys Lys Ile Ser Gly Glu Leu Leu Arg Lys Arg Lys Arg
    5                   10                  15
```

<210> 1023
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1023

```
Met Ser Leu Phe Val Leu Leu Ile Ile Thr Gln Leu Leu Tyr Gly Gly
-15                 -10                 -5                  1
Ile Leu
```

<210> 1024
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1024

```
Met Asn Cys Phe Cys Asn Phe Val Lys Thr Ser Glu Ala Tyr Met Ile
            -25                 -20                 -15
Leu Phe Leu Gly Val Leu Leu Ser Ala Ser Asp Leu Cys Val Tyr Pro
        -10                 -5                  1
Ile Gly
5
```

<210> 1025
<211> 33

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1025
Met Ser Val Ile Leu Ala Leu Trp Glu Ala Glu Ala Gly Gly Ser Pro
-10 -5 1
Glu Ile Gly Ser Ser Gly Pro Ala Ala Pro Thr Trp Arg Ser Pro Val
5 10 15
Gln

<210> 1026
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1026
Met Tyr Gly Glu Ser Thr Leu Phe Ile His Ser Ser Val His Gly His
-25 -20 -15
Leu Gly Cys Leu Leu Leu Ala Val Arg Ser Ser Ala Thr Val Asn Ile
-10 -5 1
Thr Tyr Xaa Xaa Val Cys Val Asp Ile Xaa Xaa His Phe His Met Leu
5 10 15
Met Ser Gly Ile Thr Gly Ser Tyr Gly Asn Ser Leu Ser
20 25 30

<210> 1027
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1027
Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro Met Leu
-50 -45 -40
Ser Leu Phe Arg Gly Ser His Arg Val Gln Val Thr Leu Arg Lys Thr
-35 -30 -25 -20
Phe Cys Thr Thr Ser Ser Trp Leu Tyr Leu Leu Glu Val Val Ala Pro
-15 -10 -5
Leu Ser Gly Ile His Glu Trp Arg Pro Ser His Val Cys Leu Ser Cys
1 5 10
Leu Gly Ser Thr Ser Cys Asn Pro Pro Glu
15 20

<210> 1028
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -65..-1

<400> 1028
Met Leu Arg Ser Ala Cys Val Ser Gln His Ala Gly Gly Ile Trp Val
-65 -60 -55 -50
Asp Arg Gly Gly Pro Gln Cys Gln Arg Val Phe Thr Phe Cys Arg Gly
-45 -40 -35
Leu Ser Pro Asn Phe Gly Arg Ser Glu Thr Gln Arg Glu Arg Trp Ile
-30 -25 -20
Arg Pro Gly Gln Leu Met Val Val Ala Glu Thr Ser Gln Gly Ser Trp
-15 -10 -5
Ser Ala Pro Thr Ser Pro Xaa Thr Ser Cys Pro Pro Pro Asn Thr Xaa
1 5 10 15
Thr Thr Pro Xaa

<210> 1029
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1029
Met Val Ser Arg Ser Leu Arg Gly Arg Arg Thr Trp Val Arg Cys Met
-45 -40 -35 -30
Arg Arg Leu Pro Pro Ile Pro Ala Trp Ser Gln Gly Lys Gly Met Pro
-25 -20 -15
Gly Phe Val Ser Leu Leu Val Val His Ala Ala Asp Ala Trp Val Ala
-10 -5 1
Gln Arg Leu Ser Thr Pro Tyr Phe Ser Leu Phe Leu Ser Ile Pro Arg
5 10 15
Cys Ser Phe Pro Arg Arg Ser Ile Asp Arg Thr Cys Ser Ser Xaa Leu
20 25 30 35
Asp Ser Glu Gly Ser Ser Ser Ile Xaa Pro Ser Thr Pro Phe
40 45

<210> 1030
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1030
Met Val Gly Ala Leu Pro Pro Ala Ser Leu Leu Pro Cys Ser Leu Ile
-20 -15 -10
Ser Asp Cys Cys Ala Ser Asn Glu Arg Gly Ser Met Gly Val Gly Pro
-5 1 5 10
Ser Glu Pro Arg Arg Gly
15

<210> 1031
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1031

```
Met Arg Met Thr Lys Asp Pro Leu Gly Ser Leu Ile Ala Ser Leu Ala
-20                 -15                 -10                 -5
Pro Ser Thr Gly Leu Gly
                1

<210> 1032
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1032
Met Lys Leu Gln Phe Ala Phe Cys Tyr Phe Leu Tyr Leu Asp Thr Phe
            -25                 -20                 -15
Phe Leu Phe Leu Phe Phe Xaa Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly
        -10                 -5                  1
Arg Ser Ala Val Ala Xaa Pro Gln Leu Xaa Ala Ala Ser Thr Phe Xaa
5                   10                  15                  20
Phe Gln Ala Ile Phe Leu Pro Gln Xaa
                25

<210> 1033
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69..-1

<400> 1033
Met Ala Ala Gly Glu Leu Glu Gly Gly Lys Pro Leu Ser Gly Leu Leu
                -65                 -60                 -55
Asn Ala Leu Ala Gln Asp Thr Phe His Gly Tyr Pro Gly Ile Thr Glu
            -50                 -45                 -40
Glu Leu Leu Arg Ser Gln Leu Tyr Pro Glu Val Pro Pro Glu Glu Phe
        -35                 -30                 -25
His Pro Phe Leu Ala Lys Met Arg Gly Ile Leu Lys Val Leu Leu Phe
    -20                 -15                 -10
Ser Val Val Ser Gly Leu Glu Gln Asn Pro Leu Ala Ala Gly Phe Arg
-5                  1                   5                   10
Leu Ser His Pro
            15

<210> 1034
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1034
Met Met Met Ser Asn Val Met Leu Met Leu Gln Leu Gln Pro Leu Leu
    -30                 -25                 -20
Ala Xaa Ser Leu Ile Leu Ser Pro Ser Pro Arg Pro Val Leu Gly Phe
-15                 -10                 -5                  1
Phe Arg Gln Val His Leu Leu Thr Arg Ser His Phe Ser Arg Trp
            5                   10                  15
```

<210> 1035
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1035
```
Met Ile Ile Leu Ile Asn Gln Leu Leu Phe Ile Cys Pro Pro Pro Pro
-20                 -15                 -10                 -5
Pro Ile Ser Ala Ser Ser Asn Tyr His Phe Thr Leu Tyr Leu His Asp
                1               5                   10
Ile Asn Phe Phe Ser
        15
```

<210> 1036
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1036
```
Met Thr Asp Val Leu Leu Gln Leu Leu Leu Arg Val Cys Ser Pro Arg
-15                 -10                 -5                  1
Thr Arg
```

<210> 1037
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1037
```
Met Gly Leu Phe Leu Cys Cys Ser Leu Leu Ile Phe Cys Leu Val Val
            -10                 -5                  1
Leu Ile Ile Thr Glu Leu Gly Tyr Gly
    5                   10
```

<210> 1038
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1038
```
Met Gly Ser Trp Ala Leu Thr Trp Leu His Pro Ala Glu Ala Gly Thr
                -10                 -5                  1
Arg Val Pro Phe Cys Ser Trp Glu Lys Ser Asp Gly Arg Ser
        5                   10                  15
```

<210> 1039

<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1039
Met Met Leu Xaa Xaa Xaa Arg Gly Tyr Pro His Arg Thr Glu Arg Tyr
-40 -35 -30
Asp Gly Phe Leu Lys Tyr Ser Asp Pro Asn Asp Ile Ala Leu Ser Val
-25 -20 -15
Leu Ser Leu Val Ile Asn Phe Ser Trp Ser Arg Lys Cys Phe Val Pro
-10 -5 1 5
Tyr Tyr Ile Pro Phe Lys Pro Tyr Arg Xaa Pro Tyr Pro Thr Ala Ala
10 15 20
Arg

<210> 1040
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1040
Met Tyr Val Cys Ile Tyr Ile Xaa Leu Xaa Asp Leu Tyr Asp Phe Phe
-35 -30 -25
Leu Leu Gly Thr Tyr Phe Phe Glu Arg Lys Cys Phe Val Cys Xaa Leu
-20 -15 -10
Phe Val Phe Leu Leu Ser Gly Leu Asn Tyr Phe Ser Ile Leu Ser Phe
-5 1 5
Tyr Pro Arg
10

<210> 1041
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1041
Met Cys Ile Phe Cys Leu Phe His Leu Leu Tyr His Lys Leu Leu Ser
-40 -35 -30 -25
Arg Ser Leu Phe Phe Cys Cys Ile Phe Ser Gly Phe Ile Thr Phe Ile
-20 -15 -10
Phe Ser Phe Ser Phe Cys Glu Cys Ile Val Gly Met Tyr Ile Tyr Gly
-5 1 5
Ala Arg
10

<210> 1042
<211> 40
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -27..-1

<400> 1042
Met Xaa Ile Cys Tyr Asn Ile Phe Gln Asn Ile Leu Gly Leu Leu Leu
        -25                 -20                 -15
Ile Phe Leu Tyr Leu Ser Leu Asn Leu Phe Cys Ile Phe Phe Ser Val
    -10                 -5                  1                   5
Pro Ala Leu Gln Pro Arg Arg Leu
                10

<210> 1043
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1043
Met Ala Ser Ser Met Leu Xaa Ser Phe Gln Thr Phe Met Met Leu Thr
    -25                 -20                 -15
Leu Leu Gly Phe Pro Ser Lys Ala Leu Thr Phe Ile Ser
-10                 -5                  1

<210> 1044
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1044
Met Gly Arg Ser Lys Arg Gln Leu Leu Ser Leu Pro Gly Ser Phe Ile
-20                 -15                 -10                 -5
Pro Gly Asn Cys Arg Pro Arg Ile Leu Ser Asn Gly Glu Xaa Arg Arg
                1                   5                   10
Lys

<210> 1045
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1045
Met Arg Ser Asp Gly Phe Ile Arg Gly Phe Cys Phe Cys Phe Phe Leu
-25                 -20                 -15                 -10
Ile Phe Leu Leu Pro Pro Leu Pro Ala Met Ile Leu Arg Pro Leu Gln
                -5                  1                   5
Pro Cys Gly Ile Ile Ser Pro Ile Lys Pro Leu Phe Pro Phe Phe Phe
        10                  15                  20

<210> 1046
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1046
Met Asn Thr Leu Trp Thr Ala Ser Ser Leu Pro Leu Ser Thr His Ser
-15 -10 -5
Gln Arg Thr Met Ile His Trp Asn Val Phe Leu Trp Asn Ser Phe Tyr
1 5 10 15
Ser Cys Ile Lys Ile Phe Pro
20

<210> 1047
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1047
Met Thr Trp Thr Lys Cys Pro Leu Pro Leu Gly Pro Ala Phe Phe Thr
-30 -25 -20
Gln Cys Cys Leu Ile Gly Leu Leu Val Pro Leu Leu Gly Trp Gly Asn
-15 -10 -5 1
Gln Asn Thr Gln Trp Tyr Pro Thr Ser Lys Met Pro Asp Gly
5 10 15

<210> 1048
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1048
Met Gly Arg Ser Asn Asp Phe Arg Phe Ala Phe Leu Thr Cys Phe Leu
-30 -25 -20
Gly Trp Glu Ile Val Tyr Phe Leu Val Leu Leu Arg Val Leu Tyr Thr
-15 -10 -5
Leu Gln Trp Gly Gly
1 5

<210> 1049
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1049
Met Lys Thr Asp Asn Leu Thr Ser Phe Leu Thr Tyr Met Pro Leu Ile
-15 -10 -5
Ser Ser Ser Cys Ser Ile Ala Pro
1 5

<210> 1050

<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -79..-1

<400> 1050
Met Arg Phe Arg Phe Cys Gly Asp Leu Asp Cys Pro Asp Trp Val Leu
-75 -70 -65
Ala Glu Ile Ser Thr Leu Ala Lys Met Ser Ser Val Lys Leu Arg Leu
-60 -55 -50
Leu Cys Ser Gln Val Leu Lys Glu Leu Leu Gly Gln Gly Ile Asp Tyr
-45 -40 -35
Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe Glu Ser Gly Asp
-30 -25 -20
Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu Ser Ser Ala Ala
-15 -10 -5 1
Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu Leu Gln Gln Leu
5 10 15
Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg Cys Tyr Glu Glu
20 25 30
Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys Ser Leu Arg Met
35 40 45
Asn Arg
50

<210> 1051
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1051
Met Phe Leu Ala Ala Leu Phe Thr Val Ala Lys Ile Trp Lys Gln Pro
-10 -5 1
Lys Cys Ser Ser Thr Asn Lys Trp Thr Lys Lys Met Trp Tyr Ile Tyr
5 10 15
Thr Met Glu Tyr Tyr Ser Ala Ile Lys Lys Asp Asp Ile Leu Ser Phe
20 25 30
Ala Thr Ile Trp Met Glu Leu Glu Ser Ile Thr Leu Ser Glu Ile Ser
35 40 45 50
Gly Xaa Pro Lys Asp Lys Leu Leu Met Phe Ser Leu Ile Cys Gly
55 60 65

<210> 1052
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1052
Met Glu Ser Ser Thr Phe Ala Leu Val Pro Val Phe Ala His Leu Ser
-25 -20 -15
Ile Leu Gln Ser Leu Val Pro Ala Ala Gly Ala Xaa Ser Pro
-10 -5 1

<210> 1053
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -78..-1

<400> 1053
```
Met Gly Cys Leu Leu Ala Ser Glu Tyr Pro Leu Ser Glu Pro Trp Ala
            -75                 -70                 -65
Pro Gly Pro Phe Thr Gln Tyr Leu Val Asp His His His Thr Leu Leu
        -60                 -55                 -50
Cys Asn Gly Tyr Trp Leu Ala Trp Leu Ile His Val Gly Glu Ser Leu
    -45                 -40                 -35
Tyr Ala Ile Val Leu Cys Lys His Lys Gly Ile Thr Ser Gly Arg Ala
-30                 -25                 -20                 -15
Gln Leu Leu Trp Phe Leu Gln Thr Phe Phe Phe Gly Ile Ala Ser Leu
                -10                 -5                  1
Xaa Ile Leu Ile
        5
```

<210> 1054
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1054
```
Met Cys Cys Trp Ile Trp Val Ala Ser Ile Leu Leu Arg Ile Phe Ala
    -15                 -10                 -5
Ser Val Leu Ile Arg Asp Ile Tyr Leu Trp Phe Ser Phe Phe Phe Phe
1               5                   10                  15
```

<210> 1055
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1055
```
Met Ile Ser Ser His Leu Tyr Asn Phe Ser Leu Leu Phe Phe Xaa Leu
            -20                 -15                 -10
Trp Leu Arg Tyr Lys Glu Ser Gly Arg Glu Gly Asn Cys Glu Glu Gly
        -5                  1                   5
Ala Phe Ser Arg Trp
10
```

<210> 1056
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -17..-1

<400> 1056
Met Gly Trp Gln Arg Leu Leu Leu Leu Pro Arg Pro Pro Ala Ser Thr
-15 -10 -5
Gly Ala Ser Asn Ala Thr Arg Xaa Pro Lys Xaa Leu Tyr Arg Xaa Tyr
1 5 10 15
Asn His Gly Val Leu Lys Ile Thr Ile Cys Lys Ser Cys Gln Lys Pro
20 25 30
Val Asp Lys Tyr Ile Glu Tyr Asp Pro Val Ile Ile Leu Xaa Asn Ala
35 40 45
Ile Leu Cys Lys Ala Xaa Ala Tyr Arg His Ile Leu Phe Asn Thr Gln
50 55 60
Ile Asn Asn Lys Leu Pro Ile Leu Leu Ala Phe Leu Pro Ser Cys Gly
65 70 75
Xaa Thr Ala His Asp Gly Lys Lys Lys Pro Asn Phe Ile Leu Leu Leu
80 85 90 95
Lys Xaa Tyr Tyr Tyr Leu Ala Thr Glu Asn
100 105

<210> 1057
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1057
Met Ala Ala Gly Val Ser Leu Leu Ala Leu Val Val Arg Val Ile Leu
-15 -10 -5
Ser Thr Ala Ile Leu Cys Pro Ser Gly Ala Ser Arg Arg Gln Arg Ser
1 5 10
Ser Glu Val Glu Trp Gly Thr Asp Ser
15 20

<210> 1058
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1058
Met Asn Pro Leu Phe Trp Leu Ile Leu Cys Ser Gly Leu Leu Cys Asn
-15 -10 -5 1
Lys Ser Phe

<210> 1059
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1059
Met Arg Gly Ala Trp Ile Ser Ile Phe Leu Ser Ser Leu Ser Leu Ser
-15 -10 -5

```
Leu Ser Leu Phe
        1

<210> 1060
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1060
Met Ser Gln Lys Arg Leu Asp Phe Ile Tyr Gln Leu Phe Val Leu Leu
                -20                 -15                 -10
Pro His Phe Phe Leu Ser Phe Leu Ser Pro Phe Tyr Leu His Pro Trp
            -5                  1               5

<210> 1061
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1061
Met Tyr Leu Tyr Leu Leu Ser Ile Cys Met Ser Ser Leu Lys Lys Cys
            -30                 -25                 -20
Leu Phe Lys Phe Leu Ala His Phe Leu Ile Gly Leu Thr Val Cys Phe
        -15                 -10                 -5
Gly Glu Gly Xaa Leu Met Ser Tyr Arg Ser Ser Tyr Leu Leu Leu Lys
    1               5                   10                  15
Gly Pro Pro Gly

<210> 1062
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1062
Met Gly Phe Trp Cys Glu Cys Pro Phe Cys Leu Leu Val Phe Leu Leu
        -20                 -15                 -10
Thr Glu Trp Thr Ser Ser Lys Leu Gln Lys Thr
    -5                  1               5

<210> 1063
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1063
Met Trp Trp Gly Arg Cys Phe Ile Arg Val Leu His Leu Phe Pro Leu
        -20                 -15                 -10
```

Thr Pro Ala Ser Thr Gly His Trp
    -5                  1

<210> 1064
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1064
Met Arg Asp Pro Leu Ala Asp Met Val His Ser Tyr Leu Ser Ser Ser
                -25                 -20                 -15
Leu Phe Met Ala Leu Pro Pro Val Leu Ser Ser His Gly Ser Arg Asn
            -10                 -5                  1
Leu Arg Ile Trp Gly Ser Pro Phe Gly Gly Ala Leu Thr Lys Gly Lys
    5                   10                  15
Ala Pro Pro Thr Pro Ala Gln Pro Ala Leu
20                  25

<210> 1065
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1065
Met Ser Ser Ala Trp Leu Cys Leu Pro Cys Ser Leu Cys Val Ser Gln
        -15                 -10                 -5
Leu Leu Pro Ser Tyr Ser Leu Leu Ile Pro Ala Pro
    1               5                   10

<210> 1066
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1066
Met Ser Pro Met Trp Ala Gly Leu Leu Ser Leu Leu Gly Pro Leu Xaa
    -20                 -15                 -10
Pro Pro Met Arg Ala Cys Ser Val Cys Val Leu
-5                  1               5

<210> 1067
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1067
Met Ser Leu Asn Glu Leu Ser Ile Ala Asp Leu Leu Pro Ser Ser Ser

```
            -15                 -10                 -5
Phe Ala Asn Pro Lys Leu Ser Gly Pro Ile Ser Ile Ser Val Thr Ser
        1               5                   10
Ala Gly Ser Pro Pro Gly Ala
15                  20

<210> 1068
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1068
Met Lys Asp Leu Leu Gly Thr Ala Phe Leu Glu Gly Ser Leu Ala Ala
-15                 -10                 -5                  1
Tyr Leu Thr Met Ala Asn Ile Thr His Val
            5                   10

<210> 1069
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1069
Met Ala Asn Asp Ile Lys His Leu Phe Met Cys Leu Leu Thr Ile Cys
                -15                 -10                 -5
Ile Ser Ser Leu Glu Lys Leu Pro Phe Phe Phe Phe Phe
            1               5                   10

<210> 1070
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1070
Met Tyr Gln Lys Val Thr Ser Tyr Cys Arg Ser Ala Thr Leu Val Gly
                -20                 -15                 -10
Phe Thr Val Gly Ser Val Leu Gly Gln Ile Leu Val Ser Val Ala Gly
            -5                  1                   5
Trp Ser Leu Phe Ser Leu Asn Val Ile Ser Leu Thr Cys Val Ser Val
    10                  15                  20
Ala Phe Ala Val Ala Trp Phe Leu Pro Met Pro Gln Lys Ser Leu Phe
25                  30                  35                  40
Phe His His Ile Pro Ser Thr Cys Gln Arg Val Asn Gly Ile Lys Val
                45                  50                  55
Gln Asn Gly Gly Ile Val Thr Asp Thr Gln Leu Leu Thr Pro Ser Trp
            60                  65                  70
Leu Gly

<210> 1071
<211> 19
<212> PRT
```

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1071
Met Met Pro Pro Ala Leu Phe Phe Leu Leu Arg Ile Ala Trp Leu Leu
-15 -10 -5
Gly Leu Phe
1

<210> 1072
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1072
Met Asn Cys Val Thr Leu Ile Gln Ala Leu Ser Leu Trp Ala Ser Val
-20 -15 -10
Ser Pro Ser Trp Met Cys Arg Pro Pro Ala Ser Phe Ile Ile Thr Thr
-5 1 5 10
Thr Thr Thr Thr Cys Gly
15

<210> 1073
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1073
Met Leu Ser Leu Leu Ser Leu Met Ala Arg Thr Asp Leu Val Phe Cys
-15 -10 -5
Ser Pro Arg
1

<210> 1074
<211> 255
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1074
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala
-30 -25 -20
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
-15 -10 -5
Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
1 5 10
Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro
15 20 25 30
Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys

```
                35                  40                  45
Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
            50                  55                  60
Val Met Met Lys Asn Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly
        65                  70                  75
Asn Ile Phe Met Phe Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg
    80                  85                  90
Leu Asp Ile Arg Met Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe
95                  100                 105                 110
Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Xaa
                115                 120                 125
Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg
            130                 135                 140
Val Thr Trp Ile Val Glu Phe Phe Ala Xaa Trp Ser Asn Asp Cys Gln
        145                 150                 155
Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr
    160                 165                 170
Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser
175                 180                 185                 190
Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr
                195                 200                 205
Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln
            210                 215                 220
```

<210> 1075
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1075

```
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
        -15                 -10                 -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
    1               5                   10                  15
Thr Gly Leu Thr Thr Ala Lys Met Pro Ser Val Pro Leu Ser Ser Asp
                20                  25                  30
Pro Leu Pro Thr His Thr Thr Ala Phe Ser Pro Ala Ser Thr Phe Glu
            35                  40                  45
Arg Glu Asn Asp Phe Ser Glu Thr Thr Thr Ser Leu Ser Pro Asp Asn
        50                  55                  60
Thr Ser Thr Gln Val Ser Pro Asp Ser Leu Asp Asn Ala Ser Ala Phe
    65                  70                  75
Xaa Thr Thr Gly Val Ser Ser Val Gln Thr Pro Xaa Leu Pro Thr His
80                  85                  90                  95
Ala Asp Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser
                100                 105                 110
Gly Ser Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu
            115                 120                 125
Ser Gln Met Ser Gln Glu Arg Gly Val
        130                 135
```

<210> 1076
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1076
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
        -15                 -10                 -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
    1               5                   10                  15
Thr Gly Val Ser Ser Val Gln Thr Pro Gln
                20                  25

<210> 1077
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1077
Met Thr Met Tyr Leu Trp Leu Lys Leu Leu Ala Phe Gly Phe Ala Phe
        -15                 -10                 -5
Leu Asp Thr Glu Val Phe Val Thr Gly Gln Ser Pro Thr Pro Ser Pro
    1               5                   10                  15
Thr Gly Val Ser Ser Val Gln Thr Pro His Leu Pro Thr His Ala Asp
                20                  25                  30
Ser Gln Thr Pro Ser Ala Gly Thr Asp Thr Gln Thr Phe Ser Gly Ser
            35                  40                  45
Ala Xaa Met Gln Asn Ser Thr Leu Pro Gln Ala Ala Met Leu Ser Gln
        50                  55                  60
Met Ser Gln Glu Arg Gly Val
    65                  70

<210> 1078
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1078
Met Arg Gly Ala Thr Trp Pro Trp Pro Cys Leu Pro Ala Arg Thr Ser
    -35                 -30                 -25
Thr Ala Ala Ser Ile Ala Arg Leu Phe Leu Leu Ser Gly Thr Ile Trp
-20                 -15                 -10                 -5
Ile Ala Ile Cys Lys Pro Thr Thr Asn Gly
                1                   5

<210> 1079
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -64..-1

<400> 1079
Met Gly Val Leu Pro Asp Leu Val Val Glu Ile Phe Gly Val Asn Lys
                -60                 -55                 -50
Cys Arg Leu Ser Trp Gly Leu Val Leu Glu Ser Leu Gln Gln Pro Leu
            -45                 -40                 -35

```
Ile Asn Arg His Leu Ile Tyr Cys Leu Gly Asp Ile Ile Leu Xaa Xaa
        -30                 -25                 -20
Leu Asp Leu Ser Ala Leu Leu Arg Ser Leu Leu Leu Pro Xaa Leu Xaa
    -15                 -10                 -5
Gln Ile Pro Gln Ala Thr Leu Arg
1               5
```

<210> 1080
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1080

```
Met Thr Ala Leu Gly Phe Val Leu Leu Ala Pro Arg Gly Trp Gly Ser
-15                 -10                 -5                  1
Leu Thr Val Met Val Glu Gly Lys Glu Glu Gln Val Thr Ser Tyr Thr
            5                   10                  15
Asp Gly Ser Arg Gln Arg Asp Ser Asn Phe
        20                  25
```

<210> 1081
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1081

```
Met Lys Arg Ile Arg Arg Lys Arg Arg Asn Glu Val Thr Ile Gln Pro
                -35                 -30                 -25
Phe Pro Ile Arg Leu Pro Leu Leu Pro Pro Leu Ile Ser Phe Leu His
            -20                 -15                 -10
Thr Leu Gln Val Val Cys Ser Val Ile Met Lys Ser Ile Arg Lys Ala
        -5                  1                   5
Phe Val Leu Cys Gly Phe Leu Tyr Phe Glu Phe Phe Asp Gln Lys Leu
10                  15                  20                  25
```

<210> 1082
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1082

```
Met Leu Pro Leu Leu His Cys Phe Phe Xaa Val Xaa Leu Phe Xaa Xaa
        -20                 -15                 -10
Val Xaa Val Xaa Xaa Ala Ala Leu Leu Arg Tyr Asn Xaa Ser Ile Gln
    -5                  1               5                   10
Xaa Gly Arg Ala Gln Xaa Leu Xaa Pro Xaa Ile Pro Xaa Leu Trp Glu
                15                  20                  25
Thr Lys Xaa Gly Arg Leu Leu Glu Pro Arg Asn
            30                  35
```

<210> 1083

<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1083
Met Val Ser Val Phe Arg Ser Glu Glu Met Cys Leu Ser Gln Leu Phe
    -20                 -15                 -10
Leu Gln Val Glu Ala Ala Tyr Cys Cys Val Ala Glu Leu Gly
-5                  1               5

<210> 1084
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1084
Met Ala Ala Leu Arg Ser Thr Leu Thr Trp Thr Glu Val Val Gly Trp
            -25                 -20                 -15
Trp Ser Val Ala Ser Leu Leu Ser Asp Val Ala Ala Trp Trp Pro Pro
        -10                 -5                  1
His Ser Thr Ser Thr Arg Gly Gly Val
5                   10

<210> 1085
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 1085
Met Asn Ala Leu Val Asp Gly Lys Arg Leu Xaa Xaa Cys Ile Arg Tyr
                -40                 -35                 -30
Phe Asp Ser Ile Ser Leu Tyr Ser Lys Ala Ser Leu Ser Cys Cys Leu
            -25                 -20                 -15
Val Cys Val Phe Thr Cys Ser Leu Leu Ala Phe Phe Ser Pro Cys
        -10                 -5                  1

<210> 1086
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1086
Met Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Leu Lys Gly
                -15                 -10                 -5
Val Gln Cys Glu Leu Gln Val Val Glu Ser Gly Gly Gly Leu Val Gln
            1                   5                   10
Pro Gly Arg Ser Leu Arg Leu Ser Cys Arg Thr Ser Gly Phe Ala Phe

```
    15                  20                  25
Asp Asp Tyr Asn Leu Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
30                  35                  40                  45
Glu Trp Val Gly Phe Ile Arg Ser Lys Pro Tyr Gly Glu Thr Thr Thr
                50                  55                  60
Tyr Ala Ala Trp
            65
```

```
<210> 1087
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1087
Met Ser Leu Phe Xaa Leu Xaa Xaa Leu Arg Gln Ser Phe Thr Xaa Xaa
                -10                 -5                  1
Ala Gln Ala
        5

<210> 1088
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1088
Met Ile Ser Ala His Cys Ser Phe Tyr Phe Leu Ala Ser Ser Ser Leu
                -15                 -10                 -5
Ser Thr Ser Ala Ser Xaa Arg Thr Gly Ile Thr Asp Val Ser
            1               5                   10

<210> 1089
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1089
Met Asn Ala Glu Asn Asn Phe Phe Gly Phe Val Cys Leu Phe Val Phe
                -20                 -15                 -10
Leu Tyr Thr Thr Pro Cys Asn Cys Phe Gly Leu Glu His Leu Trp Ile
            -5                  1                   5
Leu Ser Phe Met Val Val Leu Gly Xaa Thr Arg
    10                  15

<210> 1090
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1
```

<400> 1090
Met Thr Met Ala Val Gly Ala Ala Xaa Xaa Leu Pro Cys Cys Cys His
-20 -15 -10
Leu Leu Thr Cys Val Ser Ser Leu Arg Xaa Asp Ile Tyr Pro His
-5 1 5

<210> 1091
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1091
Met Arg Arg Lys Arg Arg Glu Arg Lys Glu Arg Lys Ser Ile Leu Leu
-25 -20 -15 -10
Ala Ala Leu Ser Arg Asn Ile Ser Pro Gly Gln Thr Tyr Arg Thr Ser
-5 1 5
Pro Ala

<210> 1092
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1092
Met Gly Ser Pro Tyr Val Ala His Val Gly Leu Glu Leu Leu Thr Ser
-20 -15 -10
Ser Asp Pro Pro Ser Leu Ala Ser Gln Val Leu Gly Ile His
-5 1 5

<210> 1093
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1093
Met His Leu Tyr Thr His Val Cys Trp Leu Thr Leu Thr Leu Ala His
-15 -10 -5
Ser His Ser Leu Thr His Thr His Thr Leu Thr Pro Ser His Thr Arg
1 5 10
Thr His Ser His Thr Cys Ala Cys Leu His Ala His Lys
15 20 25

<210> 1094
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1094
Met Arg Leu Ser Leu Thr Phe Tyr His Phe Pro Leu Cys Trp Gly His
-15 -10 -5 1
Gln Ala Val Pro Thr Trp Trp Xaa Xaa Ile Ile Gln Pro Cys His Cys
5 10 15
Ala Leu Cys Thr Ser Ala Glu Gly Val Gln Ser His Ile Ile Ser Xaa
20 25 30
Ile Tyr Arg
35

<210> 1095
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1095
Met Asn Val Leu Ile Ile Val Phe Val Ala Phe Ala Phe Gly Phe Leu
-10 -5 1
Val Met Lys Ser Leu Leu Lys Pro Met Ser Arg Arg Val Phe Leu Met
5 10 15
Leu Ser Ser Arg Ile Phe Met Val Ser Gly Leu Arg Phe Lys Ser Leu
20 25 30
Ile His Leu Glu Leu Ile Phe Val Tyr Lys Leu Arg Asp Glu Asp Pro
35 40 45 50
Val Ser Phe Phe Tyr Met Trp Leu Ala Asn Tyr Pro Ser Thr Ile Cys
55 60 65

<210> 1096
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1096
Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu Leu
-20 -15 -10 -5
Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys Ser Pro
1 5 10
Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu Cys Ala Gln
15 20 25
His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser His Thr Ala Gly
30 35 40
Ser Ser Cys Asn Thr Xaa Ala Ser Cys Gln Gln Gln Ala Arg Asn Val
45 50 55 60
Gln His Tyr His Met Lys Thr Leu Gly Trp Cys Asp Val Gly Tyr Asn
65 70 75
Xaa Leu Asp Trp Arg Arg Arg Ala Arg Ile Xaa Gly Pro Trp Xaa Glu
80 85 90
Leu His Gly Xaa
95

<210> 1097
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1097
```
Met Val Phe Leu Phe Leu Met Ile Ser Val Phe Ala Gly Cys Gln Ile
                -10                 -5                  1
Pro Ser Gly
        5
```

<210> 1098
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1098
```
Met Gly Ser Arg Pro Val Ser Xaa Ala Gly Leu Glu Leu Leu Ala Ser
    -20                 -15                 -10
Ser Asn Ser Ser Ala Leu Pro Phe Gln Cys Ser Gly Ile Thr Gly Met
-5                  1               5                   10
Ser Xaa His Thr Leu Ala
            15
```

<210> 1099
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1099
```
Met Leu Cys His Leu Ser Leu Val Phe Leu Gly Xaa Gly Gln Phe Trp
            -10                 -5                  1
Ser Gln Asn
    5
```

<210> 1100
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1100
```
Met Thr Asn Leu Phe Met Cys Leu Phe Ala Ile Cys Ile Ser Ser Asn
        -15                 -10                 -5
Ala Lys Cys Leu Phe Ser Leu Phe Pro Phe Phe Ile Glu Gly
    1               5                   10
```

<210> 1101
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1101
Met Leu Gly Tyr Ile Trp Xaa Gln Asp Lys Val Phe Ala Asn Cys Val
        -25                 -20                 -15
Leu Phe Thr Leu Leu Val Ser Thr Arg Ser Gly Arg Ser Arg Ala Gly
    -10                 -5                  1                   5
Cys Ala Trp Arg Trp Arg Gly Arg Trp Ser Val Gly Gln Lys Gly Xaa
                10                  15                  20

<210> 1102
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1102
Met Xaa Leu Ile Leu Ser Leu Gln Val Cys Arg Pro Ala Thr Leu Asp
-15                 -10                 -5                  1
Gln Ala Thr Arg Ala Thr Thr Pro Cys Arg Leu Arg
            5                   10

<210> 1103
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1103
Met Cys His Arg Arg Trp Leu His Leu Ser Thr Arg His Leu Gly Phe
        -35                 -30                 -25
Lys Pro Arg Ile His Tyr Val Phe Val Leu Met Leu Ser Leu Pro Leu
    -20                 -15                 -10
Pro Pro Thr Pro Gln Gln Ala Leu Gly
-5                  1

<210> 1104
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1104
Met Asp His Val Val Ile Phe Val Ile Phe Pro Ala Ala Leu Leu Leu
                -15                 -10                 -5
Cys Trp Gly Gly Leu Ile Pro Leu Cys Ile Ile Tyr Pro Pro Ile Ala
            1                   5                   10
Asp Thr Val Gly
    15

<210> 1105
<211> 30

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1105
Met Leu Thr Asn Leu Phe Phe Gln Val Ala His Pro Leu Ile Ile Ile
-25 -20 -15 -10
Leu Xaa Phe Asp Ile Tyr Ser Leu Ala Phe Ile His Asp Val
-5 1 5

<210> 1106
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1106
Met Leu Phe Gly Leu Arg Gly Met Leu Pro Leu Thr Gln Gln Ala Pro
-10 -5 1
Ile Pro His Leu Arg Cys Lys Leu Ser Val Thr
5 10

<210> 1107
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1107
Met Arg Val Cys Met Arg Leu Cys Ala Cys Val Tyr Ala Cys Val Cys
-20 -15 -10
Ala Ser Val Ser Ala Cys Val Tyr Xaa Cys Val Cys Met Xaa Val Arg
-5 1 5 10
Ala His Leu Cys Val Cys Met Cys Val Cys Met Cys Val His Leu Cys
15 20 25
Val Cys Met Cys Val Cys Val Cys Ala Ser Val Cys Val Cys Met Cys
30 35 40
Ala Cys Val Cys Met Cys Val Cys Val Arg Ala Ser Val Cys Val
45 50 55

<210> 1108
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1108
Met Val Ile Thr Ser Asn Ser Tyr Leu Ile Ala Asn Leu Val Leu Phe
-20 -15 -10
Ile Ser Ile Ala Ala Leu Arg
-5 1

```
<210> 1109
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1109
Met Glu Glu Leu Asp Arg Lys Trp Arg Glu Lys Val Leu Pro Ala Ala
    -50                 -45                 -40
Lys Leu Ile Lys Arg Arg Asn Leu Phe Ser Thr Cys Thr Pro Gln Tyr
-35                 -30                 -25                 -20
Gly Thr His Ala Ala Phe Leu Ser Leu His Ala Ser Leu Val Thr Lys
                -15                 -10                 -5
Ala Phe Ser Ile Asn Ser Trp Glu Trp
            1               5

<210> 1110
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1110
Met Val Ser Gly Ala Gln Ala Pro Ser Ser Gln Arg Pro Leu Leu Leu
-25                 -20                 -15                 -10
Cys Pro Leu Ser Ser Gly Ser Pro Cys Pro Arg
                -5                  1

<210> 1111
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1111
Met Ser Cys Leu Leu Arg Ala Tyr Ile Ile Trp Ile Phe Pro Ser Phe
        -25                 -20                 -15
Leu Pro Ser Leu Leu Ser Ser Phe Leu Leu Ser Leu Pro Pro Ser Gly
    -10                 -5                  1               5

<210> 1112
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1112
Met Phe Gln Leu Leu Ile Leu Cys Gln Met Asn Ser Leu Lys Ile Phe
    -35                 -30                 -25
Ser Pro Ile Leu Gly Trp Ser Leu His Phe Val Tyr Cys Phe Leu Cys
```

```
-20                 -15                 -10                 -5
Cys Ala Glu Ala Phe Leu Leu Asp Met Ile Pro Phe Met Gln Phe Tyr
                1               5                   10
Phe Gly Tyr Leu Cys Leu Trp Gly Ile Thr Leu Lys Ile Phe Ala Gln
        15                  20                  25
Ser Asn Trp
    30
```

<210> 1113
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -48..-1

<400> 1113

```
Met Ala Leu Leu Gly Lys Arg Cys Asp Val Pro Thr Asn Gly Cys Gly
            -45                 -40                 -35
Pro Asp Arg Xaa Xaa Xaa Gly Xaa Asn Pro Gln Xaa Arg Asp His His
        -30                 -25                 -20
Gln Xaa Xaa Val Cys Leu Arg Leu His Val Leu Ser Ala Val Gln Thr
    -15                 -10                 -5
Glu Arg Arg Gly Asp Gly
1               5
```

<210> 1114
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1114

```
Met Arg Pro Ala Leu Arg Ser Phe Trp His Ser Ser Gly Gly Pro Pro
        -30                 -25                 -20
Pro Ser Ala Thr Leu Ala Leu Leu Ser Ser Asp Ser Val Ala Thr Gly
    -15                 -10                 -5
Ser Val Val Ser Arg
1               5
```

<210> 1115
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1115

```
Met Leu Cys Ala Cys Lys Ala Arg Gly Val Met Leu Leu Leu Phe Ser
    -25                 -20                 -15
Gly Trp Leu Val Trp Trp Gly Ser Arg Ser Ser Gln Xaa Leu Arg Met
-10                 -5                  1                   5
Pro Glu Xaa Xaa Val Ser Gly Glu Gly Arg Ser Asp Xaa Xaa Pro His
            10                  15                  20
Gly
```

<210> 1116

<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1116
```
Met Ile Ser Ser Ser Leu Ser Gly Arg Val Pro Val Ile Leu Gly Asn
        -40                 -35                 -30
Leu Met Gly Val Gly Ala Ala Val Arg Arg Met Gly Phe Ser Leu Ile
    -25                 -20                 -15
Leu Pro Thr Ser Pro Ser Pro Ala His Ser Gly Ser Ala Pro Ser Ala
-10                 -5                  1               5
Gly Pro Arg
```

<210> 1117
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 1117
```
Met Gly Ile Ile Gln Xaa Ile Leu Ala Thr Ser Arg Asp Cys Tyr Ser
    -45                 -40                 -35
Phe Lys Lys Lys Pro Ile Pro Lys Lys Pro Thr Met Leu Ala Leu Ala
-30                 -25                 -20                 -15
Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr Ser Leu Leu Ser Gly Ser
                -10                 -5                  1
His Gly Lys Xaa Asn Gln Asp Val
        5                   10
```

<210> 1118
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1118
```
Met Met Leu Ser Thr Phe Ser Tyr Ala Cys Leu Pro Phe Val Cys Leu
            -20                 -15                 -10
Leu Leu Arg Asn Val Tyr Ser Asp Leu Leu Pro Asn Arg
        -5                  1               5
```

<210> 1119
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1119
```
Met Leu Ala Ile Leu Thr Gly Gly Arg Trp Tyr Leu Ile Val Val Leu
                -20                 -15                 -10
```

```
Val Cys Ile Ser Leu Val Ile Ile Asp Asp Asp Glu His Gly
            -5                  1               5

<210> 1120
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1120
Met Leu Leu Pro Leu Gly Leu Lys Val Leu Gly Leu Gln Ala Arg Gly
                -10                 -5                  1
Thr Thr

<210> 1121
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1121
Met Arg Pro Thr Met Glu Phe His Ser Val Leu Cys Gly Val Thr Pro
            -25                 -20                 -15
Thr Leu Leu Val Met Trp Leu Ser Pro Gln Met Ala Ser Ser Pro Ser
        -10                 -5                  1
Gln Ala Pro Gly Met Glu Pro Cys Ala Ser Gly Ile Ser Gln Arg Ala
5                   10                  15                  20

<210> 1122
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1122
Met Gly Lys Lys Lys Ile Trp Thr Pro Ser Ser Tyr Pro Met Pro Ser
            -30                 -25                 -20
His Lys His Val Ser Leu Cys Leu Leu Thr Val Ala Val Leu Val Leu
        -15                 -10                 -5
Thr Phe Lys Ser Leu Ile His Phe Glu Xaa Ile Phe Ala Tyr Glu Ile
    1               5                   10                  15
Gly Val Gln Gly

<210> 1123
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1123
Met Ser Pro Val Leu Cys Phe His Arg Cys Ser Cys Pro Ser Leu Leu
```

```
                -20                 -15                 -10
Ser Pro Ile Ser Pro Ser Gln Ala Cys Pro Glu Pro Leu Leu Gly
            -5                  1               5

<210> 1124
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1124
Met Leu Gln Leu Ser Phe Ser Val Phe Ile Leu Ile Met Phe Val Cys
                -20                 -15                 -10
Met Cys Val Cys Val Cys Val Cys Val Tyr Arg Leu Phe Ser Ser Ser
            -5                  1               5
Ser Pro
    10

<210> 1125
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -91..-1

<400> 1125
Met Lys Ser Thr Val Ser Ser Arg Glu Val Ala Thr Val Asp Lys Met
    -90                 -85                 -80
Lys Arg Arg His Ala Glu Tyr Cys Ala Gln Gly Leu Gln Arg Phe Lys
-75                 -70                 -65                 -60
Ala Gln Leu Ser Gln Asp Thr Leu Pro Xaa His Pro His Leu Glu Xaa
                -55                 -50                 -45
Glu Lys Gly Leu Glu Gly Leu Glu Glu Asn Val Pro Leu Lys Gly Glu
            -40                 -35                 -30
Lys Pro Gly Glu Gly Gly Pro Glu Ser Pro Lys Lys Arg Arg Arg Val
        -25                 -20                 -15
Leu Leu Gly Ala Gly Ile Pro Pro Val Ser Ser Ala Pro Arg Arg Gln
    -10                 -5                  1               5
Ser Gln Gln Ala Thr
                10

<210> 1126
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1126
Met His Asn Ser Cys Arg Pro Val His Leu Phe Phe Phe Phe Phe Xaa
-20                 -15                 -10                 -5
Glu Thr Gly Ser Arg Ser Asn Xaa Trp Leu Glu Xaa Ser Gly Ala Ile
                1                   5                   10
Ile Ala Asn Ser
        15
```

<210> 1127
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1127
```
Met Glu Ala Tyr Leu Asn Asp Ser Leu Leu Thr Pro Ser Asp Ser Pro
        -40                 -35                 -30
Asp Phe Glu Ser Val Gln Ala Gly Pro Xaa Ala Arg Pro Thr Phe Arg
    -25                 -20                 -15
Leu Tyr Leu Ser Leu Pro Val Ser Gln Ala Gly Pro
-10                 -5                  1
```

<210> 1128
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1128
```
Met Pro Ala Leu Gly Pro Ala Leu Leu Gln Gly Ser Leu Xaa Arg Val
                -10                 -5                  1
Gly Pro His Pro Pro Ala Pro Ser Thr Asn Cys Ile His Ser Gln Trp
        5                   10                  15
His Val Ser Ala Ala Xaa Gly Lys Gly Pro His Leu Arg His Pro Leu
    20                  25                  30
Xaa Gly Xaa Tyr Gln Leu Pro Val Pro Ala Glu Pro Trp Ala Ala Ala
35                  40                  45                  50
Gly Gly His Ser Val His
                55
```

<210> 1129
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1129
```
Met Val Gly Ile Leu Pro Leu Cys Cys Ser Gly Cys Val Pro Ser Leu
                -15                 -10                 -5
Cys Cys Ser Ser Tyr
            1
```

<210> 1130
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1130

Met Ala His Ser Ile Leu Leu Leu Ala Ser Gln Ala Gly Cys Leu Arg
-10 -5 1
Ser Phe Leu Gly Asn Trp
5

<210> 1131
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1131
Met Thr Glu Phe Gly Leu Ser Trp Val Phe Leu Val Ala Ile Phe Lys
-20 -15 -10 -5
Gly Val His Cys Glu Gly Xaa Ile Gly Gly Val Gly Gly Ala
1 5 10

<210> 1132
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1132
Met Asn Thr Val Phe Leu Leu Leu Phe Phe Gly Cys Phe Phe Phe Glu
-10 -5 1

<210> 1133
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1133
Met Trp Ala Ser Ser Pro Trp Pro Ser Ala Trp Ser Cys Cys Cys Leu
-20 -15 -10
Ser Ser Ser Ser Phe Ile Ala Gly Arg Arg Arg Gly Trp Thr Gln Met
-5 1 5
Trp Leu Thr Arg Pro Phe Ser Pro Gln Ala Ser Ser Pro Ser Ala
10 15 20

<210> 1134
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1134
Met Thr Met Pro Ile Ser Ser Tyr Ser Gln Asn Val Leu Ser Asn Phe
-30 -25 -20
His Asp Gly Tyr Phe Met Leu Ile Ile Leu Ser Ala Ile Leu Leu Asn

```
        -15                 -10                 -5
Ser Phe Ile Gly Cys Val Ser Phe Tyr His Cys Phe Ser Trp Gly Ser
    1               5                   10                  15
Gly

<210> 1135
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1135
Met Leu Thr His Gly Ala Ser Leu Ser Leu Val Ile Phe Leu Leu Thr
-20                 -15                 -10                 -5
Val Lys His Cys Phe Arg Tyr Arg Val Tyr Lys Thr
                1               5

<210> 1136
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1136
Met Ser Ser Val Glu Thr Asp Trp Gly Phe Trp Thr Ser Ile Pro Ile
        -20                 -15                 -10
Leu Pro Leu Ser Ser Gly Arg Gln Leu Pro Leu Pro Thr Arg Glu Trp
    -5                  1               5                   10
Gly Met Trp

<210> 1137
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1137
Met Phe Ala Ser Pro Arg Arg Trp Ser Ser Xaa Lys Ala Phe Ser Gly
            -30                 -25                 -20
Gln Arg Thr Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe
        -15                 -10                 -5
Ser Thr Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys
    1               5                   10                  15
Val Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp
                20                  25                  30
Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu Val
            35                  40                  45
Val Xaa

<210> 1138
<211> 63
<212> PRT
<213> Homo sapiens
```

<220>
<221> SIGNAL
<222> -16..-1

<400> 1138
Met Pro Ile His Ser Val Phe Leu Cys Ala Pro Ala Leu Val Phe Pro
-15 -10 -5
Arg Pro Val Ala Trp Lys Ala Glu Arg Pro Ser Leu Cys Phe Gly Ala
1 5 10 15
Ser Leu Pro Pro Leu Gly Arg Ser Leu Leu Gly Gln Gly Ser Ser Phe
20 25 30
Ile Ser Trp Gly Thr Gln Ala Ala Ile Val Glu Leu Xaa Pro His
35 40 45

<210> 1139
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -62..-1

<400> 1139
Met Val Tyr Asp Glu Lys Ser Leu Ser Cys Ser His Thr Pro Ala Thr
-60 -55 -50
Gln Phe Leu Ser Trp Asp Ala Ser Ser Val Tyr Ser Phe Leu Tyr Ile
-45 -40 -35
Leu Ser Ala Arg Val Asn Val Asp Val Xaa Xaa Tyr Ile Arg Val Tyr
-30 -25 -20 -15
Ile Leu Ala Cys Val Phe Phe Leu Ser His Pro Leu Phe Xaa Xaa Pro
-10 -5 1
Asn Gly Ser Val Tyr Cys Xaa Arg His Ser Pro Pro Tyr Leu Phe Cys
5 10 15

<210> 1140
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1140
Met Leu Pro Leu Ser Pro Thr Lys Phe Leu Asn Val Phe Leu Gly Leu
-35 -30 -25
Phe Leu Tyr Tyr Leu Gln Leu Val Cys Leu Leu Ile Ile Ser Leu Val
-20 -15 -10 -5
Leu Ile Ser Gly Leu Gly
1

<210> 1141
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1141
Met Asp Lys Val Glu Leu Pro Pro Pro Asp Leu Gly Pro Ser Ser Ala

```
                -25                 -20                 -15
Leu Asn Gln Thr Leu Met Leu Leu Arg Glu Val Leu Ala Ser His Asp
            -10                 -5                  1
Ser Ser Val Val Pro Leu Asp Ala Arg Gln Ala Asp Phe Val Gln Gly
    5                   10                  15

<210> 1142
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1142
Met Gly Gly Thr Ala Gly Trp Ser Ser Gln Asn Thr His Asn Ile Xaa
        -30                 -25                 -20
Val His His Leu Val Trp Leu Trp Phe Val Val Pro Gln Thr Ile Thr
    -15                 -10                 -5
Met Ile Thr Pro Lys Ile Thr Glu His Arg Pro Xaa Ile Thr Asp Xaa
1               5                   10                  15
Xaa Ile Met Xaa Thr Phe Glu Xaa Leu Gly Glu Leu Pro
            20                  25

<210> 1143
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1143
Met Cys Leu Ser Val Ala Leu Tyr Leu Cys Val Cys Val Cys Val Cys
            -15                 -10                 -5
Leu Ile Ala Arg Val Tyr Phe Cys Ile Tyr Val Cys Val Trp
        1               5                   10

<210> 1144
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1144
Met Leu His Leu Leu Phe Gly Leu Phe Pro Val Leu Trp Met Phe Leu
                -10                 -5                  1
Val Tyr Phe Phe Leu Ser Ser Phe Phe Phe Phe Phe Phe
        5                   10                  15

<210> 1145
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1
```

<400> 1145
Met Tyr Val Cys Xaa Cys Val Tyr Leu Phe Cys Ala Cys Met Cys Val
-15 -10 -5
Cys Ala Phe Phe Phe Phe
1

<210> 1146
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1146
Met Lys Xaa Asn Asn Leu Arg Arg Gln Ser Pro Ala Leu Arg His Cys
-35 -30 -25
Trp Arg Xaa Glu Thr Asp Phe Phe Leu Phe Thr Leu Ile Gly Ala Ser
-20 -15 -10 -5
Leu Leu Gln Ser Ala Ser Gly Pro Cys Arg Ile Ser Xaa Xaa Leu Lys
1 5 10
Trp His Ser Lys Gly Thr Leu
15

<210> 1147
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1147
Met Trp Pro Lys Xaa Gly Leu Leu Gly Leu Gly Leu Pro Leu Leu Pro
-20 -15 -10 -5
Pro Asn His Pro Ser Val Ala Gln Gly Thr Leu Val Ser Ser His Ser
1 5 10
Gly Ser Gly Ser Glu Gly Arg Val Ala Leu Arg Ser Asp Val His Ser
15 20 25
Pro Lys Thr Thr Xaa Gln
30

<210> 1148
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1148
Met Tyr Leu Ile Arg Glu Ser His Ala Ser Gly Ser Ser Ser Val Thr
-40 -35 -30
Ser Ser Cys Ser Leu Xaa Ser Xaa Ser Pro Asn Pro Gln Ala Met Ala
-25 -20 -15
Xaa Leu Phe Leu Ser Ala Pro Pro Gln Ala Glu Val Thr Phe Glu Asp
-10 -5 1 5
Val Ala Val Tyr Leu Ser Arg Glu Glu Trp Gly Arg Leu Gly Pro Ala
10 15 20

```
Gln Arg Gly Xaa Tyr Arg Asp Val Met Leu Glu Thr Tyr Xaa Asn Xaa
        25                  30                  35
Val Ser Leu Gly Val Gly Pro Ala Gly Pro Lys Xaa Gly Val Ile Ser
    40                  45                  50
Gln Leu Glu Arg Gly Asp Glu Pro Trp Val Leu Asp Val Gln Gly Thr
55                  60                  65                  70
Ser Gly Lys Glu His Leu Lys Lys Ser Thr Ala Gln Leu Leu Gly Pro
                75                  80                  85
Glu Leu Lys Tyr Lys Glu Leu
            90
```

<210> 1149
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1149

```
Met Ile Pro Arg Arg Thr Ser Ala Ser Arg Ala Pro Ser Val Pro Gln
        -35                 -30                 -25
Asn Ala Gly Leu Ser Pro Leu Pro Ala Leu Ser Ser Leu Cys Val Ser
    -20                 -15                 -10
Trp Gly Thr Ser Ser Thr Val Thr Arg Leu Arg Pro Trp Ile Ser Pro
-5                  1                   5                   10
Thr Trp Thr Ser Arg Ala Arg
            15
```

<210> 1150
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1150

```
Met Val Cys Ile Phe Cys Phe Leu Thr Ser Lys Ala Phe Pro Asn Pro
                -10                 -5                  1
Arg Ser Gln Asp Phe Leu Leu Asp Phe Ser Arg His Xaa Ile Gly Leu
        5                   10                  15
Gly Phe Thr Phe Arg Ser Ala Met His Phe Glu Asn Phe Arg Leu Xaa
    20                  25                  30
Gly Leu Gly Gln Asp Ser Leu Cys
35                  40
```

<210> 1151
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1151

```
Met Xaa Xaa Tyr Xaa Xaa Xaa Gly Phe Cys Ser Val Thr Ser Ser Pro
-20                 -15                 -10                 -5
Leu Ala Ser Ala Gly Arg Thr Thr Arg
                1                   5
```

<210> 1152
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1152
Met Ser Leu Xaa Xaa Leu Cys Asp Pro Asp Leu Val Pro Cys Pro Leu
-20 -15 -10
Leu Ile Ser Val Ala Leu Ser Val Lys Phe His Ile Xaa Gln Gln Val
-5 1 5
Asn Leu Pro Cys Ser Ser
10 15

<210> 1153
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1153
Met Met Ile Leu Ile Leu Ile Leu Glu His Ile Val Thr Xaa Lys Arg
-35 -30 -25
Asn Pro Lys Pro Val Thr Val Pro Ala Phe Leu Xaa Pro Cys Leu Thr
-20 -15 -10
Ser Phe Ser Cys Xaa Gly Ala Ser Phe Ser Leu Xaa Gly Xaa Arg Arg
-5 1 5
Gly Trp Gln His Gly Ser Cys Cys Ser Thr Ile Pro Leu Phe Xaa Thr
10 15 20 25
Leu Asn Ser Leu Gly Gln Gly Leu Ile Gly Pro Ala Tyr Ile Gly Ala
30 35 40

<210> 1154
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1154
Met Ser Thr His Ala Ile Ser Ile Leu Leu Cys Ile Gly Ala Ser Ser
-15 -10 -5
Gln Gly Arg
1

<210> 1155
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1155
Met Glu Glu Gln Glu Thr Glu Glu Val Gly Gly Arg Ser Ser Arg Lys
    -30                 -25                 -20
Asn Ala Ala Thr Val Asn Ala Ala Ser Leu Pro Pro Cys Phe Gly Val
-15                 -10                 -5                  1
Lys Ser Cys Arg Cys Arg Arg Cys Ser Cys Arg Arg Cys Leu Leu Tyr
            5                   10                  15
Phe Ser Trp Pro Arg Gly Arg Ile Ser Pro Pro Val Gly Gln Cys Ala
        20                  25                  30
Gly Arg Gly
    35

<210> 1156
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1156
Met Arg Gly Ile Gln Ala Lys Gly Ser Pro Gly Gln Ser Ser Ala Xaa
            -30                 -25                 -20
Val Leu Xaa Pro Cys Cys Cys His Ala Gly Ala Ser Ser Gly Ala Thr
        -15                 -10                 -5
Ala Trp Glu Glu Thr Pro Arg Ser Arg Cys His Ile Ala Val Xaa Ser
    1               5                   10                  15
Thr Asn Thr Ala Ser Arg Gly Arg Thr Trp Cys Arg Ala Thr Gly Pro
                20                  25                  30
Cys Pro Ser Gly Pro Thr Arg Gly Val Ser Arg Ser Arg Gly Leu Gly
            35                  40                  45
Ala Gly Phe Leu Ser Pro Phe Cys Cys Leu Phe Ala Phe His Pro Arg
        50                  55                  60
Leu Pro Trp Cys Ala Glu Val Pro Val Pro Ala Ala Ala His His Met
    65                  70                  75
Arg Cys Gly Gly Asp Leu Leu Ala Ala Pro Pro Pro Gly Pro Ser Trp
80                  85                  90                  95
Phe Ala Arg Phe Pro Pro Leu Val Pro Glu Ser Phe Pro His His Ser
                100                 105                 110
Val

<210> 1157
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1157
Met Phe Ser Ser Arg Ser Phe Met Val Ser Gly Leu Ile Trp Val Phe
                -20                 -15                 -10
Gly Leu Val Ser Val Leu Ser Xaa Phe Leu Cys Met Val Tyr Asp Gln
            -5                  1                   5
Gly Gln
    10

<210> 1158
<211> 31
<212> PRT
<213> Homo sapiens

```
<220>
<221> SIGNAL
<222> -13..-1

<400> 1158
Met Leu Leu Ala Val Ser Leu Ser Leu Val Ser Asn Cys Asn Phe Val
            -10                 -5                  1
Leu Thr Asp Gln Leu Phe Pro Ala Pro Ala Ser Leu Ile Pro Glu
    5                   10                  15

<210> 1159
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1159
Met Asn Gln Asp Phe Asn Pro Glu Ile Glu Ala Ser Pro Gln Val Lys
                -25                 -20                 -15
Thr Gly Val Phe Leu Phe Ser Ile Ile Gly Ser Phe Gly Phe Pro Gly
            -10                 -5                  1
Met Cys Asn Cys Lys Asn Pro Ala Arg
    5                   10

<210> 1160
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1160
Met Pro Cys Ser Trp Ser His Ile Val Ser Ser Leu Phe Ser Trp Leu
-20                 -15                 -10                 -5
Leu Ser Leu Thr Ser Val Pro Gly
                1

<210> 1161
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1161
Met Phe Phe Phe Gly Tyr Ser Glu Asp Ile Tyr Cys Val Ser Gly Pro
            -25                 -20                 -15
Val Leu Ser Cys Cys Cys Leu Thr Ala Gly Arg Ala Arg Leu Trp
        -10                 -5                  1

<210> 1162
<211> 58
<212> PRT
<213> Homo sapiens
```

<220>
<221> SIGNAL
<222> -16..-1

<400> 1162
```
Met Pro Tyr Ala Ala Leu Ile Cys Pro Trp Ser Ser Gln Val Pro Ser
    -15                 -10                 -5
Ser Pro Pro Ala Ser Leu Glu Ala Ser Ser Asn Val Tyr Leu Gln Glu
1               5                   10                  15
Ser Arg Ala Ala Tyr Ala Ser Val Pro Ala Gly Pro Glu Val Ala Thr
            20                  25                  30
Gln His Thr Ser Ser Pro Val Thr Pro Met
        35                  40
```

<210> 1163
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1163
```
Met Gln Leu Leu Tyr Leu Thr Tyr Ser Leu Ala Phe Leu Leu Phe Ile
            -15                 -10                 -5
Lys Ala Gly Thr
        1
```

<210> 1164
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1164
```
Met Ala Pro Ser Arg Pro Arg Ala Ala Ala Val Thr Ser Ser Ala Ala
-20                 -15                 -10                 -5
Pro Ser Arg Ala Arg Gln Gly Ala
                1
```

<210> 1165
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1165
```
Met Leu Ala Ser Ala Pro Arg Leu Asn Ser Ala Asp Arg Pro Met Lys
        -40                 -35                 -30
Thr Ser Val Leu Arg Gln Arg Lys Gly Ser Val Arg Lys Gln His Leu
    -25                 -20                 -15
Leu Ser Trp Ala Xaa Gln Xaa Gly Arg Xaa Gln Val Val Glu Ile Leu
-10                 -5                  1               5
Gln Ser Glu Lys Gln Thr Xaa Xaa Asp
            10                  15
```

<210> 1166
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 1166
```
Met Tyr Pro Leu Gly Arg Gly Glu Gln Gly Pro Ala Ala Pro Lys Ser
            -35                 -30                 -25
Trp Leu Leu Leu Pro Thr Thr Leu Ala Leu His Gly Ser Leu Asp Ala
        -20                 -15                 -10
Val Ser Gln Ala Gln Gly Arg Pro Gly His Pro Asp Ala Pro Pro
    -5                  1               5
```

<210> 1167
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1167
```
Met Arg Val Phe Ile Ala Ala Leu Phe Thr Ile Ala Glu Thr Trp Asn
    -15                 -10                 -5
Gln Pro Lys Cys Pro
1               5
```

<210> 1168
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1168
```
Met Ala Lys Gly Leu Arg Val Asn Leu Gly Glu Leu Val Glu Ser Met
-30                 -25                 -20                 -15
Arg Leu Cys Phe Leu Ser Val His Phe Arg Leu Arg Trp Gly Asp Ser
                -10                 -5                  1
Cys Pro Ser Ser Pro His Arg Glu Thr Phe Pro Ala Gly Pro Val Asn
        5                   10                  15
Gly Pro Leu Tyr His Pro Arg
    20                  25
```

<210> 1169
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1169
```
Met Pro Ser Pro Gln Leu Leu Val Leu Phe Gly Ser Gln Thr Gly Thr
        -15                 -10                 -5
```

Ala Gln Asp Val Ser Glu Arg Leu Gly Arg Glu Ala Arg Gly Arg Arg
1 5 10 15
Leu Gly Cys Arg Val Gln Ala Leu Asp Ser Tyr Pro Val Val Asn Leu
20 25 30
Ile Asn Glu Pro Leu Val Ile Phe Val Cys Ala Thr Xaa Gly Gln Gly
35 40 45
Asp Pro Pro Asp Asn Met Lys Asn Phe Trp Arg Phe Ile Phe Arg Lys
50 55 60
Asn Leu Pro Ser Thr Ala Arg
65 70

<210> 1170
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 1170
Met Ser Ser Ile Leu Gly Val Ser Ser Ser Trp Trp Tyr Leu Tyr Tyr
-40 -35 -30
Gly Tyr Cys Ile Phe Val Lys Lys Cys Ser Phe Cys Ser Phe Leu Phe
-25 -20 -15 -10
Leu Ala Cys Ile Phe Gln Gly Xaa Ser Xaa Xaa Xaa Asn Thr Gln Ser
-5 1 5

<210> 1171
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1171
Met Gly Ser Val Leu Gly Leu Cys Ser Met Ala Ser Trp Ile Pro Cys
-25 -20 -15
Leu Cys Gly Ser Ala Pro Cys Leu Leu Cys Arg Cys Cys Pro Ser Gly
-10 -5 1
Asn Asn Ser Thr Val Thr Arg Leu Ile Tyr Ala Leu Phe Leu Leu Val
5 10 15 20
Gly Val Trp

<210> 1172
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 1172
Met Ser Xaa Xaa Xaa Arg Leu Xaa Arg Gln Leu Leu Ser Gln Xaa Arg
-45 -40 -35
Xaa Met Thr Cys Glu Asn Glu Ala Gly Ala Gln Cys Gln Lys Ser Ser
-30 -25 -20 -15
Phe Ile Gly Ser Cys Ser Val Met Ser Ser Gly Ala Leu Cys Val Pro
-10 -5 1
Leu Tyr Tyr Leu Ala Lys Gly Asn Met Cys Ser Ile Cys Gly Met Leu

5 10 15
Lys Glu Met Asn Gly Leu Trp Ser Glu Cys Asp Ser Leu Lys Asn Thr
20 25 30
Phe Ile Val Trp Xaa Cys Ile Phe Ser Cys Leu Gly Met Gln Leu Xaa
35 40 45 50
Ser Ser Xaa Val Ser Asn Val Arg Leu Leu Leu Ser His
55 60

<210> 1173
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1173
Met Pro His Pro Leu Ala Thr Ser Ala Phe Leu Arg Ser Ala Phe Pro
-25 -20 -15
Phe Val Cys Leu Thr Phe Cys Val Gly Gly Gly Pro Gly Ile Ser Gly
-10 -5 1 5
Val Tyr Arg Leu Leu Met Ala Asn Ala Thr Arg Arg Glu Ser Glu Val
10 15 20
Ser Leu Arg Gly Leu Gly Arg Asp Gly Glu Gly Ala Arg Ala Thr Pro
25 30 35

<210> 1174
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1174
Met Thr Val Gly Leu His Ile Leu Arg Asp Ser Leu Met Val Phe Leu
-20 -15 -10
Asn Leu Phe Phe Leu Asn Cys Asp Pro His Arg
-5 1

<210> 1175
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1175
Met Val Arg Trp Gly His Pro Pro Met Phe Cys Val Ser Leu Leu Leu
-20 -15 -10
His His Ala Tyr Pro Leu Pro Ser Thr Met Ile Val Ser Phe Pro Arg
-5 1 5 10
Pro Pro Leu

<210> 1176
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1176
```
Met Ala Gly Ala Ala Arg Trp Val Gly Gln Xaa Ser Ser Ala Met Val
    -25                 -20                 -15
Cys Phe Gly Cys Pro Gly Gly Ala Ser Ser Arg Cys Arg Ser Pro Arg
-10                 -5                  1                   5
Gly Arg Gln Ala Ser Arg Val Pro Arg Leu Glu Asn Gly Ala Gln Arg
            10                  15                  20
Val Val Arg Thr Met Val His Leu Val Leu Gln Pro Lys Arg Val Thr
        25                  30                  35
Leu Val His Pro Pro Arg Gly Leu Glu Pro Val Cys Thr Pro Ile Ala
    40                  45                  50
Xaa Met Xaa Pro Lys Ser His Gly Leu Arg Ser Ser Leu
55                  60                  65
```

<210> 1177
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1177
```
Met Gly Val Val Ser Gly Gly Val Gly Asp Leu Thr Thr Lys Thr Gln
                -30                 -25                 -20
Glu Asn Gly Leu Leu Pro Xaa Leu Leu Ser Xaa Leu His Gly Leu Leu
            -15                 -10                 -5
Tyr Gly Ser Pro Asp Ala Glu Leu Thr Gly Pro Asp Pro Trp Asp
        1                   5                   10
```

<210> 1178
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1178
```
Met Gly Phe Leu Ser Xaa Thr Cys Val Leu Ser Cys Xaa Arg Ser Leu
-15                 -10                 -5                  1
Ser
```

<210> 1179
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1179
```
Met Glu Tyr Gly Ser Ala Lys Leu Ser Ser Gly Arg Val Phe Tyr Leu
                -35                 -30                 -25
Pro Arg Asp Phe Gly Ile Glu Arg Arg Val Leu Val Cys Phe Phe Asn
            -20                 -15                 -10
```

```
Ser Val Ser Phe Leu Phe Gly Val Ser Xaa Lys Lys Ser Xaa Gln Trp
        -5                  1               5

<210> 1180
<211> 17
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1180
Met Leu Ser Gly Leu Val Leu Asn Ser Trp Ala Leu Ala Tyr Gln Leu
            -10                 -5                  1
Ala

<210> 1181
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1181
Met Arg Leu Val Phe Phe Xaa Gly Xaa Ser Ile Ile Leu Val Leu Gly
    -15                 -10                 -5
Ser Thr Phe Xaa Ala Tyr Leu
1               5

<210> 1182
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1182
Met Leu Ser Ser Asp Phe Phe Leu Leu Phe Val Ser Leu Ser Leu Ser
    -15                 -10                 -5
Pro Phe Pro Phe Phe Leu Phe Pro Pro Leu Phe Ser Cys Phe Leu Leu
1               5                   10                  15
Pro Thr Arg

<210> 1183
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1183
Met Phe Ile Ala Ala Leu Phe Thr Val Ala Lys Ile Trp Asn Gln Pro
                -10                 -5                  1
Lys Cys Pro Ser Thr Asp Glu Trp Ile Asn Lys Met Trp Tyr Ile Tyr
        5                   10                  15
Thr Met Glu Tyr Tyr Pro Asp Ile Lys Lys Asn Gly Ile Leu Thr Phe
```

```
    20                  25                  30
Lys Ala Thr Arg Met Asn Arg Lys Thr Leu
35                  40

<210> 1184
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1184
Met Cys Val Cys Gly Cys Leu Cys Val Trp Met Cys Val Cys Gly Xaa
-15                 -10                 -5                  1
Val Cys Ile Tyr Ile Xaa Val Tyr Val Cys Thr Cys Val Arg Gly
            5                   10                  15

<210> 1185
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1185
Met Gly Val Arg Thr Val Cys His Phe Ile Gln Val Phe Leu Ser Leu
    -25                 -20                 -15
Phe Val Phe Phe Trp Leu Val Gly Phe Ser Phe Phe Phe Phe Leu Xaa
-10                 -5                  1                   5
Phe Ser Thr Lys Gln Val Arg Val Glu Gln His Cys Asp Phe Lys Ser
            10                  15                  20
Thr Pro Xaa Val Glu Ser Ser Ser Thr Val Gly His Ala
        25                  30                  35

<210> 1186
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1186
Met Tyr His Ile Leu Phe Ile His Ser Phe Ile Asp Arg Tyr Leu Ser
        -25                 -20                 -15
Cys Phe Tyr Leu Leu Ala Ile Val Ser Asn Ala Val Met Asn Met Gly
    -10                 -5                  1                   5
Val Gln Met Ser Val Leu Ser Pro Cys Phe Ala Phe Val His Ser Ile
                10                  15                  20
Lys Asn Val Lys Val Leu Cys Phe Leu Leu Phe Phe Leu Phe Gly
            25                  30                  35

<210> 1187
<211> 37
<212> PRT
<213> Homo sapiens

<220>
```

<221> SIGNAL
<222> -22..-1

<400> 1187
Met Gln Phe Thr Val Leu Met Cys Pro Val Gln Trp Leu Leu Val Tyr
-20 -15 -10
Ser Pro Ser Cys Ala Ala Thr Ile Thr Val Asn Phe Lys Thr Phe Ser
-5 1 5 10
Ser Pro Gln Thr Gly
15

<210> 1188
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1188
Met Arg Arg Ala Trp Thr Gln Glu Arg Glu Pro Arg Pro Cys Glu Pro
-35 -30 -25
Ala Glu Arg Ala Asp Pro Ala Pro Val Ser Cys Leu Ser Ala Gly Leu
-20 -15 -10
Arg Val Cys Cys Ser Gln Arg Ser
-5 1

<210> 1189
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1189
Met Leu His Leu Ile Cys Ile Ser Leu Ile Val Asn Asp Phe Phe Ile
-25 -20 -15 -10
Cys Leu Leu Ala Ile Cys Val Ser Ser Phe Glu Asn Cys Leu Phe Met
-5 1 5
Ser Leu Ala His Ser
10

<210> 1190
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 1190
Met Arg Ser Glu Arg Pro Met Val Trp Cys Cys Leu Phe Val Arg Ser
-60 -55 -50
Gln Arg Lys Arg Lys Gln Ser Thr Gln Asp Glu Asp Ala Val Ser Leu
-45 -40 -35
Cys Ser Leu Asp Ile Ser Glu Pro Ser Asn Lys Arg Val Lys Pro Leu
-30 -25 -20
Ser Arg Val Thr Ser Leu Ala Asn Leu Ile Pro Pro Val Lys Ala Xaa
-15 -10 -5 1

Pro Leu Lys Arg Phe Ser Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg
5 10 15
Ser Glu Ser Arg Pro Asp Ile Leu Ala Pro Arg Pro Trp Ser Arg Asn
20 25 30

<210> 1191
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1191
Met Val Phe Trp Thr Lys Phe Cys Ile Leu Ile Ser Thr Ala Phe Pro
-20 -15 -10 -5
Ser Leu Leu Thr Gln Ile Ile Phe Pro Lys Ser Ile Thr Phe Ala Phe
1 5 10
Gln Phe Phe Trp Asn Arg Glu Lys Gln Lys Thr Lys Thr Pro Thr Gly
15 20 25

<210> 1192
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1192
Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile
-35 -30 -25
Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe
-20 -15 -10
Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu
-5 1 5 10
Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu His
15 20 25
Gly

<210> 1193
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1193
Met Ser Val Ser Ala Leu Leu Leu Glu Xaa Leu Gln Xaa Ala Ile Pro
-15 -10 -5
Arg Xaa Thr Ser Gly Xaa Gln Asp Leu Pro Asn Trp
1 5 10

<210> 1194
<211> 50
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -39..-1

<400> 1194
Met Gln Ala Cys Tyr Met Gly Met Trp Tyr Thr Ala Glu Ala Trp Gly
-35 -30 -25
Thr Ile Glu Ser Leu Thr Gln Val Val Ser Val Ile Ala Ile Val Ser
-20 -15 -10
Phe Thr Thr Leu Cys Ser Ser Leu Tyr Ser Pro Gln Val Val Pro Ser
-5 1 5
Val Gly
10

<210> 1195
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -62..-1

<400> 1195
Met Met Leu Arg Gly Gly Gly Thr Phe Lys Xaa Cys Leu Ser His Glu
-60 -55 -50
Gly Ser Ser Phe Thr Lys Gly Leu Ala Gln Glu Cys Val Ser Xaa Ser
-45 -40 -35
Cys Gly Thr Arg Leu Ile Thr Ala Val Ala Ser Xaa Tyr Lys Ala Arg
-30 -25 -20 -15
Leu Pro Leu Ala Ala Cys Pro Leu Leu Leu Pro Ile Phe Ser His Ala
-10 -5 1
Arg Ser Ser
5

<210> 1196
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1196
Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn
-40 -35 -30 -25
Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
-20 -15 -10
Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
-5 1 5
Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
10 15 20
Glu His Thr Thr
25

<210> 1197
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 1197
Met Ser Pro Ala Pro Asp Ala Ala Pro Ala Pro Ala Ser Ile Ser Leu
-40 -35 -30
Phe Asp Leu Ser Ala Asp Ala Pro Val Phe Gln Gly Leu Ser Leu Val
-25 -20 -15 -10
Ser His Ala Pro Gly Glu Ala Leu Ala Arg Ala Pro Arg Thr Ser Cys
-5 1 5
Ser Gly Ser Gly Glu Arg Glu Ser Pro Glu Arg Lys Leu Leu Gln Gly
10 15 20
Pro Met Asp Ile Ser Glu Lys Leu Phe Cys Ser Thr Cys Asp Gln Thr
25 30 35
Phe Gln
40

<210> 1198
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1198
Met Leu Leu His Tyr Leu Lys Leu Lys Gly Asp Gln Trp Lys Leu Ser
-35 -30 -25 -20
Ser Val Ser Thr Leu Ile Leu Phe Ile Phe Ile Gly Ser Leu Gln Pro
-15 -10 -5
Val Pro Thr Arg Phe Lys Arg Phe Ser Cys Leu Xaa His Leu Ser Ser
1 5 10
Arg Asp His Arg Gln Ala Leu Arg
15 20

<210> 1199
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -153..-1

<400> 1199
Met Ala Glu Gly Asp Asn Arg Ser Thr Asn Leu Leu Ala Ala Glu Thr
-150 -145 -140
Ala Ser Leu Glu Glu Gln Leu Gln Gly Trp Gly Glu Val Met Leu Met
-135 -130 -125
Ala Asp Lys Val Leu Arg Trp Glu Arg Ala Trp Phe Pro Pro Ala Ile
-120 -115 -110
Met Gly Val Val Ser Leu Val Phe Leu Ile Ile Tyr Tyr Leu Asp Pro
-105 -100 -95 -90
Ser Val Leu Ser Gly Val Ser Cys Phe Val Met Phe Leu Cys Leu Ala
-85 -80 -75
Asp Tyr Leu Val Pro Ile Leu Ala Pro Arg Ile Phe Gly Ser Asn Lys
-70 -65 -60
Trp Thr Thr Glu Gln Gln Gln Arg Phe His Glu Ile Cys Ser Asn Leu
-55 -50 -45
Val Lys Thr Arg Arg Arg Ala Val Gly Trp Trp Lys Arg Leu Phe Thr
-40 -35 -30
Leu Lys Glu Glu Lys Pro Lys Met Tyr Phe Met Thr Met Ile Val Ser
-25 -20 -15 -10
Leu Ala Ala Val Ala Trp Val Gly Gln Gln Val His Asn Leu Leu Leu

```
                -5                   1                   5
Thr Tyr Leu Ile Val Thr Ser Leu Leu Leu Leu Pro Gly Leu Asn Gln
        10                  15                  20
His Gly Ile Ile Leu Lys Tyr Ile
    25                  30

<210> 1200
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1200
Met Ala Ala Leu Lys Ala Leu Val Ser Gly Cys Gly Arg Leu Leu Arg
    -25                 -20                 -15
Gly Leu Leu Ala Gly Pro Ala Ala Thr Ser Trp Ser Arg Leu Pro Ala
-10                 -5                  1                   5
Arg Gly Phe Arg Glu Val Val Glu Thr Gln Glu Gly Lys Thr Thr Ile
            10                  15                  20
Ile Glu Gly Arg Ile Thr Ala Thr Pro Lys Glu Ser Pro Asn Pro Pro
        25                  30                  35
Asn Pro Ser Gly Gln Cys Pro Ile Cys Arg Trp Asn Leu Lys His Lys
    40                  45                  50
Tyr Asn Tyr Asp Asp Val Leu Leu Leu Ser Gln Phe Ile Arg Pro His
55                  60                  65                  70
Gly Gly Met Leu Pro
                75

<210> 1201
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1201
Met Gly Ser Leu Leu Phe Ile Arg Gln Thr Leu Val Gly Phe Lys Gln
            -20                 -15                 -10
Val Val Ala Trp Thr Phe Ala Ser Asp Ser His Cys Xaa Xaa Val Xaa
        -5                  1                   5
Met Val Xaa Xaa Ser Gln Leu Xaa Asn Pro Pro Leu
10                  15                  20

<210> 1202
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1202
Met Leu Ala Arg Ala Ala Glu Xaa Thr Gly Ala Leu Leu Leu Arg Gly
                -20                 -15                 -10
Ser Leu Leu Ala Ser Xaa Arg Ala Xaa Xaa Xaa Pro Pro Leu Gly Leu
            -5                  1                   5
Xaa Arg Asn Thr Xaa Gly Thr Val Arg Ala Ala Ala Gly Gly Leu Gly
```

10 15 20

<210> 1203
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1203
Met Asn Ala Ser Leu Leu Ser Phe Cys Leu Cys Ser Asp Phe Ile Ser
-15 -10 -5
Gln Asp Ala Leu Leu Leu Thr Val Ile Phe Pro Pro
1 5 10

<210> 1204
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -60..-1

<400> 1204
Met Leu Asn Met Glu Pro Tyr Thr Val Ser Gly Met Ala Arg Gln Asp
-60 -55 -50 -45
Ser Ser Ser Glu Val Gly Glu Asn Gly Arg Ser Val Asp Gln Gly Gly
-40 -35 -30
Gly Gly Ser Pro Arg Lys Lys Val Ala Leu Thr Glu Asn Tyr Glu Leu
-25 -20 -15
Val Gly Val Ile Val His Ser Gly Gln Ala His Ala Gly His Tyr Tyr
-10 -5 1
Ser Phe Ile Lys Asp Arg Arg Gly Cys Gly Lys Gly Lys Trp Leu
5 10 15

<210> 1205
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1205
Met Xaa Xaa Ala His Phe Ser Leu His Leu Xaa Ser Ser Arg Xaa Pro
-20 -15 -10 -5
Pro Ile Leu Ala Ser Pro Val
1

<210> 1206
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1206

Met Ile Arg Pro Val Cys Glu Leu Ser Ile Phe Phe Thr Tyr Val Leu
-15 -10 -5
Ala Ile Tyr Ile Ser Pro Ser Val Asn Cys Leu Phe Ile Ser Phe Pro
1 5 10 15
Ala

<210> 1207
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1207
Met Arg Gly Cys Gln Leu Leu Gly Leu Arg Ser Ser Trp Pro Gly Asp
-25 -20 -15
Leu Leu Ser Ala Arg Leu Leu Ser Gln Glu Lys Arg Ala Ala Glu Thr
-10 -5 1
His Phe Gly Phe Glu Thr Val Ser Glu Glu Glu Lys Arg Gly Asp Leu
5 10 15
Thr Ser Val Val Ser Leu Glu Tyr Pro Glu Val Gln Leu Gln Gly Gln
20 25 30 35
Arg Val Tyr Ala Phe Leu Ser Pro Ile Cys Thr Tyr Gly Ser Glu Gly
40 45 50
Cys Ser Leu Lys
55

<210> 1208
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1208
Met Glu Asn Leu Pro Phe Pro Leu Lys Leu Leu Ser Ala Ser Ser Leu
-35 -30 -25 -20
Asn Thr Pro Ser Ser Thr Pro Trp Val Leu Asp Ile Phe Leu Thr Leu
-15 -10 -5
Val Phe Ala Leu Gly Phe Phe Phe Leu Leu Leu Pro Tyr Phe Ser Tyr
1 5 10
Leu Arg Cys Asp Asn Pro Pro
15 20

<210> 1209
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1209
Met Cys Val Cys Val Phe Ala Ile Phe Gly Val Arg Cys Cys Val Cys
-10 -5 1
Val Arg Cys Ile
5

<210> 1210
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 1210
```
Met Ile Cys Ile Phe Tyr Ser Lys Ile Ser Ile Ser Val Gly Cys Gly
                -40                 -35                 -30
Arg Thr Ala Ala Glu Gln Val Gly Cys Lys Gln Arg Ser Phe His Xaa
            -25                 -20                 -15
Pro Cys Pro Leu Leu Phe Pro Gly Ala Cys Phe Pro Cys Pro
        -10                 -5                  1
```

<210> 1211
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1211
```
Met Asn Leu Ile Cys Val Ser Leu Met Ala Ser Asp Gly Ala Ser Ser
    -15                 -10                 -5
Pro Val Leu Gly Gly Ser Ser His Ser Ser Ser Xaa Xaa
1               5                   10
```

<210> 1212
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 1212
```
Met Gly Ser Val Thr Gly Ala Val Leu Lys Thr Leu Leu Leu Leu Ser
        -45                 -40                 -35
Thr Gln Asn Trp Asn Arg Val Glu Ala Gly Asn Ser Tyr Asp Cys Asp
    -30                 -25                 -20
Asp Pro Leu Val Ser Ala Leu Pro Gln Ala Ser Phe Ser Ser Ser Ser
-15                 -10                 -5                  1
Glu Leu Ser Ser Ser His Ser Pro Gly Phe Ala
            5                   10
```

<210> 1213
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1213
```
Met Met Ser Glu Xaa Ser Gln Asp Leu Val Val Lys Cys Ala Pro Pro
    -30                 -25                 -20
```

```
Xaa Pro Phe Phe Leu Leu Phe Leu Phe Ser Ser Cys Asp Val Pro Val
-15                 -10                 -5                  1
Pro Leu His Leu Leu Gln Trp Leu Gln Ser Phe Leu Arg Pro Arg
            5                   10                  15

<210> 1214
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1214
Met Phe Arg Cys Val Arg Phe Leu Pro Ser Gly Gly Phe Val Val Leu
        -25                 -20                 -15
Leu Thr Ser Gly Val Lys Pro Gln Thr Phe Ala Val Ser Val Thr Ala
    -10                 -5                  1                   5
Leu Lys Gly Gly Met Pro Gly Val Val His Ser Ser Gly Gly Phe Val
                10                  15                  20
Val Leu Leu Thr Ser Gly Ala Xaa Cys Arg Pro
            25                  30

<210> 1215
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1215
Met Arg Val Gly Arg Arg Glu Gly His Pro Leu Phe Pro Asn Val Pro
-30                 -25                 -20                 -15
Arg Cys Leu Phe Leu Asn Ala Arg Leu Ala Gly Thr Leu Cys Gln Leu
                -10                 -5                  1
Lys Leu Leu Gln Phe Gly Arg Leu Gly Asn Thr Glu Ser His Leu His
        5                   10                  15
Gly Leu Ala Gly
    20

<210> 1216
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1216
Met Tyr Phe Asp Ile Gln Ile Val Ser Asp Val Val Ser Gly Ile Pro
    -30                 -25                 -20
Phe Lys Leu Leu Cys Pro Leu Thr Cys Pro His His Ser Leu Ser Thr
-15                 -10                 -5                  1
Val

<210> 1217
<211> 47
<212> PRT
<213> Homo sapiens
```

<220>
<221> SIGNAL
<222> -31..-1

<400> 1217
Met Leu Phe Ile Phe Ser Asp Ile Asp Trp Lys Met Asp Leu Cys Phe
-30 -25 -20
Phe Ser Phe Ser Pro Phe Leu Pro Ser Leu Pro Leu Leu Glu Ala Glu
-15 -10 -5 1
Arg Met Arg Val Ser Asp Gln Leu Gln Tyr Thr Thr Gly Xaa Gly
5 10 15

<210> 1218
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1218
Met Glu Leu Glu Ala Met Ser Arg Tyr Thr Ser Pro Val Asn Pro Ala
-35 -30 -25
Val Phe Pro His Leu Thr Val Val Leu Leu Ala Ile Gly Met Phe Phe
-20 -15 -10 -5
Thr Ala Trp Phe Phe Val Tyr Glu Val Thr Ser Thr Lys Tyr Thr Arg
1 5 10
Asp Ile Tyr Lys Glu Leu Leu Ile Ser Leu Val Ala Arg
15 20 25

<210> 1219
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1219
Met Lys Gly Ala Leu Lys Leu Ile Ser Thr Asn Phe Ser Leu Cys Gln
-15 -10 -5
Ser Val Gln Cys Pro Ser Glu Glu Thr Ile Thr Asp Leu Val Ser Val
1 5 10 15
Pro Cys Gln Xaa Gly Leu
20

<210> 1220
<211> 93
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69..-1

<400> 1220
Met Thr Ser Gln Pro Val Pro Asn Glu Thr Ile Ile Val Leu Pro Ser
-65 -60 -55
Asn Val Ile Asn Phe Ser Gln Ala Glu Lys Pro Glu Pro Thr Asn Gln
-50 -45 -40

Gly Gln Asp Ser Leu Lys Lys His Leu His Ala Glu Ile Lys Val Ile
        -35                 -30                 -25
Gly Thr Ile Gln Ile Leu Cys Gly Met Met Val Leu Ser Leu Gly Ile
    -20                 -15                 -10
Ile Leu Ala Ser Ala Ser Phe Ser Pro Asn Phe Thr Gln Val Thr Ser
-5                  1               5                   10
Thr Leu Leu Asn Ser Ala Tyr Pro Phe Ile Gly Pro Gly
            15                  20

<210> 1221
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1221
Met Val Asp Glu Cys Leu Thr Glu Pro Val Trp Gly Ser Lys Arg Gln
-40                 -35                 -30                 -25
Gly Cys Ser Ser Gln Ala Glu Ala Ser Cys Asp Ile Val Ser Ala Ala
                -20                 -15                 -10
Cys Lys Cys Gly Ser Ser Gln Ala Ala Ile Asp Cys Glu Thr Ser Ser
            -5                  1               5
Cys Ser Glu Asp Phe Pro Val
    10                  15

<210> 1222
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1222
Met Ala Trp Trp Phe Ser Gly Thr Phe Pro Leu Thr His Pro Cys Ser
                -10                 -5                  1
Gly Tyr Gly Ser Leu Met Ala Pro Ser Ser Pro Thr Pro Ser Gly
        5                   10                  15

<210> 1223
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -57..-1

<400> 1223
Met Val Ala Lys Asp Tyr Pro Phe Tyr Leu Thr Val Lys Arg Ala Asn
        -55                 -50                 -45
Cys Ser Leu Glu Leu Pro Pro Ala Ser Gly Pro Ala Lys Asp Ala Glu
    -40                 -35                 -30
Glu Pro Ser Asn Lys Arg Val Lys Pro Leu Ser Arg Val Thr Ser Leu
-25                 -20                 -15                 -10
Ala Asn Leu Ile Pro Pro Val Lys Ala Thr Pro Leu Lys Arg Phe Ser
                -5                  1               5
Gln Thr Leu Gln Arg Ser Ile Ser Phe Arg Ser Glu Ser Ala
        10                  15                  20

<210> 1224
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1224
```
Met Ser Pro Ala Phe Arg Ala Met Asp Val Glu Pro Arg Ala Lys Gly
            -25                 -20                 -15
Val Leu Leu Glu Pro Phe Val His Gln Val Gly Gly His Ser Cys Val
        -10                 -5                  1
Leu Arg Phe Asn Glu Thr Thr Leu Cys Lys Pro Leu Val Pro Arg Glu
5                   10                  15                  20
His Gln Phe Tyr Glu Thr Leu Pro Ala Glu Met Arg Lys Phe Thr Pro
                25                  30                  35
Gln Tyr Lys Gly Gln Ser Gln Arg Pro Leu Val Ser Trp Pro Ser Leu
            40                  45                  50
Pro His Phe Phe Pro Trp Ser Phe Pro Leu Trp Pro Gln Gly
        55                  60                  65
```

<210> 1225
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1225
```
Met Leu Gly Gly Ala Val Ile Ala Gly Arg Pro Leu Gly Arg Trp Glu
                -30                 -25                 -20
Ser Thr Ala Gln Xaa Ile Leu Ala Phe Leu Gln Ser Pro Arg Ala Ile
            -15                 -10                 -5
Leu Pro Gly Asn Phe Phe Glu Lys Asn Ala Gln Ile Gln Gly Gly Pro
        1                   5                   10
Trp Gly Gly Gly Ser Gly Lys Thr Cys Ala Pro Gly Arg Xaa Asp Pro
15                  20                  25                  30
Gly Trp Glu Cys Gly Ala Gly Gly Gly Xaa Gly Glu Ala Ala Gly Ser
                35                  40                  45
Arg Xaa Arg Xaa Ser
            50
```

<210> 1226
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1226
```
Met Ser Met Ala Cys Phe Phe His Leu Phe Val Ser Ser Leu Ile Ser
    -15                 -10                 -5
Phe Glu Gln Cys Phe Xaa Met Leu Arg Lys Leu Leu Lys Ile Ile
1               5                   10                  15
```

<210> 1227

<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1227
Met Gly Ser Arg Gly Asp Pro Leu Ile Cys Gly Leu Gln Arg Ser Val
-45 -40 -35 -30
Gly Glu Val Trp Phe Pro Gly Trp Gly His Thr Ile Thr His Cys Phe
-25 -20 -15
Pro Trp Leu Glu Val Gly Leu Phe Phe Trp Leu His Ala Ala Pro Gly
-10 -5 1
Arg Ala Ile Ala Leu Pro His Phe Ser Ser Phe Ser Val Gly Gln Xaa
5 10 15
Val His Leu Val Ser Pro Leu Xaa Xaa Leu Asp Ile Ser Val Glu
20 25 30

<210> 1228
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1228
Met His Leu Leu Gln Glu Glu Leu Leu Leu Leu Leu Pro Arg Gly Leu
-15 -10 -5
Cys Gln Val Cys Pro Arg Leu Cys Leu Gln Arg Xaa Val Gly Glu Leu
1 5 10
Gln Xaa Xaa Xaa Pro Asp Val Gly Thr Ala Leu Leu Pro Asp Val Asn
15 20 25
Arg Thr Ser Cys Thr Thr Trp
30 35

<210> 1229
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1229
Met Cys Leu Ser Cys Ile Gln Gly Ser Phe Phe Val Glu Ile Leu Gln
-25 -20 -15
Leu Val Thr Arg Leu Leu Leu Ser Pro Ser Gln Ser Thr Gln Thr His
-10 -5 1
Thr His Thr His Thr His Thr
5 10

<210> 1230
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -32..-1

<400> 1230
Met Thr Ile Leu Arg Glu Met Xaa Xaa Ser Leu Tyr Val Leu Glu Ala
-30 -25 -20
Lys Asp Thr Ala Ile Leu Leu Leu Val Xaa Val Ser Asp Lys Asn Glu
-15 -10 -5
Gln Gln Leu Gly Arg Gly Val
1 5

<210> 1231
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1231
Met Arg Leu Ser Ser Ser Cys Gly Leu Pro Val Lys Thr Leu Pro Phe
-25 -20 -15
Ile Cys Cys Asn Leu Tyr Phe Leu Leu Phe Cys Arg Ser Ser Phe Leu
-10 -5 1
Tyr Phe Gly Tyr Asp Pro Ile Asn Thr Tyr Met Tyr Tyr Asn Val Phe
5 10 15
Ser His Ser
20

<210> 1232
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -68..-1

<400> 1232
Met Leu Leu Thr Arg Pro Ala Val Ser Ala Gly Gly Ala Xaa Arg Phe
-65 -60 -55
Ser Pro Gly Ser Arg Gly Arg Gly Ser Asp Leu Glu Arg Gly Leu Cys
-50 -45 -40
Pro Ala His Pro Gly Ala Pro Pro Leu Pro Arg Pro Pro Asp Arg Leu
-35 -30 -25
Pro His Ser Phe Ser Pro Thr Gly Cys Leu Leu Xaa Pro Leu Leu Val
-20 -15 -10 -5
Ser Cys Leu Gly Ser Leu Leu Pro Val Thr Gln Thr Leu Gly Ser Phe
1 5 10
Ser Ala Gly Pro Cys Phe Arg Thr Leu
15 20

<210> 1233
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1233
Met His Ser Leu Cys Pro Leu Ser Gln Phe Leu Pro Ile Leu Xaa Ser

```
-25                 -20                 -15                 -10
Leu Ser Ser Ser Val Pro Ser Arg Ala Gly Ser Ala Phe Pro Ser Ala
                -5                  1                   5
Leu Gly Pro Leu Tyr Gln Pro Leu Leu Gly Pro Pro Ala Trp
        10                  15                  20

<210> 1234
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 1234
Met Arg Thr Gln Val Tyr Glu Gly Leu Cys Lys Asn Tyr Phe Ser Leu
                -40                 -35                 -30
Ala Val Leu Gln Arg Asp Arg Ile Lys Leu Leu Phe Phe Asp Ile Leu
            -25                 -20                 -15
Val Phe Leu Ser Val Xaa Leu Leu Phe Leu Leu Phe Leu Val Asp Ile
        -10                 -5                  1
Met Ala Asn Xaa Thr Thr Ser Leu Gly Arg Pro
5                   10                  15

<210> 1235
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1235
Met Gly Gln Phe Thr Ala Ala Met Val Gly Arg Ile Ser Cys Leu Gly
-45                 -40                 -35                 -30
Val Trp Lys Leu Pro Arg Val Glu Ser Cys Ser Gln Pro Ala Arg Pro
                -25                 -20                 -15
Leu Leu Ser Leu Ala Gln Thr Thr Thr Lys Thr Thr Ala Thr Thr Thr
            -10                 -5                  1
Thr Thr Thr Lys His Ala Thr Cys Ala Leu Ala Tyr Thr Asn Thr Pro
    5                   10                  15
Thr Glu Pro Xaa Gln Ala Asp Lys Ala Ser Arg Arg Ala Ser Gly Xaa
20                  25                  30                  35
Leu Xaa Xaa Ala Ala Arg His Ile Pro Trp His Gly Ala Thr Ala Ala
                40                  45                  50
Gln Leu Pro Ala Pro Pro Pro Ser Val Ile Ser Ala Leu
            55                  60

<210> 1236
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1236
Met Leu Ile Phe Ile Ile Ala Ile Leu Phe Pro Asn Ser Gly Ser Cys
            -15                 -10                 -5
Phe Ala Phe Ser Cys His Val Ser Phe Phe Phe Phe
```

1 5 10

<210> 1237
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1237
Met Val Arg Cys Ala Cys Phe Pro Phe Phe Pro Phe Ala Phe Cys His
-15 -10 -5 1
Asp Cys Lys Phe Leu Gly Ala Ser Gln Ser Cys Phe Leu Leu Ser Arg
5 10 15
Gln Asn Cys Val Ser Thr Gly Xaa Pro Ser Ser Lys Ser Asp Ile Asn
20 25 30
Ser Arg Ser Gly Ser Cys Ser Leu Ala Arg
35 40

<210> 1238
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1238
Met Val Ser Leu Arg Val Gly Ala Ser Pro Phe Arg Phe Pro Leu Ala
-25 -20 -15
Pro Leu Xaa Leu Val Phe Ile Ser Leu Leu Pro Ala Pro Phe Phe Pro
-10 -5 1 5
Thr Leu Ser Phe Pro Cys Cys Cys Val Ser Trp Leu Phe Ser Leu Ser
10 15 20
Val Xaa Val Ser Leu Arg Leu Ser Leu Xaa Val Ser Cys Leu Ser Leu
25 30 35
Trp Cys Leu Leu Val Leu Phe Leu Ser Pro Thr Leu Tyr Val Ser Asp
40 45 50
Ser Phe Cys Ser Phe Cys Val Leu Pro Ile Ala Leu Cys Pro Xaa Ala
55 60 65
Arg Ser
70

<210> 1239
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 1239
Met Ala His Pro Cys Leu Ala Pro Ala Glu Pro Ser Thr Leu Ser Gln
-50 -45 -40
Thr Xaa His Pro Ile Gln Arg Thr Leu Thr Thr Phe Pro Gln Ala Trp
-35 -30 -25
Val Leu Thr Ser Ser Phe Ser Ile Gln Pro Gly Leu Ala Phe Leu Ala
-20 -15 -10
Ile Leu Thr Val Leu Ala Lys Pro Gly Ser Ser Xaa Trp Ser Pro Gly

```
    -5                  1              5                   10
Gln Phe Thr Pro His Ser Leu Leu
                15

<210> 1240
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1240
Met His Phe Pro Ile Gln Ala Thr Phe Xaa Tyr Ser Pro Thr Asp Ser
    -30                 -25                 -20
Leu Cys His Leu Tyr Xaa Ser Leu Phe Ser Ser Phe Leu Cys Ser Thr
-15                 -10                 -5                  1
Pro Ala Arg

<210> 1241
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1241
Met Ala Leu His Ile Leu Glu Cys Glu Arg Asn Val Cys Phe Val Ala
    -35                 -30                 -25
Val Arg Gln Pro Ala His Glu Ser Cys Phe Val Pro Ser Leu Val Thr
-20                 -15                 -10                 -5
Gly Ala Leu Gln Gln Ser Gln Thr Gln His Pro Pro Trp Val Cys Pro
                1               5                   10
Gln Val Gln Gly Ser Tyr Pro Ser Trp Lys Asn Arg Gly
        15                  20                  25

<210> 1242
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1242
Met Ser Cys Thr His Ser Ser Ser Asn Leu Gly Lys Phe Ser Val His
        -30                 -25                 -20
Arg Glu Tyr Arg Val Leu Xaa Leu Cys Asn Ser Arg Val Ser Phe Thr
    -15                 -10                 -5
Arg Xaa His Val Lys Arg Pro Pro Xaa Arg Leu Cys Val Ser Ser Lys
1               5                   10                  15
Gly Cys Leu Phe His Leu Gly Ala Gly Arg
            20                  25

<210> 1243
<211> 40
<212> PRT
<213> Homo sapiens
```

<220>
<221> SIGNAL
<222> -19..-1

<400> 1243
```
Met Leu Lys Lys Leu Ser Ala Phe Pro Leu Leu Leu Val Ile Ile Leu
                -15                 -10                 -5
Leu Phe Gln Lys Gln Xaa Gly Leu Leu Lys Asn Tyr Xaa Ser Pro Gln
            1               5                   10
Arg Gln Val Leu Phe Cys Asn Arg
    15                  20
```

<210> 1244
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1244
```
Met Ser Tyr Phe Arg Cys Ile Phe Leu Ala Val Leu Ser Lys Ile Ser
            -15                 -10                 -5
Trp Ala Val Asn Met Cys Ser Leu Ile Ser Gly Ser Ser
        1               5                   10
```

<210> 1245
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1245
```
Met Leu Cys Ile Met Phe Gly Ile Glu Thr Asn Glu Ile Thr Lys Met
                -30                 -25                 -20
Thr Met Ser Phe Leu Leu Phe Leu Ser Ile Ser Leu Ile Thr Leu Tyr
            -15                 -10                 -5
Tyr Ser Ser Glu Ala Cys Gly
        1               5
```

<210> 1246
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1246
```
Met Cys Gln Ala Arg Ile Ala Leu Asp Arg Cys Asn Leu Arg Thr Ala
                -35                 -30                 -25
Phe Ile Leu Phe Xaa Leu Ile Leu Ser His Tyr Val Phe Xaa Leu Leu
            -20                 -15                 -10
Ala Pro Phe Leu Thr Arg Ser Ser Pro Ser Trp Asn Ser Tyr Gly Thr
        -5                  1                   5
Leu Ala Pro Glu Thr Thr Asn Ser Ser Leu Lys Phe Ser Asn Ser Asn
10                  15                  20                  25
Asn Gly Ile Ser Asp Leu Ala Xaa Leu Tyr Phe Ser His Val Xaa Lys
```

```
                30                  35                      40
Ile Gly Ser Ala Ser Thr Met Gly Tyr Gly
            45                  50

<210> 1247
<211> 99
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1247
Met Val Lys Ser Val Ile Phe Leu Ser Phe Trp Gln Gly Met Leu Leu
                -20                 -15                 -10
Ala Ile Leu Glu Xaa Cys Gly Ala Ile Pro Lys Ile His Ser Ala Arg
            -5                  1                   5
Val Ser Val Gly Glu Gly Thr Val Ala Ala Gly Tyr Gln Asp Phe Ile
    10                  15                  20
Ile Cys Val Glu Met Phe Phe Ala Ala Leu Ala Leu Arg His Ala Phe
25                  30                  35                  40
Thr Tyr Lys Val Tyr Ala Asp Lys Arg Leu Asp Ala Gln Val Pro Thr
                45                  50                  55
Tyr Gly Pro Tyr Gly Arg Cys Ala Pro Met Lys Ser Ile Ser Ser Ser
            60                  65                  70
Leu Lys Glu
        75

<210> 1248
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -86..-1

<400> 1248
Met Asp Met Arg Trp His Cys Glu Asn Ser Gln Thr Thr Asp Asp Ile
    -85                 -80                 -75
Leu Val Ala Ser Ala Glu Cys Pro Ser Asp Asp Glu Asp Ile Asp Pro
-70                 -65                 -60                 -55
Cys Glu Pro Ser Ser Gly Gly Leu Ala Asn Pro Thr Arg Ala Gly Gly
                -50                 -45                 -40
Arg Glu Pro Tyr Pro Gly Ser Ala Glu Val Ile Arg Glu Ser Ser Ser
            -35                 -30                 -25
Thr Thr Gly Met Val Val Gly Ile Val Ala Ala Ala Ala Leu Cys Ile
        -20                 -15                 -10
Leu Ile Leu Leu Xaa Ala Met Tyr
    -5                  1

<210> 1249
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1249
Met Ala Trp Thr Pro Leu Trp Pro Thr Leu Leu Thr Leu Cys Ile Gly
```

```
-20                 -15                 -10                 -5
Ser Val Val Ser Ser Asp Leu Thr Gln Asp Pro Ala Val Ser Val Ala
                1                   5                   10
Leu Gly Gln Arg Val Arg Ile Thr Cys Gln Gly Asp Asn Leu Glu Glu
        15                  20                  25
Tyr Phe Ala Ser Trp Tyr Arg Gln Arg Pro Gly Gln Ala Pro Val Leu
    30                  35                  40
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Xaa Arg Xaa
45                  50                  55                  60
Ser Gly Ser Lys Ser Gly Asn Thr Ala Leu Leu Thr Ile Xaa Gly Ala
                65                  70                  75
Gln Ala Glu Asp Xaa Ala Asp Tyr Tyr Cys Ser Xaa Arg Asp His Thr
            80                  85                  90
Asp Asn Arg Trp Val Phe Gly Gly Gly Thr Arg Leu Thr
        95                  100                 105
```

<210> 1250
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1250

```
Met Glu Ala Glu Phe Tyr Met Xaa Ile Leu Thr Cys Leu Ile Phe Arg
-20                 -15                 -10                 -5
Asn Ser Glu Gly Phe Gln Ile Xaa His Val Gln Lys Gln Gln Cys Leu
                1                   5                   10
Phe Lys Asn Glu Lys Val Val Val Gly Ser Cys Asn Arg Thr Ile Gln
        15                  20                  25
Asn Gln Gln Trp Met Trp Thr Glu Asp Glu Lys Leu Leu His Val Lys
    30                  35                  40
Ser Ala Leu Cys Leu Ala
45                  50
```

<210> 1251
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1251

```
Met Cys Val Cys Ala Cys Ala Leu Cys Val Trp Leu Cys Val Lys Ser
        -15                 -10                 -5
Cys Ser Ile
    1
```

<210> 1252
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1252

```
Met Ile Ser Asp Val Gln His Leu Phe Ile Tyr Leu Leu Ala Phe Cys
```

```
-20 -15 -10
Met Pro Ser Leu Glu Lys Cys Leu Tyr Gly Ser Leu Ala His Phe Phe
-5 1 5 10
Phe Phe
```

<210> 1253
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1253

```
Met Pro Leu Phe Arg Val Leu Phe Ser Xaa Thr Cys Ala Leu Xaa Gln
-15 -10 -5 1
Asp Phe Arg Met Gln Pro Cys Pro Pro Thr Pro Lys
5 10
```

<210> 1254
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1254

```
Met Trp Tyr Val Glu Met Trp Val Ser Phe Phe Leu Leu Phe Tyr Val
-20 -15 -10
Leu Leu Phe Arg Asn Leu Tyr Thr His Thr His His Thr Gly
-5 1 5
```

<210> 1255
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1255

```
Met Ala Ala Arg Val Gly Ala Phe Leu Lys Asn Ala Trp Asp Lys Glu
-30 -25 -20 -15
Pro Val Leu Val Val Ser Phe Val Val Gly Gly Leu Gly Cys Asn Xaa
-10 -5 1
Ala Pro Ile Glu Pro Leu Leu Gln Val Leu Arg His Asp Gln Gln Gly
5 10 15
His Ala Leu Gln Leu Xaa
20
```

<210> 1256
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1256

```
Met Gln Ala Arg Arg Trp Glu Ser Trp Met Trp Thr Cys Val Ala Pro
            -20                 -15                 -10
Val Tyr Pro Ala Cys Ser Gly Arg Arg Ala Xaa Ala Val Xaa Gln Xaa
        -5                  1               5
Xaa Pro Arg Leu Gly Xaa Xaa Leu Pro Gly Pro Gly Xaa Glu His Leu
10                  15                  20                  25
Ala His Val Cys Gly Leu Pro Ala Gly Glu Ala Gly Arg Gly Arg Gly
                30                  35                  40
Val Glu Arg Pro Gln Glu Lys Arg Ala Asp Lys Ala Val Xaa Val Arg
            45                  50                  55
Arg Gly Leu Gly Gly Ala Gly Leu Pro Gly Gly Asp Thr Pro Arg Gly
        60                  65                  70
Pro Pro Met Ser Thr Trp Pro
    75                  80
```

<210> 1257
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1257

```
Met Phe Leu Phe Phe Phe Gly Asn Ser Pro Cys Cys Gly Ala Thr Gly
                -10                 -5                  1
```

<210> 1258
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1258

```
Met Gly Leu Ser His His Arg Val Ser Ala Pro Ser Ser Leu Ser Leu
-25                 -20                 -15                 -10
Ser Leu Ser Ala Ser Leu Ile Ile Ser Pro Ser Pro Ser Ala Ser Pro
                -5                  1               5
Ser Leu Leu Xaa Pro Pro Xaa Arg
        10                  15
```

<210> 1259
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1259

```
Met Phe Val Phe Leu Val Gly Thr Pro Cys Leu Ser Met Leu Leu Arg
            -20                 -15                 -10
Leu Val Ser Asn Ser Arg Pro Pro Val Met Arg Pro Pro Arg Pro Gly
        -5                  1               5
```

<210> 1260
<211> 42

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1260
Met Lys Phe Thr His Phe Lys Cys Thr Ile Arg Leu Leu Leu Leu Tyr
-30 -25 -20
Leu Gln Asn Pro Val Thr Ile Thr Ile Leu Phe Leu Ile Val Ser Met
-15 -10 -5
Ala Leu Lys Ile Asn His Ile Pro Lys Gly
1 5

<210> 1261
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1261
Met Ser Cys Met Ser Leu Phe Pro Cys Cys Pro Ala Gln Ser Lys Asn
-10 -5 1
Tyr Met Leu Leu Leu Phe Ile Ile Leu Leu Pro Thr Gln Phe Leu Tyr
5 10 15
Ser Lys Leu Val Thr Ile Cys Cys Cys Phe
20 25

<210> 1262
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1262
Met Leu Val Cys Cys Thr Ile Asn Ser Ser Phe Ala Leu Gly Ile Ser
-10 -5 1
Arg Asn Ala Ile Pro Leu Pro Ala Pro Gly
5 10

<210> 1263
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1263
Met Gly Arg Gly Pro Gly Pro Leu Gln Glu Arg Ser Leu Phe Glu Xaa
-50 -45 -40
Lys Arg Gly Ala Pro Pro Ser Ser Asn Ile Glu Asp Phe His Gly Leu
-35 -30 -25
Leu Pro Lys Val Ile Pro Ile Cys Ala Leu Tyr Val Ile Cys Gln Phe
-20 -15 -10

```
Ile Leu Ile Arg Ser Gly Val Asn Ile Ser Met Glu Gln Val Thr Val
-5                  1               5                   10
Val Asp Ala Ser Leu
            15

<210> 1264
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1264
Met Leu Tyr Cys Val Val Val Val His Ser Val Cys Cys Ala Val Tyr
            -10                 -5                  1
Tyr Phe Val Ile Ile His Thr Ile Glu His Ile Thr Tyr Leu Cys Ile
    5                   10                  15
His Ser Thr Ile Leu Leu Cys Val
20                  25

<210> 1265
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1265
Met Cys Trp Leu Arg Xaa Trp Gly Gln Ile Leu Leu Pro Val Phe Xaa
    -25                 -20                 -15
Ser Leu Phe Leu Ile Gln Leu Leu Ile Ser Phe Ser Glu Asn Gly Phe
-10                 -5                  1                   5
Ile His Ser Pro Met
            10

<210> 1266
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1266
Met Cys Gly Leu Xaa Ile Leu Cys Gly Pro Trp Leu His Ala Ala Pro
                -10                 -5                  1
Pro Ser Pro Pro Arg
        5

<210> 1267
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1
```

<400> 1267

```
Met Phe His Gly Arg Val Met Ala Met Gly Xaa Leu Thr Lys His Leu
            -30                 -25                 -20
Asn Leu Asn Ile Ser Ile Ser Leu Leu Leu Met Leu Xaa Xaa Tyr Trp
        -15                 -10                 -5
Ser Cys Trp Ile Lys Ser Pro Pro Xaa Met
    1               5
```

<210> 1268
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -128..-1

<400> 1268

```
Met Leu Gly Arg Ser Ser Leu Leu Xaa Trp Lys Xaa Ser Pro Gly Ser
            -125                -120                -115
Lys Lys Leu Val Val Ala Thr Glu Lys Asn Val Ile Ala Ala Leu Asn
        -110                -105                -100
Ser Arg Thr Gly Glu Ile Leu Trp Arg His Val Asp Lys Gly Thr Ala
    -95                 -90                 -85
Glu Gly Ala Val Asp Ala Met Leu Leu His Gly Gln Asp Val Ile Thr
-80                 -75                 -70                 -65
Val Ser Asn Gly Gly Arg Ile Met Arg Ser Trp Glu Thr Asn Ile Gly
                -60                 -55                 -50
Gly Leu Asn Trp Glu Ile Thr Leu Asp Ser Gly Ser Phe Gln Ala Leu
            -45                 -40                 -35
Gly Leu Val Gly Leu Gln Glu Ser Val Arg Tyr Ile Ala Val Leu Lys
        -30                 -25                 -20
Lys Thr Thr Leu Ala Leu His His Leu Ser Ser Gly His Ser Ser Gly
    -15                 -10                 -5
Trp Thr Ser Pro
1
```

<210> 1269
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -57..-1

<400> 1269

```
Met Ser Thr Thr Tyr Leu Asn Glu Asp Leu Lys Lys Lys Phe Ser Ala
        -55                 -50                 -45
Val Ile Glu Gln Val Leu Phe Ala His Leu Ser Pro Leu His Val Trp
    -40                 -35                 -30
Leu Gln Leu Arg Ser Leu Cys Glu Xaa Leu Thr Cys Ile Trp Val Arg
-25                 -20                 -15                 -10
Phe Asn Phe Leu Ala Ser Ser Gln Ala Cys Ser Lys Cys Asn Ser Ser
                -5                  1               5
Phe Leu Ile Met Ser Ser Ser Ser
        10                  15
```

<210> 1270
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1270
```
Met Ala Leu Ile Val Leu Gln Leu Thr Phe Gly Ile Gly Tyr Val Thr
                -35                 -30                 -25
Leu Leu Gln Ile His Ser Ile Tyr Ser Gln Leu Ile Ile Leu Asp Leu
            -20                 -15                 -10
Leu Val Pro Val Ile Gly Leu Ile Thr Glu Leu Pro Leu His Ile Arg
        -5                  1               5
Glu Thr Leu Leu Phe Thr Ser Ser Leu Ile Leu Thr Leu Asn Thr Val
10                  15                  20                  25
Phe Val Leu Ala Val Lys Leu Lys Trp Phe Tyr Tyr Ser Thr Arg Tyr
                30                  35                  40
```

<210> 1271
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1271
```
Met Arg Val Ala Gly Ala Ala Lys Leu Val Val Xaa Val Ala Xaa Phe
                -20                 -15                 -10
Leu Leu Thr Phe Tyr Val Ile Ser Gln Val Phe Glu Ile Lys Met Asp
            -5                  1               5
Ala Ser Leu Gly Asn Leu Phe Ala Arg Ser Ala Leu Asp Thr Ala Ala
    10                  15                  20
Arg Ser Thr Lys Pro Pro
25                  30
```

<210> 1272
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1272
```
Met His Thr Leu Val Phe Leu Ser Thr Arg Gln Val Leu Gln Cys Gln
-15                 -10                 -5                  1
Pro Ala Ala Cys Gln Ala Leu Pro Leu Leu Pro Arg Glu Leu Phe Pro
            5                   10                  15
Leu Leu Phe Lys Val Ala Phe Met Xaa Lys Lys Thr Val Val Leu Arg
        20                  25                  30
Xaa Leu Val His Thr Arg
    35
```

<210> 1273
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1273
Met Thr Val Val Ile Ser Cys Leu Val Gly Glu Cys Gly Ser Trp Lys
-10 -5 1

<210> 1274
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 1274
Met Cys Thr Leu Thr Asp Thr His Thr His Val Gln Val His Lys Ser
-45 -40 -35
Lys Pro Cys Gln Leu Leu Ser Pro Pro Pro Pro Xaa His Gly Pro Leu
-30 -25 -20
Leu Leu Pro Ile Phe Gly Leu Leu Val Pro Ser Gln Ile Phe Ser Ser
-15 -10 -5 1
Leu Leu Asn Ser Leu His Leu Gly Leu Pro Ser Phe Pro Lys Met Pro
5 10 15
Leu Met Ile Phe Leu Pro Arg Trp
20 25

<210> 1275
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 1275
Met Thr Leu Ile Leu Gly Glu Ser Ser Ser Gln Pro Gln Ile Ser Ile
-60 -55 -50
Phe Leu Trp Thr Lys Val Lys Asp Leu Phe Ser Leu Met Ile Thr Trp
-45 -40 -35
Thr Val Gln Met Lys Leu Thr Ser Met Trp Met Asn Leu Ile Pro Pro
-30 -25 -20
Met Lys Gln Ile Leu Xaa Ser Thr Leu Ala Met Lys Ile His Ser Gln
-15 -10 -5 1
Gln Arg Phe Trp Pro Arg Val Arg Val Tyr Ser Arg Ile Tyr
5 10 15

<210> 1276
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1276
Met Tyr Lys Glu Lys Leu Val Leu Phe Leu Leu Asn Leu Phe Gln Lys
-15 -10 -5
Ile Glu Glu Glu Glu Leu Phe Pro Asn
1 5

<210> 1277
<211> 88

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -48..-1

<400> 1277
```
Met Asp Ser Val Pro Ala Thr Val Pro Ser Ile Ala Ala Thr Pro Gly
            -45                 -40                 -35
Asp Pro Glu Leu Val Gly Pro Leu Ser Val Leu Tyr Ala Ala Phe Ile
        -30                 -25                 -20
Ala Lys Leu Leu Glu Leu Val Ala Thr Leu Pro Asp Asp Val Gln Pro
    -15                 -10                 -5
Gly Pro Asp Phe Tyr Gly Xaa Xaa Trp Lys Leu Tyr Leu Ser Leu Pro
1               5                   10                  15
Ser Trp Glu Xaa Phe Val Cys His Phe Leu Met Glu Thr Val Leu Val
            20                  25                  30
Val Lys Xaa Arg Val Tyr Xaa Val
        35                  40
```

<210> 1278
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1278
```
Met Ala Ala Tyr Phe Ala Val Trp Ala Ser Val Ala Ser Pro Ala Ser
            -15                 -10                 -5
Ile Cys Cys Gly Xaa Trp Leu Thr Gly Leu Val Arg His Glu Arg Ile
        1               5                   10
Glu Ala Pro Trp Ala Arg Gly
15                  20
```

<210> 1279
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1279
```
Met Lys Thr Gln Phe Leu Ser Trp Gly Lys Phe Ser Phe Cys Phe Gly
                -25                 -20                 -15
Ile Leu Leu Ile Leu Gln Leu Leu Lys Xaa Ser Leu Lys Lys Cys Arg
            -10                 -5                  1
His Gly
    5
```

<210> 1280
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1280
Met Leu Pro Ala Val Ala Val Ser Glu Pro Val Val Leu Arg Phe Ile
-25 -20 -15 -10
Leu Pro Ser Ser Trp Asp Cys Arg Cys Ala Pro Pro Leu Leu Thr Gly
-5 1 5
Phe Cys Ile Phe Trp Xaa Glu Thr
10 15

<210> 1281
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1281
Met Asp Pro Ala Ala Pro Trp Leu Phe Trp Glu Ala Ala Ala Pro Ala
-30 -25 -20
Leu Lys Arg Pro Trp Leu Leu Met Val Ala Pro Arg Leu Pro Ala Gly
-15 -10 -5
Ala Arg Asp Ser Gly Gln Phe Pro Arg Lys Gly Gln Ala Gly Ser Pro
1 5 10 15
Ser Arg Gly Arg Val Arg Lys Leu Gly Gly Ala Val
20 25

<210> 1282
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1282
Met Lys Met Ser Thr Pro Ser Pro Leu Ser Lys Lys Val Leu Arg Asn
-30 -25 -20
Gln Val Ser Arg Leu Xaa Ala Leu Leu Ser Pro Tyr Ala Phe Thr Leu
-15 -10 -5 1
Xaa Arg Leu Ala Ser Gly
5

<210> 1283
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1283
Met Arg Arg Phe Leu Leu Leu Tyr Ala Thr Gln Gln Gly Gln Ala Lys
-15 -10 -5 1
Ala Ile Ala Glu Glu Met Cys Xaa Gln Ala Val Val His Gly Phe Ser
5 10 15
Ala Asp Leu His Cys Ile Ser Glu Ser Asp Lys Val Ser Val Ile Gln
20 25 30
Asn Thr Pro Thr Phe Ala Thr Gly Gly Arg
35 40

<210> 1284
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1284
```
Met Leu Ile Asp Ile Trp Ser Met Val Leu Arg Glu Asn Leu Phe Val
        -25                 -20                 -15
Asn Leu Asn Leu Cys Phe Ala Tyr Thr Phe Ala Leu Tyr Ser Cys Pro
    -10                 -5                  1               5
Ala Pro Thr Arg Cys Pro Arg Pro Ser
                10
```

<210> 1285
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1285
```
Met Leu Ser Cys Pro Trp Phe Pro Leu Ser Cys Ser Pro Ser Leu Pro
            -15                 -10                 -5
Leu Ser Ile Pro Asp Cys Leu Pro Ala Phe Leu Trp Pro Leu Gly Ile
        1               5                   10
Pro Trp Pro Asp Gly Glu Gly Leu Arg Pro Ser Arg Leu Leu Arg Thr
15                  20                  25                  30
Arg Glu Asn Ile Thr Pro Leu Ser Leu Phe Ala Met Leu Ser Gly Arg
                35                  40                  45
Glu Gly Ala Pro Leu Leu Val Pro Leu
            50                  55
```

<210> 1286
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1286
```
Met Val Val Val Ser Phe Leu Ala Ser Ser Ser Leu Pro Ala Glu Thr
            -10                 -5                  1
Pro Lys Gln Gly
    5
```

<210> 1287
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -107..-1

<400> 1287
Met Gly Xaa Leu Ala Leu Xaa Ala Trp Leu Gln Pro Arg Tyr Arg Lys
-105 -100 -95
Asn Ala Tyr Leu Phe Ile Tyr Tyr Leu Ile Gln Phe Cys Gly Xaa Ser
-90 -85 -80
Trp Ile Phe Ala Asn Met Thr Val Arg Phe Phe Ser Phe Gly Lys Asp
-75 -70 -65 -60
Ser Met Val Asp Thr Phe Tyr Ala Ile Gly Leu Val Met Arg Leu Cys
-55 -50 -45
Gln Ser Val Ser Leu Leu Glu Leu Leu His Ile Tyr Val Gly Ile Glu
-40 -35 -30
Ser Asn His Leu Leu Pro Arg Phe Leu Gln Leu Thr Glu Arg Ile Ile
-25 -20 -15
Ile Leu Phe Val Val Ile Thr Ser Arg Arg Gly Ser Pro Thr Arg Asn
-10 -5 1 5
Met Trp Cys Val Cys Tyr Ser Ser Leu Asp Leu Trp Ile Trp Leu Xaa
10 15 20
Thr Leu Ile Ala Xaa Xaa Ser Val Ile Gly Ile Ser Tyr Ala Val Leu
25 30 35
Thr

<210> 1288
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1288
Met Asp Thr Phe Pro Ser Leu Thr Leu Thr Ala Leu Leu Val Pro Ser
-15 -10 -5
Arg Val Gln Pro Gln
1

<210> 1289
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1289
Met Gly Leu Thr Lys Gln Tyr Leu Arg Tyr Val Ala Ser Ala Val Phe
-20 -15 -10 -5
Gly Val Ile Gly Ser Gln Lys Gly Asn Ile Val Phe Val Thr Leu Arg
1 5 10
Gly Glu Lys Gly Arg Tyr Val Ala Val Pro Ala Cys Glu His Val Phe
15 20 25
Ile Xaa Asp Leu Arg Lys Gly Glu Lys Ile Leu Ile Leu Gln Gly Leu
30 35 40
Lys Gln Glu Val Thr Cys Leu Cys Pro Ser Pro Asp Gly Leu His Leu
45 50 55 60
Ala Val Gly Tyr

<210> 1290
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1290
Met Met Gly Ile Phe Leu Val Tyr Val Gly Phe Val Phe Phe Ser Val
-20 -15 -10
Leu Tyr Val Gln Gln Gly Leu Ser Ser Gln Ala
-5 1

<210> 1291
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1291
Met Ser Leu Gly Leu His Ser Asn Ser Trp Val Leu Asp Pro Ala Leu
-20 -15 -10
Leu Leu Thr Cys Leu Thr Phe Pro Ile Tyr Lys Leu Leu Trp Val Arg
-5 1 5 10
Gly Gly Thr Arg Xaa Thr Leu Xaa Ala Leu His Ser Ala Arg Thr
15 20 25

<210> 1292
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -60..-1

<400> 1292
Met Ala Ala Asn Ser Ser Gly Gln Gly Phe Gln Asn Lys Asn Arg Val
-60 -55 -50 -45
Ala Ile Leu Ala Glu Leu Thr Lys Arg Lys Glu Asn Tyr Leu Cys Arg
-40 -35 -30
Thr Ser Leu Gln Gln Ile Ile Leu Glu Leu Gly Ile Asp Thr Ile Met
-25 -20 -15
Trp Val Xaa Cys Xaa Phe Cys Phe Val Leu Phe Cys Phe Glu Thr Glu
-10 -5 1
Ser Arg Pro Val
5

<210> 1293
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1293
Met Ser Ala Gly Ser Ala Thr His Pro Gly Ala Gly Gly Arg Arg Ser
-35 -30 -25 -20
Lys Trp Asp Gln Pro Ala Pro Ala Pro Leu Leu Phe Leu Pro Pro Ala
-15 -10 -5
Ala Pro Gly Gly Glu Val Thr Ser Ser Gly Gly Ser Pro Gly Xaa Thr

```
                    1                        5                        10
Thr Ala Ala Pro Ser Gly Ala Leu Asp Ala Ala Ala Ala Val Ala Ala
        15                  20                  25
Lys Ile Asn Ala Met Leu Met Ala Lys Gly Lys Leu Lys Pro Thr Gln
30                  35                  40                  45
Xaa Ala Ser Glu Lys Leu Gln Ala Pro Gly Lys Gly Leu Thr Ser Asn
                50                  55                  60
Lys Ser Lys Asp Asp Leu Val Val Ala Glu Val Glu Ile Asn Asp Val
            65                  70                  75
Pro Leu Thr Cys Arg Asn Leu Leu Thr Arg Gly Gln Xaa Gln Asp Glu
        80                  85                  90
Ile Ser Arg Leu Ser Gly Ala Ala Val Ser
    95                  100
```

<210> 1294
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1294

```
Met Ser Pro Leu Asp Gln Ala Val Ile Arg Ala Val Cys Leu Ser Gly
    -20                 -15                 -10
Gly Ser Cys Trp Gly Gly Val Arg Cys Leu Val Arg Gly Gly Pro Asn
-5                  1               5                   10
Ile Gly Pro Ala Ala Gln Leu Leu Gly Gly Ile Pro Leu Cys Trp Pro
            15                  20                  25
Pro Ala Val Thr Ala Gly Glu Val Lys Leu
        30                  35
```

<210> 1295
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1295

```
Met Asn Ser Phe His Phe Ile Xaa Phe Leu Pro Phe Pro Trp Ala Glu
-15                 -10                 -5                  1
Xaa Ala Gln
```

<210> 1296
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1296

```
Met Gly Trp His Ser His Ser Ser Gln Gly Val Xaa Ala Met Pro Leu
                -25                 -20                 -15
Leu Leu Ser Thr His Thr Trp Thr Asp Thr Ala Leu Ala Phe Ser Thr
            -10                 -5                  1
His Thr His
    5
```

<210> 1297
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1297
Met Xaa Ala Val Arg Asn Ala Gly Ser Trp Phe Leu Arg Ser Trp Thr
-20 -15 -10
Trp Pro Gln Thr Ala Gly Arg Val Val Ala Arg Xaa Pro Ala Gly Thr
-5 1 5 10
Ile Cys Thr

<210> 1298
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1298
Met Cys Ala Leu Phe Ile Leu Val Ser Ile Ser Leu Phe Tyr Ala Leu
-15 -10 -5 1
Phe Ile Ser Pro Ser Ile Gln
5

<210> 1299
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1299
Met Tyr Leu Val Cys Thr Thr Cys Thr Trp Cys Val Phe Ser Glu Met
-50 -45 -40
Phe Val His Gly Leu Asn Ile Thr Gln Leu Val Leu Ser Gln Leu Asp
-35 -30 -25
Tyr Phe Phe His Ser Asn Leu Thr Asn Leu Val Leu Tyr Phe Leu Val
-20 -15 -10
His Leu Leu Phe Ser Leu Ser Leu Phe Met Pro Leu Thr
-5 1 5

<210> 1300
<211> 138
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -78..-1

<400> 1300
Met Lys Leu Lys Leu Tyr Leu Cys Ile Leu Gly Pro Trp Gly Cys Xaa
-75 -70 -65

```
Xaa Lys Val Pro Leu Ile Gly Phe Leu Lys Arg Ile Xaa Xaa Tyr Xaa
        -60                 -55                 -50
Leu Thr Val Leu Lys Pro Xaa Ser Leu Xaa Ser Xaa Ser Ala Gly Leu
    -45                 -40                 -35
Val Pro Ser Glu Asp Ser Lys Lys Glu Ser Val Ser Cys Leu Ser Pro
-30                 -25                 -20                 -15
Arg Phe Trp Trp Trp Leu Gly Ser Leu Xaa Val Thr Trp Leu Ile His
                -10                 -5                  1
Ala Ser Leu Gln Ser Leu Ser Pro Phe Ser His Ala Ile Phe Ser Cys
        5                   10                  15
Val Ser Val Phe Ser Phe Ala Tyr Lys Asp Thr Ser His Ile Glu Leu
    20                  25                  30
Gly Pro Ala Leu Ile Thr Ser Ser Gln Leu Pro Leu Gln Gly Thr Asn
35                  40                  45                  50
Phe Gln Ile Met Ser His Ser His Val Ala
                55                  60
```

<210> 1301
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1301

```
Met Asn Glu Lys Lys Lys Leu Leu Gly Thr Glu Gln Lys Gln Lys Lys
            -30                 -25                 -20
Arg Met Gly Asn Leu Lys Leu Leu Phe Leu Ile Leu Ile Leu Ile Ala
        -15                 -10                 -5
Gly Tyr Arg
    1
```

<210> 1302
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1302

```
Met Gly Leu Gln Ser Leu Thr Leu Pro Val Ser Cys Ser Pro Ser Ala
        -25                 -20                 -15
Leu Met Leu Pro Leu Gly Cys Ala Val Arg Thr Arg Met Leu
    -10                 -5                  1
```

<210> 1303
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1303

```
Met Asp Ser Asn Lys Lys Leu Val Leu Ser Ile Thr Gly Asn Thr Val
    -30                 -25                 -20
Trp Ile Leu Thr Thr Leu Glu Ser Leu Ala Gly Ser Val Xaa Ser Glu
-15                 -10                 -5                  1
```

Gln Asp Leu Ser Ala Tyr
5

<210> 1304
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 1304
Met Thr Cys Met Leu Ala Cys Arg Cys Ser Leu Xaa Gly Pro Gln Asp
-45 -40 -35
Phe Arg Phe Cys Ser Val Phe Ser Leu Leu Leu Lys Leu Gly Asn Phe
-30 -25 -20
Tyr Phe Ser Phe Xaa Xaa Cys Leu Phe Leu Xaa Leu Xaa Xaa Ser Glu
-15 -10 -5 1
Met Glu Ser His Ser Phe Ser
5

<210> 1305
<211> 113
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -65..-1

<400> 1305
Met Glu Asp Val Glu Ala Arg Phe Ala His Leu Leu Gln Pro Ile Arg
-65 -60 -55 -50
Asp Leu Thr Lys Asn Trp Glu Val Asp Val Ala Ala Gln Leu Gly Glu
-45 -40 -35
Tyr Leu Glu Glu Leu Asp Gln Ile Cys Ile Ser Phe Asp Glu Gly Lys
-30 -25 -20
Thr Thr Met Asn Phe Ile Glu Ala Ala Leu Leu Ile His Gly Ser Ala
-15 -10 -5
Cys Val Tyr Ser Lys Lys Val Glu Tyr Leu Tyr Ser Leu Val Tyr Gln
1 5 10 15
Ala Leu Asp Phe Ile Ser Gly Lys Arg Arg Ala Lys Gln Leu Ser Ser
20 25 30
Val Gln Glu Asp Arg Ala Asn Gly Val Ala Ala Pro Gly Ser Pro Gly
35 40 45
Gly

<210> 1306
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1306
Met Phe Val Ser Tyr Leu Ile Leu Thr Leu Leu His Val Gln Thr Ala
-15 -10 -5 1
Val Leu Ala Arg
5

<210> 1307
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1307
Met Pro Glu Ala Ala Leu Phe Leu Phe Phe Leu Phe Ile Phe Leu Leu
-25 -20 -15 -10
Tyr Phe Lys Phe Trp Gly Thr Cys Ala Glu Arg Ala Gly Leu Leu His
-5 1 5
Arg Tyr Thr Arg Ala Met Glu Val Cys Cys Thr His Gln Pro Ser Ser
10 15 20
Thr Leu Gly Ile Ser Pro Asn Ala Leu Leu Pro Leu
25 30 35

<210> 1308
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1308
Met Arg Met Gly Thr Arg Ala Ser Pro Pro Leu Cys Met His Leu Ser
-20 -15 -10
Ile His Pro Xaa Xaa Cys Ala Cys Ile Cys Pro Ser Ile Gln
-5 1 5

<210> 1309
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1309
Met Tyr Pro Arg Val Trp Gly Cys Phe Gln Leu Leu His Xaa Leu Xaa
-35 -30 -25
Xaa Thr Arg Thr Thr Gly Lys Xaa Val Cys Val Cys Val Cys Val Cys
-20 -15 -10 -5
Val Cys Val Cys Val Cys
1

<210> 1310
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1310
Met Ala Ala Val Val Leu Ala Ala Thr Arg Leu Leu Arg Gly Ser Gly
-10 -5 1

Ser Trp Gly Cys Ser Arg Leu Arg Phe Gly Pro Pro Ala Tyr Arg Arg
5 10 15
Phe Ser Ser Gly Gly Ala Tyr Pro Asn Ile Pro Leu Ser Ser Pro Leu
20 25 30
Pro Gly Val Pro Lys Pro Val Phe Ala Thr Val Asp Gly Gln Glu Lys
35 40 45 50
Phe Glu Thr Lys Val Thr Thr Leu Asp Asn Gly Leu Arg Val Ala Ser
55 60 65
Gln Asn Lys Phe Gly Gln Phe Cys Thr Val Gly Ile Leu Ile Asn Ser
70 75 80
Gly Ser Arg Tyr
85

<210> 1311
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1311
Met Tyr Cys Leu Xaa Cys Val Glu Lys Ile Ala Lys Ala Leu Tyr Leu
-25 -20 -15 -10
Ser Leu Asn Leu Tyr Phe Ala Asn Ser Leu Tyr Tyr Met Cys Val Cys
-5 1 5
Ser Tyr Ile Tyr Phe Tyr Leu Xaa Ile Tyr Xaa Tyr Xaa Leu Ile Lys
10 15 20
Xaa Xaa Ser Tyr Tyr Val Ala Gln Thr Gly Leu
25 30

<210> 1312
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1312
Met Cys Gln Leu Arg Arg Gly Leu Gly Lys Arg Pro Leu Ser Glu Ala
-25 -20 -15
Ser Ala Val Phe Leu Thr Ala Val Phe Ser Ser His Ser Trp Leu Val
-10 -5 1
Gly Pro Arg Tyr
5

<210> 1313
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1313
Met Ser Val Arg Ser Thr Trp Cys Arg Ala Gln Phe Asn Ser Trp Val
-30 -25 -20
Ser Leu Leu Thr Phe Cys Leu Ile Asp Leu Ser Asn Val Asp Ser Gly
-15 -10 -5 1

Xaa

<210> 1314
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1314
Met Val Ser Gly Val Pro Ser Gly Leu Gly Lys Ser Ala Arg Pro Arg
-50 -45 -40
Gly Arg Arg Ala Arg Lys Leu Leu Pro Ala Pro Arg Ala Ala Pro Arg
-35 -30 -25
Thr Ala Pro Asp Tyr Pro Gly Pro Leu Arg Leu Thr Trp Leu Val Ala
-20 -15 -10
Ala Gly Leu Glu Gly Arg Val His Leu Ala Asp Thr Ser Ser Gly Arg
-5 1 5 10
Lys Thr Trp Pro Gly Cys Gly His Gln Trp Lys Trp Lys Ala Leu Leu
15 20 25
Ile Leu Val Arg Ala Phe Pro Ala
30 35

<210> 1315
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1315
Met Gly Gly Cys Val Xaa Trp Arg Phe Leu Gly His Ser Ser Ala Leu
-30 -25 -20
Arg Thr Val Cys Ser Ser Leu Arg Ser Xaa Arg Pro Cys Trp Cys Asp
-15 -10 -5 1
Gly Leu Arg Leu Arg
5

<210> 1316
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1316
Met Asn Ser Lys Gly Gln Tyr Pro Thr Gln Pro Thr Tyr Pro Val Gln
-50 -45 -40
Pro Pro Gly Asn Ser Ser Ile Pro Ser Asp Leu Ala Ser Ser Ser Gly
-35 -30 -25 -20
Ser Thr Leu Tyr Arg Cys Ser Thr Cys Leu Leu Arg Ala Leu Ser Ser
-15 -10 -5
Glu Leu Cys Ala Pro Arg Gly Cys His Ser Pro His His Val Ser Arg
1 5 10
Ile Ser Trp Thr Leu Ser Val Ser Ser His Gly Pro Val Cys Gly Cys
15 20 25
Trp Ala Phe Arg Phe His Asn Pro His Gly Leu Leu Ser Ser Arg Ser

30 35 40 45
His Leu Ser Xaa Trp Leu His Ser Ala Gly
50 55

<210> 1317
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1317
Met Val Val Val Ser Ala Phe Ile Tyr Leu Phe Phe Glu Thr Gly Ser
-20 -15 -10
Pro Ser Val Ala Gln Ser Gly Val Gln Trp Cys Asp Leu Gly Leu Leu
-5 1 5 10
Gln Pro Pro Pro Pro Gly Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu
15 20 25
Gly Xaa Xaa Asp Cys Arg Arg Ala Pro Pro Gly
30 35

<210> 1318
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1318
Met Phe Val Ser Xaa Thr Xaa Phe Phe Phe Xaa Leu Xaa Phe Leu Gly
-20 -15 -10
Met Phe Leu Ser Gly Met Val Ala Gln Ile Asp Ala Asn Trp Asn Phe
-5 1 5
Leu Asp Phe Ala Tyr His Phe Thr Val Phe Val Phe Tyr Phe Gly Ala
10 15 20
Phe Leu Leu Glu Ala Ala Ala Thr Ser Leu His Asp Leu His Cys Asn
25 30 35 40
Thr Thr Ile Thr Xaa Gln Pro Leu Leu Ser Asp Asn Gln Tyr Asn Ile
45 50 55
Asn Val Ala Ala Ser Ile Phe Ala Phe Met Thr Thr Ala Cys Tyr Gly
60 65 70
Cys Ser Leu Gly Leu Ala Leu
75

<210> 1319
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1319
Met Ser Ser Glu Ile Phe Xaa Xaa Xaa Xaa Ile Ala Tyr Ala Xaa Tyr
-25 -20 -15
Leu Leu Val Gly Leu Phe Pro Leu Lys Cys His Xaa Ser Xaa Phe Ser
-10 -5 1 5
Lys Xaa Gln Ile Ser Ser Phe Val Glu

10 15

<210> 1320
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1320
Met Ala Ala Ser Ser Leu Thr Val Thr Leu Gly Arg Leu Ala Ser Ala
-15 -10 -5
Cys Ser His Ser Ile Leu Arg Pro Ser Gly Pro Gly Ala Ala Ser Leu
1 5 10
Trp Ser Ala Ser Arg Arg Phe Asn Ser Gln Ser Thr Ser Tyr Leu Pro
15 20 25 30
Gly Tyr Val Xaa Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Arg
35 40 45

<210> 1321
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1321
Met Leu Ile Ala Ala Cys Ile Cys Ser Cys Leu Phe Phe Ser Gln Tyr
-15 -10 -5
Leu Xaa Xaa Ser Asn Pro Ala Ala
1 5

<210> 1322
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1322
Met Lys Cys Trp Val Leu Ser Tyr Met Trp Gln Ser Ala Ser Leu Gly
-15 -10 -5
Phe Ser Asn Arg Ile Lys Ser Xaa Leu Arg Pro Pro Ala Gly
1 5 10

<210> 1323
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69..-1

<400> 1323
Met Ser Val Gly Leu Cys Phe Leu Ile Trp Gln Met Gly Ile Met Leu
-65 -60 -55

Leu Pro Arg Glu Cys Trp Lys Val Lys Asp Ser Lys Lys Tyr Lys Ser
-50 -45 -40
Cys Arg Glu Ser Val Leu Pro Ala Gln Ala Cys Thr Gly Glu Ser Pro
-35 -30 -25
Val Leu Ser Gly Val Arg Val Leu Gly Ile Arg Leu Ser Cys Val Leu
-20 -15 -10
Ser His Leu Gln Ala Trp Asp Ser Trp Asp Asn Gln Lys Val Cys Tyr
-5 1 5 10
Leu Gly Ala Pro Cys Phe Gly Lys Arg Leu Ser Pro Thr Thr Trp Leu
15 20 25
Thr Phe Trp Val Gly
30

<210> 1324
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1324
Met Phe Ala Phe Leu Ala Gly Cys Ser Gly Ser Cys Leu Trp Ser Arg
-10 -5 1
His Phe Gly Arg Leu Arg Arg Ala Ala Pro Leu Ser Pro Glu Phe Glu
5 10 15
Thr Gly Leu Gly Asn Met Val Glu Pro Gln Trp
20 25

<210> 1325
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1325
Met Pro Thr Tyr Phe Leu Phe Val Pro His Leu Ile Ser Cys Asn Trp
-15 -10 -5
Cys Glu Pro Arg Gly Asn Asn Pro Gln Ile Pro Leu Leu Ala Ile His
1 5 10 15
Thr Arg Lys Lys Asn Gln His Phe Ile Thr
20 25

<210> 1326
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1326
Met Leu Trp Thr Ser Phe Gln Asn Pro Leu Gln Val Val Leu Leu Thr
-25 -20 -15
Ser Val Ser Leu Xaa Xaa Xaa Xaa Xaa Xaa Gly Ser Val Arg Ile Xaa
-10 -5 1 5
Leu Ser His Trp Ser Ser Ser Ala Phe Phe Phe Leu Ile Xaa Xaa Xaa
10 15 20

```
Xaa Leu Ser His Val Thr Lys Gln Met His Leu
            25                  30

<210> 1327
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1327
Met Leu Thr Cys Leu Cys Gly Cys Phe Ile Val Leu Leu Val Cys Val
                -10                 -5                  1
Leu Lys Cys Val Phe Val Val Ala Ser Asn Gly Leu Phe Phe Pro
        5                   10                  15

<210> 1328
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1328
Met Val Val Ser Phe Ala Val Gln Lys Leu Phe Ser Leu Ile Arg Ser
                -25                 -20                 -15
His Leu Ser Ile Leu Ala Phe Val Ala Ile Ala Phe Gly Val Leu Asp
            -10                 -5                  1
Met Lys Ser Leu Pro Thr Pro Gly
    5                   10

<210> 1329
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -65..-1

<400> 1329
Met Gly Gly Arg Lys Met Ala Thr Asp Glu Glu Asn Val Tyr Gly Leu
-65                 -60                 -55                 -50
Glu Glu Asn Ala Gln Ser Arg Gln Glu Ser Thr Arg Arg Leu Ile Leu
                -45                 -40                 -35
Val Gly Arg Thr Gly Ala Gly Lys Ser Ala Thr Gly Asn Ser Ile Leu
            -30                 -25                 -20
Gly Gln Arg Arg Phe Phe Ser Arg Leu Gly Ala Thr Ser Val Xaa Arg
        -15                 -10                 -5
Ala Cys Thr Thr Xaa Ser Arg Arg Trp Asp Lys Cys His Val Glu Val
    1               5                   10                  15
Val Xaa Leu Gly His Xaa Xaa Xaa Gly Lys Cys Pro Arg Gln Ile Leu
                20                  25                  30
Ala Val Arg Arg Glu Val Thr Ala
            35

<210> 1330
<211> 80
<212> PRT
```

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1330
Met Gln Leu Gln Val Leu Gly Arg Pro Gln Gly Ala Pro Gln Leu Ala
-30 -25 -20
Pro Gln Ala Leu Ala Leu Thr Xaa Thr Leu Leu Pro Ala Pro Gly Glu
-15 -10 -5 1
His Asp Ser Pro Met Xaa Ile Gly Gln Phe Pro Xaa Asn Pro Pro Ser
5 10 15
Glu His Pro Gly Ala Ser Pro Arg Arg Xaa Xaa Thr Gly Trp Xaa Pro
20 25 30
Gln Ser Trp Asp Arg Arg Val Ser Pro Ala Glu Ala Glu Thr Arg Arg
35 40 45

<210> 1331
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 1331
Met Gly Val Tyr Thr Cys Pro Ile Phe Val His Tyr Tyr Glu Asn His
-40 -35 -30
Gly Pro Thr Pro Ser Phe Xaa Ala Phe Ile Ser Phe His Leu Phe Thr
-25 -20 -15 -10
Leu Gly Phe Leu Cys Ser Leu Cys Pro His Pro His Gly
-5 1

<210> 1332
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1332
Met Lys Lys Ser Val Ser Cys Cys Ser Ser Leu Trp Val Ser Leu Ser
-15 -10 -5
Lys Asp Glu Asn Ala Glu Met
1 5

<210> 1333
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1333
Met Leu Leu Pro Leu Ala Met Ala Gly Arg Cys Tyr Thr Ala Lys His
-30 -25 -20 -15
Ser Thr Val Leu Leu Ser Gly Ser Pro Arg Ala Val Val Ser Ala Val

```
                -10                     -5                      1
Val Met Val Gly Thr Gly Cys
        5

<210> 1334
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1334
Met Pro Ser Cys Cys Tyr Leu Arg Ala Phe Leu Leu Ser Val Pro Leu
                -15                 -10                 -5
Gly Lys Gly Ser Ala Leu Lys Asp Pro Val
            1                   5

<210> 1335
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1335
Met Val Ala Asp Lys Glu Val Gln Thr Arg Thr Leu Leu Leu Ser Ser
                -20                 -15                 -10
Leu Trp Ile Val Cys Cys Leu His Leu Asp Ser Leu Ile Ser Xaa Lys
            -5                  1                   5
Tyr Pro Leu His Ala Ile Arg Arg Tyr Leu Ser Thr Leu Arg Asn Gln
    10                  15                  20
Arg Ala Glu Glu Gln Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu
25                  30                  35                  40
Asn Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu
                45                  50                  55
Pro Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly
            60                  65                  70
Leu Lys Gln Cys Glu
        75

<210> 1336
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1336
Met His Ile Cys Leu Phe Phe Ser Phe Ser Xaa Xaa Phe Xaa Leu Phe
                -10                 -5                  1
Phe Phe Phe Phe
        5

<210> 1337
<211> 45
<212> PRT
<213> Homo sapiens
```

<220>
<221> SIGNAL
<222> -19..-1

<400> 1337
Met Trp Leu Pro Cys Gln Ile Leu Ala Arg Leu Cys Arg Met Gln Thr
-15 -10 -5
Cys Trp Cys Leu Ser Phe Pro Thr Ser Ser Phe Thr Glu Ser Val Met
1 5 10
Arg Ser Leu Gly Glu Cys Pro Arg Lys Arg Trp Gly Gly
15 20 25

<210> 1338
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84..-1

<400> 1338
Met Xaa Lys Leu Xaa Ser Asn Pro Ser Glu Lys Gly Thr Lys Pro Pro
-80 -75 -70
Ser Val Glu Asp Gly Phe Gln Thr Val Pro Leu Ile Thr Pro Leu Glu
-65 -60 -55
Val Asn His Leu Gln Leu Pro Ala Pro Glu Lys Val Ile Val Lys Thr
-50 -45 -40
Arg Thr Glu Tyr Gln Pro Glu Gln Lys Asn Lys Gly Lys Phe Arg Val
-35 -30 -25
Pro Lys Ile Ala Glu Phe Thr Val Thr Ile Leu Val Ser Leu Ala Leu
-20 -15 -10 -5
Ala Phe Leu Ala Cys Ile Val Phe Leu Val Val Tyr Lys Ala Phe Thr
1 5 10
Tyr Asp His Ser Cys Pro Glu Asp Ser Ser Xaa Ser Thr Gly
15 20 25

<210> 1339
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1339
Met Phe Xaa Ala Ala Ala Gly Val Glu Val Leu Ser Leu Leu Phe Xaa
-20 -15 -10
Cys Ile Tyr Trp Gly Gln Tyr Ala Thr Asp Gly Ile Gly Asn Glu Ser
-5 1 5 10
Val Lys Ile Leu Ala Lys Leu Leu Phe Ser Ser Ser Phe Leu Ile Phe
15 20 25
Leu Leu Met
30

<210> 1340
<211> 35
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -26..-1

<400> 1340
Met Leu Thr Gly Arg Phe Leu Gly Gly Ser Gln Gly Phe Phe Leu Ser
    -25                 -20                 -15
Phe Leu Ser Phe Phe Phe Phe Ser Phe Phe Leu Phe Leu Xaa Phe Phe
-10                 -5                  1                   5
Phe Phe Phe

<210> 1341
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1341
Met Phe Ile Xaa Xaa Xaa Met Lys Gln Xaa Phe His Ile Ile Asp Phe
            -25                 -20                 -15
Val Phe Met Ser Lys Leu Leu Leu Phe Ser Phe Ser Phe Leu Xaa Lys
        -10                 -5                  1
Ala Arg Met Xaa Thr Ala Ala Pro Gly
5                   10

<210> 1342
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1342
Met Val Thr Pro Val His Ile Leu Thr Ala Val Leu Pro Leu Val Ser
            -15                 -10                 -5
His Gln Gln Asn His Leu Gly Gly Arg Phe Ala Ser Leu Gly Ser Ser
    1                   5                   10
Gly Ile Arg His Gly
15

<210> 1343
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1343
Met Leu Ile Leu His Leu Ala Thr Leu Leu Asn Leu Phe Ile Ser Ser
-15                 -10                 -5                  1
Asn Ser Phe

<210> 1344
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1344
Met Pro Leu Ala Ser Phe Gly Pro Phe Arg Ser Ser Cys Phe Ala Ala
-15 -10 -5 1
Arg Ser Ile Ile Trp Lys Ser Gly Arg Gln Gly
5 10

<210> 1345
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1345
Met Glu Thr Trp Asn Gly Thr Ser Ile Ile Val Ala His Leu Xaa Ser
-30 -25 -20
Phe Ser Phe Leu Leu Ser Phe Leu Ser Phe Arg Ser Pro Leu Cys His
-15 -10 -5 1
His Pro Leu Gly
5

<210> 1346
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1346
Met Gln Phe Leu Ser Leu Ile Phe Ala Ser Cys Ser Ser Thr Thr Pro
-10 -5 1
Leu Pro Leu Xaa Gln Cys Cys Thr Leu Pro
5 10

<210> 1347
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1347
Met Val Thr Ser Lys Ser Arg Gly Pro Xaa Val Gln Thr Leu Gly His
-50 -45 -40
Ala Gly Asn Leu Arg Ser Leu Arg Glu Trp Pro Asp Leu Cys Cys Leu
-35 -30 -25
Arg Leu Phe Val Pro Asp His Thr Val Leu Ala Leu Val Cys His Ser
-20 -15 -10
Ala Ser Ile Ser Val Phe Pro Ser Gln Val Thr Cys Arg Leu Pro Arg
-5 1 5 10
Thr Gly Ser His Pro Ile Cys Val Ile Ser Gln Gly Ala Phe His Asp
15 20 25
Pro His Pro Asn

30

<210> 1348
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1348
Met Pro Arg Ser Ile Asp Xaa Lys Ala Leu Ile Trp Thr Val Arg Leu
-25 -20 -15
Val Val Leu Phe Ala Ser Pro Xaa Val Arg Pro Ala Ser Ser Met Ser
-10 -5 1 5
Ser Arg Leu Leu Leu Pro Xaa Leu His Tyr Ser Asp Trp Thr Cys Trp
10 15 20
Leu Pro Glu Arg Arg
25

<210> 1349
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 1349
Met Thr Ser Leu Leu Thr Thr Pro Ser Pro Arg Glu Glu Leu Met Thr
-50 -45 -40
Thr Pro Ile Leu Gln Pro Thr Glu Ala Leu Ser Pro Glu Asp Gly Ala
-35 -30 -25
Ser Thr Ala Leu Ile Ala Val Val Ile Thr Val Val Phe Leu Thr Leu
-20 -15 -10
Leu Ser Val Val Ile Leu Ile Phe Phe Tyr Leu Tyr Lys Asn Lys Gly
-5 1 5 10
Ser Tyr Val Xaa Tyr Glu Pro Thr Glu Gly Glu Pro Ser Ala Ile Val
15 20 25
Gln Met Glu Xaa Xaa Leu Ala Lys Gly Ser Glu
30 35

<210> 1350
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1350
Met Thr Lys Ala Xaa Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala Leu
-15 -10 -5
Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val Leu Gln
1 5 10
Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser Asp Trp Leu
15 20 25 30
Cys Trp

<210> 1351

<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1351
Met Ala Gln Leu Ile Met Trp Leu Lys Asn Gln Leu Ile Leu Leu Gly
-20 -15 -10
Ile Phe Arg Gly Ile Arg His Gln Ile Tyr Leu Ile Arg Thr Leu Gln
-5 1 5
Ile Arg Gln Trp
10

<210> 1352
<211> 91
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1352
Met Gly Pro Val Pro Gly Ala Ala Ala Gly Val Xaa Pro Xaa Xaa Gly
-30 -25 -20 -15
Glu Leu Ala Xaa Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Val Ser
-10 -5 1
Ile Thr Ser Tyr Tyr Trp Ser Trp Ile Arg Gln Ala Pro Gly Lys Gly
5 10 15
Pro Glu Trp Ile Gly Xaa Ile Asp His Ser Gly Asp Thr Asp Tyr Asn
20 25 30
Pro Ser Leu Gln Ser Arg Val Thr Leu Ser Val Asp Thr Ser Lys Asn
35 40 45 50
Gln Phe Ser Leu Arg Leu Leu Ser Val Ser Ala
55 60

<210> 1353
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1353
Met Trp Phe Gln Thr Arg Ser Cys Gly His His Asp Pro Val Gly Ile
-35 -30 -25
Thr Gly Val Thr Lys Val Ile Leu Pro Leu Phe Leu Cys Pro Leu Gly
-20 -15 -10 -5
Met Val Glu Thr Ser Phe Gly
1

<210> 1354
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -109..-1

<400> 1354
Met Ser Tyr Val Val Thr Lys Thr Lys Ala Ile Asn Gly Lys Tyr His
-105 -100 -95
Arg Phe Leu Gly Arg His Phe Pro Arg Phe Tyr Val Leu Tyr Thr Ile
-90 -85 -80
Phe Met Lys Gly Leu Gln Met Leu Trp Ala Asp Ala Lys Lys Ala Arg
-75 -70 -65
Arg Ile Lys Thr Asn Met Trp Lys His Asn Ile Lys Phe His Gln Leu
-60 -55 -50
Pro Tyr Arg Glu Met Glu His Leu Arg Gln Phe Arg Gln Asp Val Thr
-45 -40 -35 -30
Lys Cys Leu Phe Leu Gly Ile Ile Ser Ile Pro Pro Phe Ala Asn Tyr
-25 -20 -15
Leu Val Phe Leu Leu Met Tyr Leu Phe Pro Arg Gln Leu Leu Ile Arg
-10 -5 1

<210> 1355
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1355
Met Tyr Asn Tyr Tyr Phe Leu Ser Leu Pro Ser Phe Leu Cys Thr Cys
-15 -10 -5
Cys Gln Phe Phe Pro His Asp Pro Ile Ser Ser Gln Tyr Ser Ser Pro
1 5 10
Gln Gly Lys Pro Cys Gln Val Thr Tyr Lys Phe Leu Phe Ile Leu Leu
15 20 25
Gly His Val Tyr Pro Arg Asp Gly Gly
30 35

<210> 1356
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -79..-1

<400> 1356
Met Gln Gly Gly Asn Ser Gly Val Arg Lys Arg Glu Glu Glu Gly Asp
-75 -70 -65
Gly Ala Gly Ala Val Ala Ala Pro Pro Ala Ile Asp Phe Pro Ala Glu
-60 -55 -50
Gly Pro Asp Pro Glu Tyr Asp Glu Ser Asp Val Pro Ala Xaa Ile Gln
-45 -40 -35
Val Leu Lys Glu Pro Leu Gln Gln Pro Thr Phe Pro Phe Ala Val Ala
-30 -25 -20
Asn Gln Leu Leu Leu Val Ser Leu Leu Glu His Leu Ser His Val His
-15 -10 -5 1
Glu

<210> 1357
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1357
Met Val Phe Tyr Cys Phe Ala Leu Cys Ile Ile Leu Ile Cys Val Met
-15 -10 -5
Ser Cys Arg His Leu
1

<210> 1358
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1358
Met Leu Trp Glu Thr Asp Leu Ser Thr Asn Lys Thr Pro Val Ser Cys
-40 -35 -30
Thr Ala Gly Ser Ala Cys Ala Leu Ser Leu Leu Gln Phe Pro Val Leu
-25 -20 -15
Ile Thr Gln Leu Cys Leu Gly Lys Gly Gln Ser Glu Pro Ile Gly Pro
-10 -5 1 5
Leu Gln Asp Phe Val Ser Leu Glu Ser Thr Ser His Phe Tyr Ser Phe
10 15 20
Phe

<210> 1359
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1359
Met Thr Arg Arg Arg Thr Ser Leu Trp Cys Cys Ser Pro Ser Ser Arg
-20 -15 -10 -5
Thr Ser Ser Ser Leu Ser Trp Arg Met Gly Ser Gln Ile Arg Pro Ser
1 5 10

<210> 1360
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1360
Met Ala Phe Tyr Leu Trp Cys Phe His Ala Val Phe Phe Thr Val Cys
-15 -10 -5
Val Cys Val Arg
1

<210> 1361
<211> 60

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -33..-1

<400> 1361
Met Thr Leu Asn Glu His Ala Ala Phe Lys His Leu Phe Asn Lys Ala
-30 -25 -20
His Leu Ala Pro Pro Leu Ile His Leu Thr Leu Ser Gly His Ser Thr
-15 -10 -5
Cys Phe Arg Glu His Arg Val Gly Gly Lys Val Ile Asp Glu Gln His
1 5 10 15
Pro Lys Ala Glu Glu Ser Phe Leu Val Gln Glu Gly
20 25

<210> 1362
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1362
Met Ser Phe Ser Ser Ser Leu Pro Pro Ser Leu Pro Pro Ser Leu Ala
-25 -20 -15
Ser Phe Leu Leu Leu Thr Phe Leu Pro Ser Leu Pro Arg
-10 -5 1

<210> 1363
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -46..-1

<400> 1363
Met Arg Ala Gln Gly Leu Ser Cys Gly Tyr Pro Ala Arg Pro Leu Gln
-45 -40 -35
Pro Phe Leu Glu His Leu Ala Gly Ser Gly Ile Thr Lys Arg Thr Ala
-30 -25 -20 -15
Pro Gly Cys Ala Pro Leu Arg Trp Val Pro Gln Ile Arg Gly Cys Pro
-10 -5 1
Leu Thr Arg Leu Ala Gln Arg Gly Ala Asp Thr Arg Thr Arg Glu Asn
5 10 15
Leu Phe Tyr Ser Arg Phe Pro Gly Leu Gln Leu Pro Ala Ala Xaa Xaa
20 25 30
Ser Ala Ser Ala Leu Ser Leu Cys Thr Pro Arg Ser Pro Pro Leu Pro
35 40 45 50
Leu Pro Leu Pro Ile Asn Ser Pro Gly
55

<210> 1364
<211> 52
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -37..-1

<400> 1364
Met Ala Ala Ser Ser Thr Ser His Leu Lys Asn Lys Thr Lys Thr Phe
-35 -30 -25
Leu Ala Pro Met Thr Asn Cys His Ser Ile Ser Phe Leu Pro Phe Gln
-20 -15 -10
Ala Ser Ile Phe Gly Lys Thr Arg Leu Gln Ser Leu Arg Pro Ser His
-5 1 5 10
Pro Tyr Pro His
15

<210> 1365
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1365
Met Pro Lys Asp Ala Asp Leu Ala Phe Ser Ala Ser Leu Phe Glu Arg
-35 -30 -25
Ala Glu Ser Leu Tyr Thr Leu Ile Ser Lys Phe Xaa Ser Cys Xaa Cys
-20 -15 -10
Val Ser Thr Leu Ala Tyr Thr Lys Gly Arg Gly
-5 1

<210> 1366
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1366
Met Phe Val Asn Arg Thr Cys Phe Asn Ser Ser Phe Pro Ile Trp Met
-25 -20 -15
Pro Phe Leu Phe Leu Thr Leu Phe His Cys Leu Gly Arg Arg
-10 -5 1

<210> 1367
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1367
Met Xaa Gly Ser Ser Arg Xaa Xaa Gly Leu Gln Ile Thr Ala Ser Arg
-35 -30 -25
Thr Gly Lys Val Tyr Pro Ala Cys His Phe Leu Xaa Ala Val Ser Ala
-20 -15 -10
Ser Ser Ser Xaa Ala Cys Leu Trp Tyr Arg Pro Ile Ala Arg Arg Pro
-5 1 5 10
Ala Gly Pro Gly Gly Ser Leu Ser Ser Ala Gln Val His Pro Ala
15 20 25

<210> 1368
<211> 100
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1368
Met Ile Leu Phe Asp His Leu His Cys Ser Ala Ser Gly Val Thr Phe
    -25                 -20                 -15
Trp Leu Leu Cys Arg Ile Cys Thr Phe Gly Phe His Gly Phe Ser Lys
-10                 -5                  1               5
Tyr Thr Val Ser Arg Gly Thr Gln Gln Gly Ala Gly Xaa Xaa Xaa Gly
            10                  15                  20
Leu His Gln Asn Trp Glu Gln Trp Arg Gly Leu Val Gly Lys Ser Ser
        25                  30                  35
Ser Ala Ala Val Val Phe Cys Leu Thr Phe Asp Leu Val Thr Ser Phe
    40                  45                  50
Gln Leu Ala Ser Ala Ile Glu Ser Thr His Phe His Ala Gly Arg Asp
55                  60                  65                  70
Gly Ser His Leu

<210> 1369
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1369
Met Glu Leu Ser Leu Pro Pro Ser Met Cys Asp Tyr Pro Xaa Phe Cys
                -25                 -20                 -15
Leu Leu Leu Phe Pro Ala Ser Leu Arg Leu Leu Cys Val His Pro
            -10                 -5                  1

<210> 1370
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1370
Met Asp Gln Lys Pro Leu Phe Thr Val Gly Cys Ala Gly Leu Ala Gly
-20                 -15                 -10                 -5
Ser Cys Arg Gly Ile Ser Phe Leu Arg Thr Arg
                1                   5

<210> 1371
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1371
Met Ser Val Asn Xaa Ile Phe Ile Phe Tyr Phe Ile Leu Leu Leu Leu
-20 -15 -10
Ile Gln Asp Leu Thr Met Ser Pro Thr Ala Gly Met Gln Trp His Asn
-5 1 5
His Gly Pro Pro Gln Ala Leu Pro Cys Pro Leu Arg Xaa
10 15 20

<210> 1372
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1372
Met Ser Phe Leu Asn Val Asp Ile Thr Asp Cys Leu Tyr Asn Pro Ser
-45 -40 -35 -30
Val Cys Pro Val Ala Gln Ser Ser Leu Thr Cys Asp Phe Ile Asp Gly
-25 -20 -15
Ile Cys Leu Gly Ser Pro Leu Ala Glu Cys Leu Leu Gly Xaa Xaa Xaa
-10 -5 1
Xaa Ile Xaa Gly Ile Asn Xaa Xaa Cys Phe Pro Cys Gly Val Lys Cys
5 10 15
Ala Gly Val Val Leu Gly Leu Ser Thr Leu Trp Tyr Val Val
20 25 30

<210> 1373
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1373
Met Lys Val Gly Lys Asp Ser Leu Glu Ser Leu Pro Ser Leu Cys Glu
-35 -30 -25
Lys His Ile Gly Pro Ser Gly Leu Phe Thr Phe Leu Ser Pro Ser Phe
-20 -15 -10
His Ser Val His Leu Ser Glu Leu Asn Glu Leu Tyr Thr Ile Ala Ala
-5 1 5 10
Gly

<210> 1374
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1374
Met Glu Ser Lys Val Leu Ile Ser Ala Ser Leu Leu Arg Ala Ser Gln
-15 -10 -5
Leu Lys Ile Lys Xaa Asn Lys Met Thr Asn Phe Leu Ile Leu
1 5 10

<210> 1375
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1375
Met Ala Ala Ser Val Leu Asn Thr Val Leu Arg Arg Leu Pro Met Leu
-20 -15 -10
Ser Leu Phe Arg Gly Ser His Xaa Xaa Phe Arg Phe Pro Ser Arg Leu
-5 1 5
Phe Ala Pro Lys Leu Pro Leu Arg Lys Ile Leu Cys Pro Gln Phe Pro
10 15 20
Phe Leu Leu Ile Arg Met Ser Pro Gly Asn Ile Trp Asn Gln Lys Asn
25 30 35 40
Thr Arg Ser Asp Met Val Leu Ala Pro Ser Gly Leu Thr Thr Ala Ala
45 50 55
Thr Thr Arg Val Val Tyr Pro His Ser Gly Leu Gly Arg His Val Phe
60 65 70
Val Gly Ile Lys Leu Leu Gly Ile Pro Ala Pro Ser Val Glu Ile Thr
75 80 85
Ser Cys Met Leu Thr Leu
90

<210> 1376
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1376
Met Lys Ser Asn Leu Thr Leu Leu Thr Cys Leu Xaa Leu Xaa Gly Gly
-15 -10 -5
Glu Gly Trp Lys Gly Ala Ala Val Cys Phe Glu Thr Val Glu Gln Phe
1 5 10
Cys Ser Leu Arg Lys Trp His Val Thr Tyr Leu Xaa Lys Asp Ser Gly
15 20 25 30
Leu Cys Gln Gln Gln Glu Lys Leu Tyr Thr Lys Phe Leu Val Cys Ile
35 40 45
Lys Gly Ala Ser Asn Glu Glu Ile Lys Lys Thr Tyr
50 55

<210> 1377
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1377
Met Leu Ala Ser Pro Cys Val Leu Val Gln Gly Ser Gly Xaa Ser Leu
-10 -5 1
Val Arg Thr Pro Trp Cys Pro Glu
5 10

<210> 1378
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1378
Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile Tyr
-15 -10 -5
Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg Arg Lys
1 5 10
Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His
15 20 25

<210> 1379
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -39..-1

<400> 1379
Met Asp Leu Ile Gly Phe Gly Tyr Ala Ala Leu Val Thr Phe Gly Ser
-35 -30 -25
Ile Phe Gly Tyr Lys Xaa Arg Gly Gly Val Pro Ser Leu Ile Ala Gly
-20 -15 -10
Leu Phe Val Gly Cys Leu Ala Gly Tyr Xaa Ala Tyr Arg Val Ser Asn
-5 1 5
Asp Lys Arg Asp Val
10

<210> 1380
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1380
Met Glu Gly Val Ala Xaa Xaa Thr Phe Leu Ala Ala Xaa Arg Arg Leu
-15 -10 -5
Val Thr Gly Gln Thr Ser Pro Arg Gly Thr Trp Cys Leu Tyr Pro Gly
1 5 10
Phe Cys Arg Ser Val Ala Cys Ala Met Pro Cys Cys Ser His Arg Ser
15 20 25
Cys Arg Glu Asp Pro Gly Thr Ser Glu Ser Arg Glu Met Val Arg Val
30 35 40 45
Arg Asp His Gly

<210> 1381
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -21..-1

<400> 1381
Met Thr Gly Gln Phe Thr Lys Glu Ile Gly Leu Ile Gly Leu Thr Val
-20 -15 -10
Pro Cys Gly Trp Gly Ser Leu Ile Thr Met Ala Glu Gly Arg Glu Glu
-5 1 5 10
Gln Val Thr Ser Gly
15

<210> 1382
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1382
Met His Leu Gly Phe Ile Leu Ser Phe His Gly Leu Ile Ala Asn Phe
-10 -5 1
Phe Phe Cys Leu Asn Ala Pro Ala
5 10

<210> 1383
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1383
Met Gly Arg Thr Arg Glu Ala Gly Cys Val Ala Ala Gly Val Val Ile
-20 -15 -10 -5
Gly Ala Gly Ala Ala Thr Val Tyr Thr Asp
1 5

<210> 1384
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 1384
Met Glu Ser His Ser Val Ala Gln Ala Arg Met Arg Xaa Xaa Asn Leu
-35 -30 -25
Ser Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Pro Xaa Ser Cys Leu
-20 -15 -10
Ser Leu Leu Ser Asn Xaa Asp Tyr Arg His Ala Pro Pro Phe Leu Ala
-5 1 5 10
Asn Phe Xaa Ile Phe His Arg Asp Gly Val Ser Pro
15 20

<210> 1385
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -55..-1

<400> 1385
Met Phe His Gly Ile Pro Ala Thr Pro Gly Ile Gly Ala Pro Gly Asn
-55 -50 -45 -40
Lys Pro Glu Leu Tyr Glu Val Arg Gln His Gly Arg Ala Val Cys Gly
-35 -30 -25
Gly Glu Asp Asn Ala Ser Pro Gly Glu Gly Leu His Gln Gly Leu Cys
-20 -15 -10
Leu Pro Gln Arg Val His Cys Ser Leu Leu Pro Ala Pro
-5 1 5

<210> 1386
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1386
Met Pro His Ser Phe Val Ser Cys Asn Leu Phe Leu Ser Val Leu Asn
-20 -15 -10
Phe Leu Phe Leu Leu Ser Phe Ser Thr
-5 1

<210> 1387
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1387
Met Ala Val Phe Leu Gln Lys Arg Lys His Thr Met Arg His His Leu
-25 -20 -15
Leu Leu Ser Thr Leu Ala Thr Ile Ala Gly Asn Ile Tyr Arg
-10 -5 1

<210> 1388
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1388
Met Ala Asp Ser Glu Ala Leu Pro Ser Leu Ala Gly Asp Pro Val Ala
-25 -20 -15
Val Glu Ala Leu Leu Arg Ala Val Phe Gly Val Val Val Asp Glu Ala
-10 -5 1 5
Ile Gln Lys Gly Thr Ser Val Ser Gln Lys Val Cys Xaa Trp Lys
10 15 20

<210> 1389

<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1389
Met Arg Leu Ala Met Val Gln Leu Val Leu Asn Asn Leu Lys Thr Phe
    -35                 -30                 -25
Tyr Pro Phe Ala Asp His Asp Leu Ala Glu Leu Pro Val Ser Ser Pro
-20                 -15                 -10                 -5
Leu Cys His Ala Val Leu Lys Thr Leu Gln Cys Trp Glu Gln Val Leu
                1               5                   10
Leu Arg Arg Leu Glu Ile His Gly Gly Pro Pro Gln Asn Tyr Ile Ala
        15                  20                  25
Ser His Thr Ala Xaa Xaa Ser Leu Ser Ala Gly Pro Ala Ile Leu Arg
    30                  35                  40
His Lys Ala Leu Leu Glu Pro
45                  50

<210> 1390
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1390
Met Phe Lys Leu Phe Leu Phe Leu Phe Ile Leu Xaa Tyr Phe Xaa Xaa
-20                 -15                 -10                 -5
Tyr Thr Leu Ser Ser Gly Ile Tyr Val Gln Asn Val Gln Val Cys Tyr
                1               5                   10
Ile Gly Ile His Met Pro Trp Trp Phe Ala Ala Pro Met Asn Leu Ser
        15                  20                  25
Ser Ala Leu
    30

<210> 1391
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1391
Met Ile Tyr Ser Arg Ser Leu Glu Leu Ile Pro Leu Leu Ser Glu Ile
    -20                 -15                 -10
Leu Tyr Ala Leu Ala Asn Ile Ser Pro Ile Pro Gln Thr
-5                  1                   5

<210> 1392
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -16..-1

<400> 1392
```
Met Val His Val Ile Phe Tyr Phe Val Leu Phe Leu Gly Ile Met Thr
    -15                 -10                 -5
Gln Arg
1
```

<210> 1393
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1393
```
Met His Lys Phe Phe Arg His Phe Tyr Ser Asp Phe Leu Ile Tyr Phe
-25                 -20                 -15                 -10
Phe Gln Leu His Ser Cys Cys His Asp Lys Val Thr Ala Xaa Arg Ala
                -5                  1                   5
Tyr Xaa His Tyr Ser Ser Leu Leu Thr Pro Tyr Leu Ser Gln His Pro
        10                  15                  20
Cys Pro His Pro Gly
    25
```

<210> 1394
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1394
```
Met Ala Ala Leu Gly Ser Pro Ser His Thr Phe Arg Gly Leu Leu Arg
    -25                 -20                 -15
Glu Leu Arg Tyr Leu Ser Ala Ala Thr Gly His Pro Ile Ala Thr Pro
-10                 -5                  1                   5
Arg Pro Ile Gly Thr Xaa Val Lys Ala Phe Arg Ala His Arg Val Thr
            10                  15                  20
Ser Glu Lys Leu Cys Arg Ala Gln His Glu Leu His Phe Gln Ala Ala
        25                  30                  35
Thr Tyr Leu Cys Leu Leu Arg Xaa Ser Gly Asn Met Trp Pro Tyr Ile
    40                  45                  50
Arg Asn Phe Met Ala Arg Val Ser Ala Arg Trp Arg Ser Leu Leu Ala
55                  60                  65                  70
Trp Trp Val Ser Ser Cys Pro Ile Ser Leu Glu Gly Arg Ala Gly Ser
                75                  80                  85
His Glu His Gly Glu Tyr Pro Trp Met
            90                  95
```

<210> 1395
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1395
Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val
-25 -20 -15
Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Ala Ala Val
-10 -5 1

<210> 1396
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1396
Met Ala Glu Gly Ala Leu Ser Phe Leu Cys Ser Leu Ser Gln Asn Ala
-15 -10 -5
Leu Asn Ile Ser Leu Ile Ser Arg Lys
1 5

<210> 1397
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1397
Met Tyr Pro Ser Phe Leu Leu Cys Phe Thr Leu Val Gly Thr Gln Leu
-15 -10 -5
Arg Asn Ser Ser Leu Ala Met
1 5

<210> 1398
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1398
Met Glu Ser Cys Thr Val Gly Cys Ala Thr Ala Ser Ser Trp Gly Cys
-15 -10 -5 1
Thr Ser Arg

<210> 1399
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1399
Met Ala Met Ser Phe Glu Trp Pro Trp Gln Tyr Arg Phe Pro Pro Phe
-40 -35 -30
Phe Thr Leu Gln Pro Asn Val Asp Thr Arg Gln Lys Gln Leu Ala Ala

```
        -25                     -20                     -15
Trp Cys Ser Leu Val Leu Ser Phe Cys Arg Leu His Lys Gln Ser Ser
    -10                 -5                  1               5
Met Thr Val Met Glu Ala Gln Glu Ser Pro Leu Phe Asn Asn Val Lys
                10                  15                  20
Leu Gln Arg Lys Leu Pro Val
            25
```

<210> 1400
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1400

```
Met Arg Leu His Val His Ser Leu Ser Pro Phe Ser Phe Ala Cys Leu
                -10                 -5                  1
Pro Phe Leu Ser Pro Pro Leu
        5
```

<210> 1401
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1401

```
Met Leu His Phe Xaa Tyr Met Ile Xaa Val Cys Leu Glu Arg Met Cys
    -25                 -20                 -15
Ile Leu Gln Leu Leu Ser Ala Val Leu Tyr Arg Phe
-10                 -5                  1
```

<210> 1402
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1402

```
Met Ser Ser Glu Pro Pro Pro Pro Pro Gln Pro Pro Thr His Gln Ala
-30                 -25                 -20                 -15
Ser Val Gly Leu Leu Asp Thr Pro Leu Gly Ala Val Ser Ala His His
                -10                 -5                  1
Pro Leu Cys
        5
```

<210> 1403
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1403
Met Phe Leu Asp His Val Arg Phe Leu Thr Ser Ile Ser Phe Leu Ala
-20 -15 -10 -5
Leu Val Leu Trp Asn Val Phe Leu Asn Ser Thr Arg Leu
1 5

<210> 1404
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1404
Met Arg Glu Lys Pro Gln Pro Ala Leu Leu Thr Ser Ser Glu Leu Pro
-15 -10 -5
Ala Leu Ala Ser Gln Ile His Cys Arg Val
1 5

<210> 1405
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1405
Met Pro His Asn His Leu Glu Gly Asp Ala Leu Leu Arg Val Pro Val
-25 -20 -15
Leu Cys Ile Trp Arg Ala Trp Leu Arg Ala Glu Val Gly Gly Arg Ala
-10 -5 1 5
Pro Leu Pro Gly Arg Met
10

<210> 1406
<211> 27
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1406
Met Lys Asn Thr Leu Tyr Tyr Asn Phe Cys Leu Phe Trp Ile Xaa Leu
-20 -15 -10
Pro Pro His Thr Cys Thr His Thr Asp Thr His
-5 1 5

<210> 1407
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1407
Met Cys Leu Asn Pro Ala Cys Ser Gly Pro Leu Ser Leu Arg Ser Pro
-35 -30 -25 -20
Arg Leu Pro Pro Leu Phe Cys Thr Phe Leu Ser Leu Ser Leu His Pro
-15 -10 -5
Trp Gly Gly Phe Phe Leu Cys Ala Trp Ile Ser Xaa Phe Leu Pro Trp
1 5 10
Val Cys Val Xaa Ala
15

<210> 1408
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -89..-1

<400> 1408
Met Ala His Ser Lys Thr Arg Thr Asn Asp Gly Lys Ile Thr Tyr Pro
-85 -80 -75
Pro Gly Val Lys Glu Ile Ser Asp Lys Ile Ser Lys Glu Glu Met Val
-70 -65 -60
Arg Arg Leu Lys Met Val Val Lys Thr Phe Met Asp Met Asp Gln Asp
-55 -50 -45
Ser Glu Glu Glu Lys Glu Leu Tyr Leu Asn Leu Ala Leu His Leu Ala
-40 -35 -30
Ser Asp Phe Phe Leu Lys His Pro Asp Lys Asp Val Arg Leu Leu Val
-25 -20 -15 -10
Ala Cys Cys Leu Ala Asp Ile Phe Arg Ile Tyr Ala Pro Glu Ala Pro
-5 1 5
Tyr Thr Ser Pro Lys
10

<210> 1409
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1409
Met Xaa Ser Cys Glu Ile Ala Trp Thr Ala Thr Pro Ser Ser Ala Ala
-15 -10 -5
Phe Ala Gln Ala Phe Pro Thr Ala Cys Asn
1 5

<210> 1410
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1410
Met Cys His Tyr Leu Trp Lys Lys Leu Tyr Ser Thr Leu Leu Tyr Ile
-25 -20 -15 -10
Leu Ser Arg Ser Ser Gly Arg Arg Gly Lys Asn Leu Ile Thr Ala Val

```
                    -5                      1                   5
Ala Ser Arg Ala Gly Asn Leu Gly Val Trp Thr Glu Lys Gly
        10                      15                      20
```

<210> 1411
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1411

```
Met Xaa Ser His Arg Leu Phe Gly Cys Phe Pro Ser Asp Leu Ser Arg
        -25                 -20                 -15
Met Val Leu Leu Ser Ser Ala Leu Leu Ser Thr Glu Asn
    -10                 -5                  1
```

<210> 1412
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1412

```
Met Arg Pro Ser His Ser Ser Ala Tyr Leu Cys Leu His Leu Cys Ala
    -20                 -15                 -10
Phe Ser Thr Glu Gly Trp Met Asn Arg Leu Ser Ser Ser Leu Arg Leu
-5                  1               5                   10
Ala Pro Leu Pro Leu Tyr Pro Phe Cys Leu Pro Ser Asn Ser Pro
            15                  20                  25
```

<210> 1413
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1413

```
Met Trp Ser Arg Leu Val Trp Leu Gly Leu Arg Ala Pro Leu Gly Gly
    -15                 -10                 -5
Arg Gln Gly Phe Thr Ser Lys Ala Asp Pro Gln Gly Ser Gly Arg Ile
1               5                   10                  15
Thr Ala Ala Val Ile Glu His Leu Glu Arg Leu Ala Leu Val Asp Phe
            20                  25                  30
Gly Ser Arg Glu Ala Val Ala Arg Leu Glu Lys Ala Ile Ala Phe Ala
        35                  40                  45
Asp Arg Leu Arg Ala Val Asp Thr Asp Gly Val Glu Pro Met Glu Ser
    50                  55                  60
Val Leu Glu Asp Arg Cys Leu Tyr Leu Arg Ser Asp Asn Val Val Glu
65                  70                  75                  80
Gly Asn Cys Ala Asp Glu Leu Leu Gln Asn Ser His Arg Val Val Glu
                85                  90                  95
Glu Tyr Phe Val Ala Pro Pro Gly Asn Ile Ser
            100                 105
```

<210> 1414
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -81..-1

<400> 1414
Met Ala Pro Pro Val Arg Tyr Cys Ile Pro Gly Glu Arg Leu Cys Asn
    -80                 -75                 -70
Leu Glu Glu Gly Ser Pro Gly Ser Gly Thr Tyr Thr Arg His Gly Tyr
-65                 -60                 -55                 -50
Ile Phe Ser Ser Leu Xaa Gly Cys Leu Met Lys Ser Ser Glu Asn Gly
                -45                 -40                 -35
Ala Leu Pro Val Val Ser Val Val Arg Glu Thr Glu Ser Gln Leu Leu
            -30                 -25                 -20
Pro Asp Val Gly Ala Ile Val Thr Cys Lys Ser Leu Ala Ser Ile His
        -15                 -10                 -5
Ala Leu Pro
    1

<210> 1415
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -60..-1

<400> 1415
Met Val Gly Asn Gln Gly Pro Gln Pro Pro Pro Phe Pro Met Glu Pro
-60                 -55                 -50                 -45
Thr Met Ala Gln Tyr Gln Ala Ile Ser Lys His Leu Pro Lys Val Cys
                -40                 -35                 -30
Gln Glu Pro His Leu Pro Arg Gly His Leu Gln Pro Gln Gln His Arg
            -25                 -20                 -15
Leu Leu Val Ala Arg Leu His Met Ala Ser Leu Ala Arg Arg Cys Thr
        -10                 -5                  1
Glu Trp Ala Lys Leu His Cys Ser Asp Ala Arg Leu Pro Trp Val Ser
5                   10                  15                  20

<210> 1416
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1416
Met Lys Pro Gln Thr Leu Ala Val Ser Val Thr Val Leu Lys Asp Gly
            -25                 -20                 -15
Val Ala Gly Val Cys Phe Phe Arg Arg Ser Asp Ala Ser Glu Val Ser
        -10                 -5                  1
Ser Phe Trp
5

<210> 1417
<211> 47

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1417
```
Met Val Val Leu Ile Cys Leu Ser Leu Met Ile Ser Asn Thr Glu Leu
            -40                 -35                 -30
Phe Phe Ile Arg Phe Leu Thr Ala Cys Met Pro Ser Phe Glu Lys Cys
        -25                 -20                 -15
Leu Phe Leu Ser Phe Ala His Phe Leu Met Gly Arg Thr His Arg
    -10                 -5                  1
```

<210> 1418
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1418
```
Met Ser Ser Leu Tyr Ile Leu Asp Ile Ser Leu Leu Ser Asp Ile Leu
        -20                 -15                 -10
Phe Ala Asn Ile Phe Ser His Ser Trp Asp Val Phe Pro Leu Ser Phe
    -5                  1               5                   10
Leu Phe Phe Ser
```

<210> 1419
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -84..-1

<400> 1419
```
Met Gly Gln Gly Ala Arg Gly Trp His Arg Glu Pro Gly Leu Gly Leu
                -80                 -75                 -70
Arg His Ser Pro Arg Arg Leu Ser Gly Ala Leu His Leu Glu Ala Gly
            -65                 -60                 -55
Cys Asp Arg Asn Ala Thr Thr Val Arg Pro Leu Arg Ala Lys Xaa Gly
        -50                 -45                 -40
Asp Ala Leu Pro Glu Glu Ile Arg Glu Pro Ala Leu Arg Asp Ala Gln
    -35                 -30                 -25
Trp Val Arg Asp Gln Leu Ala Ser Ser Leu Leu Ile Ile Leu Leu Pro
-20                 -15                 -10                 -5
Asn Thr Gln Asp Leu Arg Ile Gln Lys Asp Pro Thr Pro Gly Pro
                1               5                   10
```

<210> 1420
<211> 87
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -48..-1

<400> 1420
Met Arg Lys Arg Lys Ile Ser Val Cys Gln Gln Thr Trp Ala Leu Leu
-45 -40 -35
Cys Lys Asn Phe Leu Lys Lys Trp Arg Met Lys Arg Glu Ser Leu Met
-30 -25 -20
Glu Trp Leu Asn Ser Leu Leu Leu Leu Leu Cys Leu Tyr Ile Tyr Pro
-15 -10 -5
His Ser His Gln Val Asn Xaa Xaa Ser Ser Leu Leu Thr Met Asp Leu
1 5 10 15
Gly Arg Val Asp Xaa Xaa Asn Glu Ser Arg Phe Ser Val Val Tyr Thr
20 25 30
Pro Val Thr Asn Thr Thr Pro
35

<210> 1421
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1421
Met Cys Thr Cys Leu Cys Val Cys Leu Tyr Met Tyr Asn Met Gln Phe
-30 -25 -20 -15
Leu Xaa Phe Val Phe Val Cys Xaa Leu Leu Lys Cys Met Ser Val Pro
-10 -5 1
Leu

<210> 1422
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1422
Met Ala Ala Ser Ala Ala Ala Ala Glu Leu Gln Ala Ser Gly Gly Pro
-30 -25 -20
Arg His Pro Val Cys Leu Leu Val Leu Gly Met Ala Gly Ser Gly Lys
-15 -10 -5 1
Thr Thr Phe Val Gln Arg Leu Thr Gly His Leu His Ala Gln Gly Thr
5 10 15
Pro Pro Tyr Val Ile Asn Leu Asp Pro Ala Val His Glu Val Pro Xaa
20 25 30
Pro Ala Asn Ile Asp Ile Arg Asp Thr Val Lys Tyr Lys Glu Val Met
35 40 45
Lys Gln Tyr Gly Leu Gly Pro Asn Gly Gly Ile Val Thr Ser Leu Asn
50 55 60 65
Leu Phe Xaa Thr Arg Phe Asp Gln Val Met Lys Leu Leu Arg Arg Pro
70 75 80
Arg Thr Cys Pro Asn Met Cys
85

<210> 1423
<211> 38
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -20..-1

<400> 1423
Met Tyr Ala Cys Ala Met Leu Val Leu Leu Thr His Gly Leu Ile His
-20 -15 -10 -5
Tyr Ser Phe Thr His His Leu His Tyr Val Phe Ile Leu Ile Leu Pro
1 5 10
Leu Pro Pro Pro Pro Gln
15

<210> 1424
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1424
Met Gly Phe Leu Gly Ser Pro Arg Gln Arg Asn Ser Met Cys Leu Leu
-20 -15 -10
Leu Asp Val Ser Ser Xaa Lys Ser Thr Asp Asn Xaa Xaa Xaa Xaa Xaa
-5 1 5
Leu Ile Ile Tyr Tyr Leu Ile Thr Arg Lys Gly Pro Gly
10 15 20

<210> 1425
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1425
Met Ser Cys Gln Xaa Xaa Leu Ala Xaa Thr Leu Thr Trp Leu Met Ile
-40 -35 -30
Arg Gly Arg His Pro Tyr Leu Thr Arg Arg Ser Ala Arg Asn Phe Asn
-25 -20 -15
Ile Phe Leu Ala Ala Pro Ser Pro Val Trp Gln Pro Gln Arg Thr Arg
-10 -5 1 5
Arg Pro Gln

<210> 1426
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1426
Met Cys Pro Ala Trp Leu Pro Cys Trp Thr Ala Gln Thr Glu His Leu
-30 -25 -20
Asp Arg Tyr Arg Lys Phe His Gln Met Ala Leu Xaa Pro Gly Thr Ser
-15 -10 -5
Arg Ala Gln Ala Leu Leu Tyr Asn Glu Val Leu Glu Arg Phe Met Phe
1 5 10
Thr Arg Leu

15

<210> 1427
<211> 44
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1427
Met Asn Val Met Lys Arg Ile Cys Thr Phe Leu Leu Pro Ser His Ser
-15 -10 -5
Thr Ser Gly Pro Leu Cys Cys Ser Asn Ala His Leu Pro Ala Thr Ser
1 5 10
Ser Thr Leu Lys His Cys Arg Ala Trp Arg Glu Ala
15 20 25

<210> 1428
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -121..-1

<400> 1428
Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
-120 -115 -110
Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Val Phe Lys Met Ala
-105 -100 -95 -90
Ala Ser Met His Gly Gln Pro Ser Pro Ser Leu Glu Asp Ala Lys Leu
-85 -80 -75
Arg Arg Pro Met Val Ile Glu Ile Ile Glu Lys Asn Phe Asp Tyr Leu
-70 -65 -60
Arg Lys Glu Met Thr Gln Asn Ile Tyr Gln Met Ala Thr Phe Gly Thr
-55 -50 -45
Thr Ala Gly Phe Ser Gly Ile Phe Ser Asn Phe Leu Phe Arg Arg Cys
-40 -35 -30
Phe Lys Val Lys His Asp Ala Leu Lys Thr Tyr Ala Ser Leu Ala Thr
-25 -20 -15 -10
Leu Pro Phe Leu Ser Thr Val Val Thr Asp Lys Leu Phe Val Ile Asp
-5 1 5
Ala Leu Tyr Ser Asp Asn Ile Ser Lys Glu Asn Cys Val Phe Arg Ser
10 15 20
Ser Leu Ile Gly Ile Val Cys Gly Val Phe Tyr Pro Ser Ser Xaa Ala
25 30 35
Phe Thr
40

<210> 1429
<211> 63
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -38..-1

<400> 1429
Met Ala Glu Ile Thr Asn Ile Arg Pro Ser Phe Asp Val Ser Pro Val

```
            -35                     -30                 -25
Val Ala Gly Leu Ile Gly Ala Ser Val Leu Val Val Cys Val Ser Val
        -20                 -15                 -10
Thr Val Phe Val Trp Ser Cys Cys Xaa Gln Gln Ala Glu Lys Lys His
    -5                  1                   5                   10
Lys Asn Pro Pro Tyr Lys Phe Ile His Met Leu Lys Gly Xaa Ser
                15                  20                  25
```

<210> 1430
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1430

```
Met Val Ile Leu Thr Met Leu Ile Leu Leu Ile His Glu His Gly Ile
-15                 -10                 -5                  1
Phe Phe Ser Leu Val Cys Val Leu Phe
            5                   10
```

<210> 1431
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1431

```
Met Phe Ser His Asn His Ser Tyr Thr Tyr Thr Pro Gln His Ser Pro
                -25                 -20                 -15
Leu Thr His Thr His Thr Cys Thr Pro Pro Ser Thr Ala His Pro Arg
            -10                 -5                  1
Gly
```

<210> 1432
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1432

```
Met Phe Xaa Met Ile Leu Leu Cys Phe Leu Ala Val Ser Asn Phe Asn
-15                 -10                 -5                  1
Lys Leu Leu Trp Gly Xaa
            5
```

<210> 1433
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1433
Met Phe Leu Ile Leu Gly Lys Phe Ser Arg Val Met Gly Leu Pro Leu
-25 -20 -15
Ala Cys Phe Ser Leu Phe Gly Xaa Leu Pro Gln Gly Leu Leu Ile
-10 -5 1 5

<210> 1434
<211> 30
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1434
Met Val Ala Leu Gly Gln Leu Ala Xaa Leu Pro Gly Xaa Xaa His Gly
-15 -10 -5
Gly Leu Ser Ala Val Thr Val Val Leu Pro Ile Leu Leu Cys
1 5 10

<210> 1435
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1435
Met Pro Val Ser Phe Val Cys Leu Leu Phe Arg Asn Val Tyr Ser Asn
-15 -10 -5 1
Leu Leu Pro Ser Phe Phe
5

<210> 1436
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -27..-1

<400> 1436
Met Gly Ser Gly Gly Asp Ser Leu Leu Gly Gly Arg Gly Ser Leu Pro
-25 -20 -15
Leu Leu Leu Pro Ala His His Gly Arg His Gly Ser Gly Leu Pro Ala
-10 -5 1 5
Pro Asp Pro Ser Pro Pro Pro Gly Pro Ala Val Pro Gly Pro Trp Pro
10 15 20
Cys Gln Asp Glu Leu Pro Ser Leu Arg Pro Ala Thr Ser His His Phe
25 30 35

<210> 1437
<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1437
Met Ala Val Gly Gly Thr Ala Val Ile Thr Arg Arg Leu Leu Gly Arg
-25 -20 -15 -10
Ser Gly Phe Ser Phe Gln Val Ser Gly Trp Gly Trp Gly Glu Arg Val
-5 1 5
Asp Asp Phe Leu Phe Ser Ser Gly Ile Asp Gly
10 15

<210> 1438
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1438
Met Arg His His Val Arg Xaa Pro Ala Leu Ser Ser Leu Ala His His
-20 -15 -10
Pro Arg Thr Ser Gly Gln Lys Arg Glu Pro Ile Ala Pro Ala Gln Leu
-5 1 5 10
Ser Pro

<210> 1439
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -73..-1

<400> 1439
Met Leu Ile Leu Asn Gly Phe Arg Gly His Ala Thr Asp Ser Val Lys
-70 -65 -60
Asn Ser Met Glu Ser Met Asn Thr Asp Met Val Ile Ile Pro Gly Gly
-55 -50 -45
Leu Thr Ser Gln Leu Gln Val Leu Asp Val Val Val Tyr Lys Pro Leu
-40 -35 -30
Asn Asp Ser Val Arg Ala Gln Tyr Ser Asn Trp Leu Leu Ala Gly Asn
-25 -20 -15 -10
Leu Ala Leu Ser Pro Thr Gly Asn Ala Lys Lys Pro Pro Leu Gly Leu
-5 1 5
Phe Leu Glu Trp Val Met Val Ala Trp Asn Ser Ile Ser Ser Glu Ser
10 15 20
Ile Val Gln Gly Xaa Lys Glu Val Pro Tyr Leu Xaa Gln Leu Gly Gly
25 30 35
Gly Arg Arg
40

<210> 1440
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1440
Met Ile Cys Thr Thr Val Tyr Ile Thr Met Ala Pro Tyr Cys Leu Ser

```
-25                 -20                  -15                 -10
Asn Cys Leu Leu Xaa Xaa Ser Trp Gly Leu His Leu Tyr Arg Phe Leu
                -5                   1               5
Ala Pro

<210> 1441
<211> 16
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1441
Met Val Ser Leu Cys Val Ala Ala Leu Phe Pro Leu Gln Ala Tyr Gly
                -10                 -5                   1

<210> 1442
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1442
Met Leu Ser Ile Phe Ser Phe Phe Cys Arg Pro Phe Val Tyr Leu Leu
                -20                 -15                 -10
Leu Arg Asn Leu Xaa Ser Tyr Ser Leu Pro Thr Thr
            -5                   1

<210> 1443
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -77..-1

<400> 1443
Met Phe Pro Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Thr Asn
        -75                 -70                 -65
Lys Ser Leu Pro Arg Ser Ala Ser Thr Pro Glu Thr Arg Thr Lys Phe
    -60                 -55                 -50
Thr Gln Asp Asn Leu Cys Xaa Ala Gln Arg Glu Arg Leu Asp Ser Ala
-45                 -40                 -35                 -30
Asn Leu Trp Val Leu Val Asp Cys Ile Leu Arg Asp Thr Ser Glu Asp
                -25                 -20                 -15
Leu Gly Leu Gln Cys Asp Ala Val Asn Leu Ala Phe Gly Arg Arg Cys
            -10                 -5                   1
Glu Glu Leu Glu Asp Ala Arg His Lys Leu Gln Xaa His Leu
    5                   10                  15

<210> 1444
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
```

<222> -15..-1

<400> 1444
Met Pro Leu Val His Ser Phe Leu Trp Leu Ser Ser Ile Leu Tyr Ile
-15 -10 -5 1
Tyr His Leu Arg
5

<210> 1445
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1445
Met Ile Ser Asn Gly Lys Phe Phe Cys Phe Phe Xaa Val Phe Xaa Phe
-20 -15 -10
Xaa Phe Leu Xaa Arg Xaa Leu Xaa Xaa Xaa Pro Arg Leu Glu Cys Asn
-5 1 5
Gly Lys Xaa Ser Ala His Xaa Asn Leu Arg Leu Leu Ser Xaa Ser Asn
10 15 20
Ser Leu Ala Ser Ala Pro Arg Gly
25 30

<210> 1446
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -90..-1

<400> 1446
Met Glu Asp Ser Ala Ser Ala Ser Leu Ser Ser Ala Ala Ala Thr Gly
-90 -85 -80 -75
Thr Ser Thr Ser Thr Pro Ala Ala Pro Thr Ala Arg Lys Gln Leu Asp
-70 -65 -60
Lys Glu Gln Val Arg Lys Ala Val Asp Ala Leu Leu Thr His Cys Lys
-55 -50 -45
Ser Arg Lys Asn Asn Tyr Gly Leu Leu Leu Asn Glu Asn Glu Ser Leu
-40 -35 -30
Phe Leu Met Val Val Leu Trp Lys Ile Pro Ser Lys Glu Leu Arg Val
-25 -20 -15
Arg Leu Thr Leu Pro His Ser Ile Arg Ser Asp Ser Glu Asp Ile Cys
-10 -5 1 5
Xaa Phe Thr Lys Asp
10

<210> 1447
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1447
Met Asn Ala Glu Gly Ala Ser Pro Gly Lys Glu Thr Asn Thr Gly Thr

```
                    -25                      -20                      -15
Leu Ile Glu Leu Asn Leu Xaa Ser Pro Val Ala Leu Gln Trp Pro Leu
                -10                      -5                   1
Ser Ser Pro Ser Cys Leu Arg Ile Leu Ser Asn Lys Val Pro Arg Asn
    5                   10                      15
Leu Arg Trp Gln Lys His Tyr Ser Thr His Gln
20                  25                      30
```

<210> 1448
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -63..-1

<400> 1448

```
Met Leu Gly Leu Asp Glu Leu Gly Arg Ser Gly Cys Gly His Cys Thr
            -60                 -55                 -50
Gln Ala Asp Leu Arg Phe Gly Asp Ala Ala Gly Xaa Glu Pro Arg Xaa
        -45                 -40                 -35
Arg Xaa Thr His Arg Asn Thr Ala Ala Ala Arg Val Pro Pro Pro Pro
    -30                 -25                 -20
Arg Val Met Ala Ala Ala Ala Ala Leu Arg Ala Pro Ala Gln Ser Ser
-15                 -10                 -5                   1
Val Thr Phe Glu Asp Val Ala Val Asn Phe Ser Leu Glu Glu Trp Ser
            5                   10                  15
Leu
```

<210> 1449
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1449

```
Met Ser Ala Leu Lys Asp Phe Arg Glu Phe Leu Asn Trp Trp Gly Asn
    -25                 -20                 -15
Leu Ser Phe His Leu Gln Glu Ala His Gly Ser Glu Ile Ala Glu Met
-10                 -5                   1                   5
Gly Ala Gly Ile Leu Glu Glu Lys Asn Tyr Gly Gln Gln Xaa His Cys
            10                  15                  20
Asn
```

<210> 1450
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1450

```
Met Ser Leu Pro Pro Phe Phe His Pro Ser Pro Ala Pro Ser Leu Ala
-30                 -25                 -20                 -15
Pro Pro Pro Ser Leu Phe Leu Ser Leu Pro Pro Ser Leu Ser Pro Pro
                -10                  -5                   1
Leu Pro Ala Arg
```

5

<210> 1451
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1451
Met Phe Phe Leu Cys Gly Phe Leu Tyr Leu Cys Phe Ile Ser Phe Phe
-10 -5 1
Phe Phe
5

<210> 1452
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1452
Met Lys Ala Gly Pro Cys Ser Cys Gln Glu Gly Gly Arg Gln Trp Ala
-40 -35 -30
His Gly Ser Val Pro Leu Gln Pro Thr Ala Arg Leu Ala Ala Leu Gly
-25 -20 -15
Ile Phe Leu Cys Pro Gly Glu Thr Leu Ser Ala Ser Leu His Trp Asn
-10 -5 1 5
Pro Ile Gly

<210> 1453
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1453
Met Leu Ser Gln Ser Phe Gln Lys Asn Lys Thr Asn Leu Leu Cys Leu
-20 -15 -10
Thr Phe Gln Arg Cys Gln Ser Tyr Asn Trp Leu Asn Ile Phe Glu Ala
-5 1 5
Thr Tyr Met Thr Thr Leu Phe Ile Ser Val Ile Xaa Thr Asn Phe Leu
10 15 20 25
Lys Arg Tyr Leu Leu
30

<210> 1454
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1454
Met Phe Leu Phe Cys Trp Glu Lys Ser Pro Arg Met Gln Leu Leu Gly
-25 -20 -15 -10
Cys Met Val Leu Tyr Asp Cys Phe Ser Phe Lys Lys Leu Pro Gly
-5 1 5

<210> 1455
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1455
Met Ser Phe Ile Ser Val Ile Phe Pro Leu Ile Leu Leu Asn Arg Phe
-30 -25 -20 -15
Ser Phe Val Cys Phe Phe His Val Phe Tyr Cys Val Phe Cys Asn Val
-10 -5 1
Ser Ser Leu Phe Ser Tyr Gln Phe Leu Leu His Phe Cys Asp Asp
5 10 15

<210> 1456
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1456
Met His Glu Tyr Leu Pro Arg Asn Phe His Asp Phe Asn Ser Pro Asn
-30 -25 -20
Ser Lys Leu Gly Met Gly Met Gly Phe Phe Ser Gly Val Lys Ser Trp
-15 -10 -5 1
Ile Gly Gly

<210> 1457
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -36..-1

<400> 1457
Met Ala Ser Xaa Val Pro Val Lys Asp Lys Lys Leu Leu Glu Val Lys
-35 -30 -25
Leu Gly Glu Leu Pro Ser Trp Ile Leu Met Arg Asp Phe Ser Pro Ser
-20 -15 -10 -5
Gly Ile Phe Gly Ala Phe Gln Arg Gly Tyr Tyr Arg Tyr Tyr Asn Lys
1 5 10
Tyr Ile Asn Val Lys Lys Gly Ser Ile Ser Gly Ile Thr Met Val Leu
15 20 25
Ala Cys Tyr Val Leu Phe Ser Tyr Ser Phe Ser Tyr Lys His Leu Lys
30 35 40
His Glu Ser
45

<210> 1458

<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1458
```
Met Val Ile Ser Ala Gly Ala Leu Leu Trp Met Ala Trp Asp Gly Gln
            -15                 -10                 -5
Leu Ser Arg Pro Glu Gly Ala Arg
        1               5
```

<210> 1459
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1459
```
Met Val His Cys Asn Leu Glu Leu Leu Gly Ser Ser Tyr Asn Pro Ile
            -15                 -10                 -5
Ser Ala Ser Pro Val Ala Arg Thr Ile Ser Cys Pro Ala Ile Val
        1               5                   10
```

<210> 1460
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -88..-1

<400> 1460
```
Met Leu Gly Ser Gly Phe Lys Ala Glu Arg Leu Arg Val Asn Leu Arg
            -85                 -80                 -75
Leu Val Ile Asn Arg Leu Lys Leu Leu Glu Lys Lys Lys Thr Glu Leu
        -70                 -65                 -60
Ala Gln Lys Ala Arg Lys Glu Ile Ala Asp Tyr Leu Ala Ala Gly Lys
    -55                 -50                 -45
Asp Glu Arg Ala Arg Ile Arg Val Glu His Ile Ile Arg Glu Asp Tyr
-40                 -35                 -30                 -25
Leu Val Glu Ala Met Glu Ile Leu Glu Leu Tyr Cys Asp Leu Leu Leu
                -20                 -15                 -10
Ala Arg Phe Gly Leu Ile Gln Ser Met Lys Glu Leu Asp Ser Gly Leu
            -5                  1               5
Ala Glu Ser Val Ser Thr Leu Ile Trp Ala Ala Pro Arg Leu Gln Ser
    10                  15                  20
Glu Val Ala Glu Leu Lys Ile Val Ala Asp Gln Leu Cys Pro Ser
25                  30                  35
```

<210> 1461
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -43..-1

<400> 1461
Met Arg Gly Trp Xaa Ala Pro Ala Trp Arg Xaa Leu Xaa Thr Arg Arg
-40 -35 -30
Leu Pro Met Gly Ser Arg His Gly Ala Ser Pro Ala Ser Ala Val Trp
-25 -20 -15
Cys Leu Xaa Leu Lys Leu Val Pro Ala Leu Cys Ile Ser Gly Leu Thr
-10 -5 1 5
Leu Gly Ile Gln Gly Phe
10

<210> 1462
<211> 49
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1462
Met Tyr Phe Lys Thr Thr Thr Xaa Xaa His Ser Ala His Met Leu Leu
-30 -25 -20
Gln Ile Cys Phe Phe Arg Leu Thr Ile Leu Xaa Phe His Asp Asn Thr
-15 -10 -5
Trp Gly Ser Thr Ser Phe Ser Xaa Val Ala Ala Met Leu Phe His Tyr
1 5 10
Arg
15

<210> 1463
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1463
Met Ser Ser Asn Ile Gln Arg Leu Gly Phe Pro Leu Leu Phe Leu Phe
-20 -15 -10
Phe Leu Phe Leu Phe Phe Phe Phe Phe Phe
-5 1

<210> 1464
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -67..-1

<400> 1464
Met Cys Asp Ala Phe Val Gly Thr Trp Lys Leu Val Ser Ser Glu Asn
-65 -60 -55
Phe Asp Asp Tyr Met Lys Glu Val Gly Val Gly Phe Ala Thr Arg Lys
-50 -45 -40
Val Ala Gly Met Ala Lys Pro Asn Met Ile Ile Ser Val Asn Gly Asp
-35 -30 -25 -20
Val Ile Thr Ile Pro His Leu Val Leu Pro Leu Pro Met Leu Pro Thr

-15 -10 -5
Ser Asn Arg Lys Arg
1

<210> 1465
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1465
Met Phe Leu Tyr Arg Ser Phe Gly Gly Gln Leu Leu Ser Phe Leu Leu
-20 -15 -10
Gly Thr Tyr Leu Gly Arg Arg Glu Val Ala Gly Pro Gln His Gly Gln
-5 1 5 10
Phe Ser Lys

<210> 1466
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1466
Met Xaa Gly Phe Phe Cys Leu Cys Ala Phe Asn Ser Phe Leu Leu Ser
-15 -10 -5
Pro Glu Gly
1

<210> 1467
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -66..-1

<400> 1467
Met Ile Phe Pro His Cys Met Tyr Cys Leu Glu Cys Ile Thr Lys Asn
-65 -60 -55
Gly Leu Leu Gly Leu Lys Val Leu Pro Leu Tyr Gly Ile Met Leu Ile
-50 -45 -40 -35
Phe Phe Pro Lys Val Val Tyr Asn Asn Gln Pro Leu His Tyr Lys Ser
-30 -25 -20
Val Met Val Phe Gln Leu Thr Ser Phe Leu Ser Ile Xaa Ile Phe Val
-15 -10 -5
Asn Pro Thr Arg
1

<210> 1468
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -54..-1

<400> 1468
Met Val Ser Met Ser Phe Lys Arg Asn Arg Ser Asp Arg Phe Tyr Ser
-50 -45 -40
Thr Arg Cys Cys Gly Cys Cys His Val Arg Xaa Gly Thr Ile Ile Leu
-35 -30 -25
Gly Thr Trp Tyr Met Val Val Asn Leu Leu Met Ala Xaa Leu Leu Thr
-20 -15 -10
Val Glu Val Thr His Pro Asn Ser Met Pro Ala Val Asn Ile Gln Tyr
-5 1 5 10
Glu Val Ile Gly Asn Tyr Tyr Ser Ser Glu Arg Met Ala Asp Asn
15 20 25

<210> 1469
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1469
Met Ala Ala Ala Thr Leu Thr Ser Lys Leu Tyr Ser Leu Leu Phe Arg
-30 -25 -20
Arg Thr Ser Thr Phe Ala Leu Thr Ile Xaa Arg Xaa Xaa Ser Cys Ser
-15 -10 -5 1
Ser Xaa Ala Pro Ser Ile Lys Ala Arg Thr Leu Ser Thr Thr Thr Ser
5 10 15
Thr Arg Gly Ser Cys Gly Asn Thr Ser Ser Thr Ser Met Arg Thr Ser
20 25 30
Ser Ser Leu Glu Ala Pro Ile Gln Ala Arg Arg Thr Arg Ser Thr Gln
35 40 45
Gln Leu Phe Ala Gln Ser Trp Ser Leu Ser Xaa Lys Met Met
50 55 60

<210> 1470
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 1470
Met Lys Ala Ile Lys Lys Ser Leu Thr Glu Glu Glu Tyr Leu Tyr Leu
-40 -35 -30
Asp Phe Ser His Gln Thr Glu Gly Cys Ile Phe Pro Leu His Thr Ser
-25 -20 -15 -10
Val Thr Leu Phe Leu Leu Ser Tyr Cys Asp Cys Lys Ile Phe Lys Ile
-5 1 5
Cys Leu Val Val Thr Lys Glu Val Ser Arg Asp Xaa Ser Leu Leu Arg
10 15 20
Asp Asp Leu Ile Gln Asp Val Glu Ile Gln Ile Ile Ser Arg Gln Glu
25 30 35
Leu Pro Pro
40

<210> 1471
<211> 20
<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1471
Met Phe Leu Cys Val Cys Tyr Phe Ile Arg Lys Ser Thr Ser Phe Phe
-10 -5 1
Ser Ile Ser Ser
5

<210> 1472
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1472
Met Gly Lys Pro Arg Gly Gly Glu Met Leu Glu Val Val Lys Thr Val
-45 -40 -35 -30
Ser Thr Phe Thr Leu Gly Gly Trp Lys Gly Thr Ala Pro Val Ser Cys
-25 -20 -15
Ala Trp Trp Leu Leu Leu Pro Val Trp Lys Leu Gly Gly Gln Leu Glu
-10 -5 1
Arg Arg Lys Asn Pro Lys Glu Tyr Cys Leu Gly Ser Trp Val Trp Leu
5 10 15
Ser Pro Gln Leu Ala Pro Arg
20 25

<210> 1473
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1473
Met Leu Ile Phe Thr Phe Ile Ser Thr Leu Leu Phe Val Phe Leu Gly
-15 -10 -5
Val Val
1

<210> 1474
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -37..-1

<400> 1474
Met Glu Val Leu Ser Xaa Pro Asn Ser Phe Gln Thr Gln Ala Leu Trp
-35 -30 -25
Asp Ser Leu His Ser Pro Gly Val Pro Gly Ser Gly Leu Cys Ser Met
-20 -15 -10
Ala Ala Val Gln Ala Gly Asn Gln Ala Ile Tyr Ser Ala Ser Gly

-5 1 5 10

<210> 1475
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -42..-1

<400> 1475
Met Gln Ala Thr Ala Ser Gln Pro Ile His Phe Phe Xaa Ser Ser Pro
-40 -35 -30
Gln Ala Pro Arg His His Ser Gly His Pro Val Pro Leu Leu Leu Thr
-25 -20 -15
Gln Ala Gly Phe Pro Arg Arg Gly Glu Ala Ala Pro Pro Leu Leu
-10 -5 1 5

<210> 1476
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1476
Met Arg Gly Xaa Asn Xaa Val Phe Arg Val Phe Ser Glu Ser Leu Lys
-30 -25 -20 -15
Gly Leu Cys Thr Phe Thr Leu Asn Leu Thr Ala Val Arg Thr Ile Xaa
-10 -5 1
Leu Asp

<210> 1477
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1477
Met Gly Arg Ile Ile Pro Met Val Glu Lys Ala Asp Thr Ala Gln Lys
-30 -25 -20
Phe Gln Gly Arg Leu Thr Ile Ser Thr Xaa Leu Ser Thr Ser Xaa Xaa
-15 -10 -5
Phe Met Glu Leu Ser Ser Leu Arg
1 5

<210> 1478
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -67..-1

<400> 1478
Met Asn Leu Val Ile Cys Val Leu Leu Leu Ser Ile Trp Lys Asn Asn

```
        -65                     -60                     -55
Cys Met Thr Thr Asn Gln Thr Asn Gly Ser Ser Thr Thr Gly Asp Lys
    -50                 -45                 -40
Pro Val Glu Ser Met Gln Thr Lys Leu Asn Tyr Leu Arg Arg Asn Leu
-35                 -30                 -25                 -20
Leu Ile Leu Val Gly Ile Ile Ile Met Val Phe Val Phe Ile Cys Phe
                -15                 -10                 -5
Cys Tyr Leu His Tyr Asn Cys Leu Ser Asp Asp Ala Ser Lys Ala Gly
            1               5                   10
Met Val Lys Lys Lys Gly Ile Ala Ala Lys Ser Ser Lys Thr Ser Phe
    15                  20                  25
Ser Glu Ala Lys Thr Ala Ser Gln Cys Ser Ser Glu Thr Gln Thr Gly
30                  35                  40                  45
```

<210> 1479
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -28..-1

<400> 1479

```
Met Gln Ile Ser Ala Ala Ser Leu Asn Phe Ser Ser Lys Asn Gly Ile
            -25                 -20                 -15
Phe Phe Ser Leu Thr Leu Ser Gly Cys Lys Phe Ser Lys Leu Leu Cys
        -10                 -5                  1
Pro Phe Gly
5
```

<210> 1480
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -52..-1

<400> 1480

```
Met Ile Phe Glu Pro Val Val Leu Lys Pro Val Phe Leu Asn Ile Phe
        -50                 -45                 -40
Phe Phe Ser His His Val Phe Thr Val Phe Phe Ser Gly Ser His Val
    -35                 -30                 -25
Asp Ile Leu Ser Arg Thr Val Leu Val Trp Asp Cys Leu Leu Pro Pro
-20                 -15                 -10                 -5
Pro Ser Phe Phe Leu Leu Leu Leu Ser Ser Ser Xaa Ser Xaa Leu Leu
                1               5                   10
Leu Xaa Xaa Ser Ser Ser Ser Arg
        15                  20
```

<210> 1481
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1481

```
Met Leu Val Pro Leu Leu Ser His Leu Leu Phe Lys Phe Thr Trp Pro
```

-10 -5 1
Lys Xaa Ser Gln
5

<210> 1482
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 1482
Met Asp Arg Asn Pro Ser Pro Pro Pro Pro Gly Arg Asp Lys Glu Glu
-45 -40 -35
Glu Glu Glu Val Ala Gly Gly Asp Cys Ile Gly Ser Thr Val Tyr Ser
-30 -25 -20
Lys His Trp Leu Phe Gly Val Leu Ser Gly Leu Xaa Gln Xaa Val Ser
-15 -10 -5
Pro Gly Lys His Gln Asn Leu Gly Ser Xaa Xaa Glu Glu Gln Leu Thr
1 5 10 15
Glu Leu Asp Glu Arg Asn
20

<210> 1483
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -23..-1

<400> 1483
Met Lys Leu Ser Leu Ala Gly Tyr Glu Ile Leu Gly Cys His Phe Phe
-20 -15 -10
Ser Leu Ala Leu Leu Asn Thr Gly Pro Gln Tyr Leu Leu Ala Tyr Arg
-5 1 5
Val Ser Ala Glu Arg
10

<210> 1484
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -40..-1

<400> 1484
Met Ala Thr Ser Val Gly His Arg Cys Leu Gly Leu Leu His Gly Val
-40 -35 -30 -25
Ala Pro Trp Arg Ser Ser Leu His Pro Cys Glu Ile Thr Ala Leu Ser
-20 -15 -10
Gln Ser Leu Gln Pro Leu Arg Lys Leu Pro Phe Arg Ala Ser Xaa Thr
-5 1 5

<210> 1485
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -49..-1

<400> 1485
```
Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
                -45                 -40                 -35
Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
            -30                 -25                 -20
Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
        -15                 -10                 -5
Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
    1               5                   10                  15
Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
                20                  25                  30
Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
            35                  40                  45
Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
        50                  55                  60
Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp
    65                  70                  75
```

<210> 1486
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1486
```
Met Ala Ala Val Thr Val Thr Val Thr Lys Thr Ala Ala Ala Ala Thr
                -25                 -20                 -15
Ala Phe Asn Lys Ala Val Trp Phe Thr Pro Cys Ser Cys Gln Glu Val
            -10                 -5                  1
Ser Ser Arg Leu Pro Ala Arg Thr Ala Ala Thr Arg Gln Asp Arg Ala
    5                   10                  15
Asp Lys Lys Glu Arg Pro Cys
20                  25
```

<210> 1487
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1487
```
Met Leu Gln Phe Glu Lys Pro Gly Ser Ala Ile Cys Leu Trp His Ser
                -15                 -10                 -5
Thr Leu Gly Gly Xaa Gly Gly Arg Glu Ile Xaa Ser Leu Arg Pro Ala
            1                   5                   10
Cys Gly
    15
```

<210> 1488
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1488
```
Met Leu Ile Ser Tyr Leu Ala Ile Leu Leu Lys Trp Val Ser Asn Ser
            -15                 -10                 -5
Lys Ser Phe Leu Val Lys Ala Ser
        1               5
```

<210> 1489
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1489
```
Met Lys Leu Gln Thr Leu Ala Phe Trp Ser Ala Tyr Val Pro Cys Gln
-15                 -10                 -5                  1
Thr Gln Asp Arg Asp Ala Pro Arg Leu Thr Leu Glu Gln Ile Asp Leu
            5                   10                  15
Ile Arg Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser
        20                  25                  30
Ala Lys Ala Leu Asn Asp Thr Gln Lys Leu Ala Cys Leu Ile Gly Val
    35                  40                  45
Glu Gly Gly His Ser Leu Asp Asn Ser Leu Ser Arg
50                  55                  60
```

<210> 1490
<211> 23
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1490
```
Met Pro Ala Cys Leu Ser Ser Phe Val Ile Pro Ser Leu Leu Ser Pro
                -10                 -5                  1
Ser Ser Pro Pro Ser Ile Gly
        5
```

<210> 1491
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1491
```
Met Val Val Ser Phe Ala Gly Ser Cys Thr Ile Leu Gly Ala Ser Ser
    -15                 -10                 -5
His Ser Phe Pro Ile Glu Val Ser Leu Phe Pro Val Asp Cys Gly Phe
1               5                   10                  15
Leu Leu
```

<210> 1492
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1492
Met Cys Cys Pro Gly Trp Asn Ala Val Ser Gln Ser Trp Leu Ala Ala
-20 -15 -10 -5
Pro Ser Thr Ser Trp Val Gln Glu Ile Leu Val Leu Gln Pro Pro Gly
1 5 10

<210> 1493
<211> 69
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -54..-1

<400> 1493
Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr
-50 -45 -40
Val Pro Leu Lys Xaa Xaa Xaa Val Asp Asp Asp Asp Ser Lys Ile Trp
-35 -30 -25
Ser Xaa Tyr Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe
-20 -15 -10
Leu Xaa Xaa Val Ser Gly Thr Xaa Asp Val Phe Phe Arg Gln Ile Leu
-5 1 5 10
Ala Leu Thr Gly Trp
15

<210> 1494
<211> 45
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1494
Met Asp Ala Ser His Ser His Leu Ser Leu Val Gly His Ser Arg Ala
-15 -10 -5
Cys Gly Val Thr Ser Arg Pro His Ala Arg His Arg Gly Arg Cys Leu
1 5 10 15
Gly Pro Cys Ser Arg Ser Gly Pro Arg Leu Cys Ser Ala
20 25

<210> 1495
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1495

```
Met Gly Ser Asn Ala Val Val Trp His Thr Lys Pro Ser Leu Leu Asn
                -30                 -25                 -20
His Pro Ala Ser Ser Leu Ile Ser His Asp Pro Trp Pro Arg Gly Ala
            -15                 -10                 -5
Phe Ala Leu Ser Cys Pro Ser Ala Ser Phe Met Leu Phe Ser Ser Leu
        1               5                   10
Gln Cys Pro Phe Pro Tyr Xaa Xaa Thr Glu Cys Asn Xaa
15                  20                  25
```

<210> 1496
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1496

```
Met Lys Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val
            -15                 -10                 -5
Tyr Gly Asp Gln Asp Met His Glu Val Val Arg Lys His Xaa Met Asp
        1               5                   10
Tyr Leu Met Lys Asn Ala Asp Tyr Phe Ser Xaa Tyr Val Thr Glu Asp
15                  20                  25                  30
Phe Thr Thr Tyr Ile Xaa Arg Lys
                35
```

<210> 1497
<211> 24
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -21..-1

<400> 1497

```
Met Val His Leu Ile Leu Thr Glu Val Leu Ile Met Ile Xaa Glu Ala
    -20                 -15                 -10
Xaa Asn Val Trp Cys Gly Asp Ser
-5                  1
```

<210> 1498
<211> 51
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -47..-1

<400> 1498

```
Met Tyr His Asn Leu Phe Ala Leu Leu Leu Ile Asp Ile His Val Val
        -45                 -40                 -35
Leu Val Phe Tyr Cys Leu Asp Leu Leu Met Ile His Ile Phe Tyr Cys
    -30                 -25                 -20
Lys Tyr Cys Leu Xaa Phe Gly Ile Leu Ala Ser Glu Val Tyr Ser Trp
-15                 -10                 -5                  1
Asn Ile Tyr
```

<210> 1499
<211> 44

<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -29..-1

<400> 1499
```
Met Glu Ser Pro Ser Arg Ala Gly Gly Val Xaa Leu Xaa Lys Ala Ala
                -25                 -20                 -15
Ser Pro Leu Cys Ser Xaa Ser Ser Gly Tyr Cys Xaa Ala Phe Pro Arg
            -10                 -5                  1
Arg Ser Ala Arg Arg His Leu His Pro Gly His Gly
    5                   10                  15
```

<210> 1500
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -25..-1

<400> 1500
```
Met Trp Arg Tyr Val Ser Arg Leu Ser Ser Val Pro Leu Ile Ser Leu
-25                 -20                 -15                 -10
Ser Val Leu Met Pro Val Gln His Ser Pro Asp Phe Cys Ser Phe Ile
                -5                  1               5
Val Ser Thr Val Ile Pro Trp Phe Pro Trp Gly Ile Gly Ser Arg Thr
        10                  15                  20
Leu Met Asp Ile Lys Ile Leu Gly Cys Ser Ser Pro Gly
    25                  30                  35
```

<210> 1501
<211> 33
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1501
```
Met Asp Val Ser Cys Lys Ile Leu Tyr Asn Val Ile Glu Lys Phe Cys
-30                 -25                 -20                 -15
Asn Asn Leu Leu Lys Leu Ser Ser His Ser Pro Thr Cys Ala Cys Lys
                -10                 -5                  1
Leu
```

<210> 1502
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1502
```
Met Ile Phe Lys Asp Val Phe Ser His Leu Ser Gly Ser Ser Leu Gln
-20                 -15                 -10                 -5
Leu Cys Val Ala Gln Phe Leu Xaa Leu Ser Ala Val Asp
```

1 5

<210> 1503
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -44..-1

<400> 1503
Met Lys Leu Thr Lys Asn Ile Leu Xaa Val Ile Ile Gly Cys Phe Lys
-40 -35 -30
Leu Ile Ala Tyr Lys Asn Ser Val Leu Tyr Phe Tyr Ser Asn Phe Ser
-25 -20 -15
Phe Ser Phe Leu Phe Phe Phe Phe Leu Ser Phe Phe Phe Phe Phe Phe
-10 -5 1
Phe Phe
5

<210> 1504
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -87..-1

<400> 1504
Met Asn Asn Gln Lys Gln Xaa Xaa Pro Thr Leu Ser Gly Gln Arg Phe
-85 -80 -75
Lys Thr Arg Lys Arg Asp Glu Lys Glu Arg Phe Asp Pro Thr Gln Phe
-70 -65 -60
Gln Asp Cys Ile Ile Gln Gly Leu Thr Glu Thr Gly Thr Asp Leu Glu
-55 -50 -45 -40
Ala Val Ala Lys Phe Leu Asp Ala Ser Gly Ala Lys Leu Asp Tyr Arg
-35 -30 -25
Arg Tyr Ala Glu Thr Leu Phe Asp Ile Leu Val Ala Gly Xaa Met Leu
-20 -15 -10
Ala Pro Gly Gly Thr Leu Ala Asp Asp Met Met Xaa
-5 1 5

<210> 1505
<211> 35
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1505
Met Ala Asp Ser Leu Glu Ile Lys Leu Pro Phe Leu Pro Phe Ala Gln
-15 -10 -5
Gln Ile Asp Ile Lys Ser Cys Phe Tyr Phe Phe Phe Xaa Asn Xaa Xaa
1 5 10 15
Phe Pro Arg

<210> 1506
<211> 115
<212> PRT

<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1506
Met Asp Arg Lys Trp Thr Trp Lys Arg Gly Gln Arg Ser His Leu Glu
-35 -30 -25 -20
Ser Gly Gln Ala Ala Pro Ala Thr Ala Ala Ala Thr Ala Ala Ser Ala
-15 -10 -5
Thr Thr Gly Ala Ser Val Trp Arg Ser Thr Met Gly Xaa Leu Cys Asp
1 5 10
Cys Thr Xaa Xaa Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser
15 20 25
Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro
30 35 40 45
Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr
50 55 60
Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr
65 70 75
Gln Ala Pro
80

<210> 1507
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -43..-1

<400> 1507
Met Ala Pro Gln Met Tyr Glu Phe His Leu Pro Leu Ser Pro Glu Glu
-40 -35 -30
Leu Leu Lys Ser Gly Gly Val Asn Gln Tyr Val Val Gln Glu Val Leu
-25 -20 -15
Ser Ile Lys His Leu Pro Pro Gln Leu Arg Ala Phe Gln Ala Ala Phe
-10 -5 1 5
Arg Ala Gln Gly Pro Leu Ala Met Leu Gln His Phe Asp Thr Ile Tyr
10 15 20
Ser Ile Leu His His Phe Arg Ser Ile Asp
25 30

<210> 1508
<211> 84
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -15..-1

<400> 1508
Met Ala Ala Val Gln Val Val Gly Ser Trp Pro Ser Val Gln Pro Arg
-15 -10 -5 1
Glu Ala Pro Arg Glu Ala Ile Pro Glu Arg Gly Asn Gly Phe Arg Leu
5 10 15
Leu Ser Ala Arg Leu Cys Ala Leu Arg Pro Asp Asp Ser Ser Ser Ala
20 25 30
Arg Thr Glu Ile His Leu Xaa Phe Asp Gln Leu Ile Ser Glu Asn Tyr
35 40 45

Ser Glu Gly Ser Gly Val Ala Pro Glu Asp Val Ser Ala Leu Leu Val
50 55 60 65
Gln Ala Cys Gly

<210> 1509
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -30..-1

<400> 1509
Met Phe His Gly Cys His Ile Leu Ser Phe Leu Arg Ile Ser Thr Arg
-30 -25 -20 -15
Gly Phe Leu Phe Phe Leu Gln Phe Ser Phe Pro Leu Tyr Tyr Leu Phe
-10 -5 1
Arg Xaa Xaa Phe Pro Gln Ser Phe Met Leu Glu Ala Phe Val Arg Cys
5 10 15

<210> 1510
<211> 42
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -26..-1

<400> 1510
Met Tyr Arg His Ser Lys Gln Arg Asn Asn Val Pro Cys Leu Val Leu
-25 -20 -15
Tyr Ala Pro Trp Val Pro Pro Leu Leu Leu Ala Phe Trp Gly Trp Trp
-10 -5 1 5
Leu Leu Glu Gln Gly Leu Phe Phe Phe Phe
10 15

<210> 1511
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -50..-1

<400> 1511
Met Gly Asp Pro Ser Lys Gln Asp Ile Leu Thr Ile Phe Lys Arg Leu
-50 -45 -40 -35
Arg Ser Val Pro Thr Asn Lys Val Cys Phe Asp Cys Gly Ala Lys Asn
-30 -25 -20
Pro Ser Trp Ala Ser Ile Thr Tyr Gly Val Phe Leu Cys Ile Asp Cys
-15 -10 -5
Ser Gly Ser His Arg Ser Leu Gly Val His Leu Ser Phe Ile Arg Ser
1 5 10
Thr Glu Leu Asp Ser Asn Trp Ser Trp Phe Gln Leu Arg Cys Met Gln
15 20 25 30
Val Gly Gly Asn Ala Ser Ala Ser Ser Phe Phe His Gln His Gly Cys
35 40 45
Ser Thr Asn Asp Thr Asn Ala Lys Tyr Asn Ser Arg Ala Ala Gln Leu
50 55 60
Tyr Arg Glu Lys Ile Lys Ser Leu Ala Ser Gln Ala Thr Arg Lys His

65 70 75
Gly Thr Asp Leu Trp Leu Asp Ser Cys
80 85

<210> 1512
<211> 26
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -22..-1

<400> 1512
Met Pro Leu Pro Pro Asn Gln Ser Pro Leu Leu Leu His Leu Val Phe
-20 -15 -10
His Gln Arg Thr Leu Ile Ser Leu Pro Pro
-5 1

<210> 1513
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1513
Met Phe Leu Thr Phe Phe Phe Cys Thr Gln Val His Gly Pro Ser Ile
-10 -5 1
Leu Asp Ser Pro Ala
5

<210> 1514
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1514
Met Val Thr Leu Trp Ile Phe Gln Phe Phe Leu Cys Leu Thr Cys Lys
-10 -5 1
Ala Tyr Asn Leu Arg Asn Cys Asn Asp Gly Lys Gly Xaa Xaa Ser Xaa
5 10 15
Val Leu Gly Leu Glu Gln Xaa Leu Pro Glu Ser Ala Gly Met Val Xaa
20 25 30
Phe Leu Gly Leu Lys His Arg Trp
35 40

<210> 1515
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -14..-1

<400> 1515

Met Val Leu Trp Ala Gly Pro Xaa Val Pro Leu Leu Cys Ala Ala Xaa
-10 -5 1
Gly Leu Gly Ala Leu His Pro Arg Cys Ser Ser Gln Gly Leu Arg Leu
5 10 15
Ala Xaa Ser Glu Ala
20

<210> 1516
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -41..-1

<400> 1516
Met Asn Trp Arg Arg Lys Ser Val Ile Gly Leu Ser Phe Asp Phe Val
-40 -35 -30
Ala Leu Asn Leu Thr Gly Phe Val Ala Tyr Ser Val Phe Asn Ile Gly
-25 -20 -15 -10
Leu Leu Trp Val Pro Xaa Xaa Xaa Gly Ala Val Ser Pro Gln Ile Pro
-5 1 5
Gln Arg Ser Glu Pro Arg Glu Gln Gln Arg Arg Leu Leu
10 15 20

<210> 1517
<211> 149
<212> PRT
<213> Homo sapiens
<400> 1517
Met Glu Pro Leu Ala Ala Tyr Pro Leu Lys Cys Ser Gly Pro Arg Ala
1 5 10 15
Lys Val Phe Ala Val Leu Leu Ser Ile Val Leu Cys Thr Val Thr Leu
20 25 30
Phe Leu Leu Gln Leu Lys Xaa Leu Lys Pro Lys Ile Asn Ser Phe Tyr
35 40 45
Ala Phe Glu Val Lys Asp Ala Lys Gly Arg Thr Val Ser Leu Glu Lys
50 55 60
Tyr Lys Gly Lys Val Ser Leu Val Val Asn Val Ala Ser Asp Cys Gln
65 70 75 80
Leu Thr Asp Arg Asn Tyr Leu Gly Leu Lys Glu Leu His Lys Glu Phe
85 90 95
Gly Pro Ser His Phe Ser Val Leu Ala Phe Pro Cys Asn Gln Phe Gly
100 105 110
Glu Ser Glu Pro Arg Pro Ser Lys Glu Val Glu Ser Phe Ala Arg Lys
115 120 125
Asn Tyr Gly Val Thr Phe Pro Ile Phe His Lys Ile Lys Ile Leu Gly
130 135 140
Ser Glu Gly Glu Leu
145

<210> 1518
<211> 132
<212> PRT
<213> Homo sapiens
<400> 1518
Met Asn Glu Ala Met Ala Thr Asp Ser Pro Arg Arg Pro Ser Arg Cys
1 5 10 15
Thr Gly Gly Val Val Val Arg Pro Gln Ala Val Thr Glu Gln Ser Tyr
20 25 30
Met Glu Ser Val Val Thr Phe Leu Gln Asp Val Val Pro Gln Ala Tyr
35 40 45

Ser Gly Thr Pro Leu Thr Glu Glu Lys Glu Lys Ile Val Trp Val Arg
50 55 60
Phe Glu Asn Ala Asp Leu Asn Asp Thr Ser Arg Asn Leu Glu Phe His
65 70 75 80
Glu Ile His Ser Thr Gly Ser Glu Pro Pro Leu Leu Ile Met Ile Gly
85 90 95
Tyr Ser Asp Gly Met Gln Val Trp Ser Ile Pro Ile Xaa Gly Glu Xaa
100 105 110
Lys Ser Ser Ser Leu Phe Asp Met Ala Gln Phe Glu Arg Leu Glu Ser
115 120 125
Cys Leu Leu His
130

<210> 1519
<211> 46
<212> PRT
<213> Homo sapiens
<400> 1519
Met Pro Val Thr Arg Ala Ser Gln Pro Arg Lys Pro Ser Ser Ala Gln
1 5 10 15
Gln Gln Lys Ala Ala Leu Leu Xaa Asn Asn Thr Ala Leu Gln Ser Val
20 25 30
Ser Leu Arg Ser Lys Thr Thr Ile Arg Glu Arg Pro Ser Ser
35 40 45

<210> 1520
<211> 41
<212> PRT
<213> Homo sapiens
<400> 1520
Met Asn Gly Phe Gly Arg Leu Glu His Phe Ser Gly Ala Val Tyr Glu
1 5 10 15
Gly Gln Phe Lys Asp Asn Met Phe His Gly Leu Gly Thr Tyr Thr Phe
20 25 30
Pro Asn Gly Ala Lys Tyr Thr Gly Ile
35 40

<210> 1521
<211> 131
<212> PRT
<213> Homo sapiens
<400> 1521
Met Ala Lys Ile Ala Lys Thr His Glu Asp Ile Glu Ala Gln Ile Arg
1 5 10 15
Glu Ile Gln Gly Lys Lys Ala Ala Leu Asp Glu Ala Gln Gly Val Gly
20 25 30
Leu Asp Ser Thr Gly Tyr Tyr Asp Gln Glu Ile Tyr Gly Gly Ser Asp
35 40 45
Ser Arg Phe Ala Gly Tyr Val Thr Ser Ile Ala Ala Thr Glu Leu Glu
50 55 60
Asp Asp Asp Asp Asp Tyr Ser Ser Ser Thr Ser Leu Leu Gly Gln Lys
65 70 75 80
Lys Pro Gly Tyr His Ala Pro Val Ala Leu Leu Asn Asp Ile Pro Gln
85 90 95
Ser Thr Glu Gln Tyr Asp Pro Phe Ala Glu His Arg Pro Pro Lys Ile
100 105 110
Ala Asp Arg Glu Asp Glu Tyr Lys Lys His Arg Arg Thr Met Ile Ile
115 120 125
Ser Gln Ser
130

<210> 1522
<211> 82

<212> PRT
<213> Homo sapiens
<400> 1522
Met Pro Ile Asn Lys Ser Glu Lys Pro Glu Ser Cys Asp Asn Val Lys
1 5 10 15
Val Val Val Arg Cys Arg Pro Leu Asn Glu Arg Glu Lys Ser Met Cys
20 25 30
Tyr Lys Gln Ala Val Ser Val Asp Glu Met Arg Gly Thr Ile Thr Val
35 40 45
His Lys Thr Asp Ser Ser Asn Glu Pro Pro Lys Thr Phe Thr Phe Asp
50 55 60
Thr Val Phe Gly Pro Glu Ser Lys Gln Leu Asp Val Tyr Asn Leu Thr
65 70 75 80
Ala Arg

<210> 1523
<211> 40
<212> PRT
<213> Homo sapiens
<400> 1523
Met Pro Asn Arg Gly Gly Asn Gly Leu Ala Pro Gly Glu Asp Arg Phe
1 5 10 15
Lys Pro Val Val Pro Trp Pro His Val Glu Gly Val Glu Val Asp Leu
20 25 30
Glu Ser Ile Arg Arg Ile Asn Lys
35 40

<210> 1524
<211> 35
<212> PRT
<213> Homo sapiens
<400> 1524
Met Ser Leu Trp Leu Cys Phe Gln Cys Pro Leu Gly Val Ser Lys Ser
1 5 10 15
Asn Lys Lys Arg Ile Asn Leu Cys Asn Gly Phe Trp Asn Glu Lys Ile
20 25 30
Lys Asn Arg
35

<210> 1525
<211> 47
<212> PRT
<213> Homo sapiens
<400> 1525
Met Gly Thr His Val Phe Ala Ile Asn Lys Arg Thr Tyr Val Ile Ser
1 5 10 15
Arg Asp Arg Glu Leu Ser Thr Ala Lys Pro Xaa Cys Ser Ser Leu Leu
20 25 30
Thr Ala Pro Val Leu Cys Tyr Trp Arg Ala Cys Pro Leu Gln Thr
35 40 45

<210> 1526
<211> 56
<212> PRT
<213> Homo sapiens
<400> 1526
Met Phe Cys Phe Leu Phe Ser Trp Trp Leu Arg Gly Gly Leu His Val
1 5 10 15
Leu Leu Asn Thr Cys Leu Tyr Val Pro Tyr Gly Tyr Leu Ser Leu Ile
20 25 30
Cys Leu Leu Cys Leu Trp Tyr Leu Asn Leu Tyr Lys Phe Ser Ile Phe
35 40 45
Phe Ser Phe Leu Ser Phe Phe Phe

50 55

<210> 1527
<211> 55
<212> PRT
<213> Homo sapiens
<400> 1527
Met Thr Thr Thr Ser Lys His Ala Ala Tyr Cys Leu Lys Gly Ser Cys
1 5 10 15
Leu Xaa Gln Ala Arg Val Gln Trp Pro Leu Lys Xaa Thr Thr Ala Ser
20 25 30
Asn Phe Trp Ala Gln Val Ile Leu Ser Leu Pro Val Val Phe Val Asp
35 40 45
Cys Leu Met Glu Xaa His Gly
50 55

<210> 1528
<211> 121
<212> PRT
<213> Homo sapiens
<400> 1528
Met Glu Gly Gly Gly Gly Ile Pro Leu Glu Thr Leu Lys Glu Glu Ser
1 5 10 15
Gln Ser Arg His Val Leu Pro Ala Ser Phe Glu Val Asn Ser Leu Gln
20 25 30
Lys Ser Asn Trp Gly Phe Leu Leu Thr Gly Leu Val Gly Gly Thr Leu
35 40 45
Val Ala Val Tyr Ala Val Ala Thr Pro Phe Val Thr Pro Ala Leu Arg
50 55 60
Lys Val Cys Leu Pro Phe Val Pro Ala Thr Met Lys Gln Ile Glu Asn
65 70 75 80
Val Val Lys Met Leu Arg Cys Arg Arg Gly Ser Leu Val Asp Ile Gly
85 90 95
Ser Gly Asp Gly Arg Ile Val Ile Ala Ala Ala Lys Lys Gly Phe Xaa
100 105 110
Ala Val Gly Tyr Glu Leu Asn Pro Trp
115 120

<210> 1529
<211> 154
<212> PRT
<213> Homo sapiens
<400> 1529
Met Ala Thr Pro Leu Ala Val Asn Ser Ala Ala Ser Leu Trp Gly Pro
1 5 10 15
Tyr Lys Asp Ile Trp His Lys Val Gly Asn Ala Leu Trp Arg Arg Gln
20 25 30
Pro Glu Ala Val Xaa Leu Leu Asp Lys Ile Leu Lys Lys His Lys Pro
35 40 45
Asp Phe Ile Ser Leu Phe Lys Asn Pro Pro Lys Asn Val Gln Gln His
50 55 60
Glu Lys Val Gln Lys Ala Ser Thr Glu Gly Val Ala Ile Gln Gly Gln
65 70 75 80
Gln Gly Thr Arg Leu Leu Pro Glu Gln Leu Ile Lys Glu Ala Phe Ile
85 90 95
Leu Ser Asp Leu Phe Asp Ile Gly Glu Leu Ala Ala Val Glu Leu Leu
100 105 110
Leu Ala Gly Glu His Gln Gln Pro His Phe Pro Gly Leu Thr Arg Gly
115 120 125
Leu Val Ala Val Leu Leu Tyr Trp Asp Gly Lys Arg Cys Ile Ala Asn
130 135 140
Ser Leu Lys Ala Leu Ile Gln Ser Arg Arg
145 150

<210> 1530
<211> 125
<212> PRT
<213> Homo sapiens
<400> 1530
Met Asn Gly Arg Ala Asp Phe Arg Glu Pro Asn Ala Glu Val Pro Arg
1 5 10 15
Pro Ile Pro His Ile Gly Pro Asp Tyr Ile Pro Thr Glu Glu Glu Arg
20 25 30
Arg Val Phe Ala Glu Cys Asn Asp Glu Ser Phe Trp Phe Arg Ser Val
35 40 45
Pro Leu Ala Ala Thr Ser Met Leu Ile Thr Gln Gly Leu Ile Ser Lys
50 55 60
Gly Ile Leu Ser Ser His Pro Lys Tyr Gly Ser Ile Pro Lys Leu Ile
65 70 75 80
Leu Ala Cys Ile Met Gly Tyr Phe Ala Gly Lys Leu Ser Tyr Val Lys
85 90 95
Thr Cys Gln Glu Lys Phe Lys Lys Leu Glu Asn Ser Pro Leu Gly Glu
100 105 110
Ala Leu Arg Ser Gly Gln Ala Arg Arg Ser Ser Pro Pro
115 120 125

<210> 1531
<211> 35
<212> PRT
<213> Homo sapiens
<400> 1531
Met His Met Ser Lys Leu Ile Asn Leu Tyr Thr Ser Xaa Met Cys Asn
1 5 10 15
Leu Leu Xaa Ile His Leu Xaa Xaa Ile Ser Cys Leu Xaa Asn Asn Lys
20 25 30
Xaa Thr Leu
35

<210> 1532
<211> 111
<212> PRT
<213> Homo sapiens
<400> 1532
Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser
1 5 10 15
Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His
20 25 30
Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp
35 40 45
Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp
50 55 60
Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu
65 70 75 80
Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Ser Ala
85 90 95
Ala Ala Ala Pro Ser Pro Val Leu Gly Asn Ile Pro Pro Gly Asp
100 105 110

<210> 1533
<211> 107
<212> PRT
<213> Homo sapiens
<400> 1533
Met Asn Pro Glu Tyr Asp Tyr Leu Phe Lys Leu Leu Leu Ile Gly Asp
1 5 10 15
Ser Gly Val Gly Lys Ser Cys Leu Leu Leu Arg Phe Ala Asp Asp Thr

20 25 30
Tyr Thr Glu Ser Tyr Ile Ser Thr Ile Gly Val Asp Phe Lys Ile Arg
35 40 45
Thr Ile Glu Leu Asp Gly Lys Thr Ile Lys Leu Gln Ile Trp Asp Thr
50 55 60
Ala Gly Gln Glu Arg Phe Arg Thr Ile Thr Ser Ser Tyr Tyr Arg Gly
65 70 75 80
Ala His Gly Ile Ile Val Val Tyr Asp Val Thr Asp Gln Glu Ser Tyr
85 90 95
Ala Xaa Val Lys Gln Trp Leu Gln Glu Ile Asp
100 105

<210> 1534
<211> 31
<212> PRT
<213> Homo sapiens
<400> 1534
Met Asn Ser Lys Ala Xaa Lys Ser Ser Thr Ala Asn Gln Gly Asp Gly
1 5 10 15
Asp Glu Glu Xaa Val Gly Arg Xaa Glu Xaa Ser Val Gly Glu Phe
20 25 30

<210> 1535
<211> 48
<212> PRT
<213> Homo sapiens
<400> 1535
Met Leu Tyr Ser Thr Leu Lys His Thr Leu Gln Tyr Val Ile Ile Asn
1 5 10 15
Cys Gly His His Ala Val Gln Lys Ile Ser Lys Thr Tyr Ser Ser Cys
20 25 30
Leu Thr Glu Xaa Leu Tyr Pro Leu Pro Asn Ile Ser Pro Ile Pro Pro
35 40 45

<210> 1536
<211> 94
<212> PRT
<213> Homo sapiens
<400> 1536
Met Asn Asp Glu Val Asn Pro Arg Arg Val Leu Glu Leu Met Gly Ser
1 5 10 15
Glu Val Thr Gln Ile Ala Cys Gly Arg Gln His Thr Leu Xaa Phe Val
20 25 30
Pro Ser Ser Gly Leu Ile Tyr Ala Phe Gly Cys Gly Ala Arg Gly Gln
35 40 45
Leu Gly Thr Gly His Thr Cys Asn Val Lys Cys Pro Ser Pro Val Lys
50 55 60
Gly Tyr Trp Ala Ala His Ser Gly Gln Leu Ser Ala Arg Ala Asp Arg
65 70 75 80
Phe Lys Tyr His Ile Val Lys Gln Ile Phe Ser Gly Gly Asp
85 90

<210> 1537
<211> 22
<212> PRT
<213> Homo sapiens
<400> 1537
Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Val Pro Trp Gly
1 5 10 15
Pro Asn His Cys Asp Lys
20

<210> 1538

<211> 94
<212> PRT
<213> Homo sapiens
<400> 1538
Met Gly Asp Asn Pro Phe Gln Pro Lys Ser Asn Ser Lys Met Ala Glu
1 5 10 15
Leu Phe Met Glu Cys Glu Glu Glu Glu Leu Glu Pro Trp Gln Lys Lys
20 25 30
Val Lys Glu Val Glu Asp Asp Asp Asp Asp Glu Pro Ile Phe Val Gly
35 40 45
Glu Ile Ser Ser Ser Lys Pro Ala Ile Ser Asn Ile Leu Asn Arg Val
50 55 60
Asn Pro Ser Ser Tyr Ser Arg Gly Leu Lys Asn Gly Ala Leu Ser Arg
65 70 75 80
Gly Ile Thr Ala Ala Phe Lys Pro Thr Ser Gln His Tyr Thr
85 90

<210> 1539
<211> 67
<212> PRT
<213> Homo sapiens
<400> 1539
Met Val Thr Gln Ala Gln Gln Glu Ile Thr Val Gln Gln Leu Met Ala
1 5 10 15
His Leu Asp Ala Ile Arg Lys Asp Met Val Ile Leu Glu Lys Ser Glu
20 25 30
Phe Ala Asn Leu Arg Ala Glu Asn Glu Lys Met Lys Ile Glu Leu Asp
35 40 45
Gln Val Lys Gln Gln Leu Met His Glu Thr Ser Xaa Ile Arg Ala Asp
50 55 60
Asn Lys Leu
65

<210> 1540
<211> 38
<212> PRT
<213> Homo sapiens
<400> 1540
Met Lys Phe Gly Asn Val Arg Met Xaa Ser Ile Gln Ile Phe Ile Val
1 5 10 15
Ser Ile Trp Ser Phe Phe Leu Phe Tyr Gly Lys Tyr Thr Tyr Ile Arg
20 25 30
Leu Ile Leu Ser Gln Gly
35

<210> 1541
<211> 35
<212> PRT
<213> Homo sapiens
<400> 1541
Met Thr Phe Asp Leu Ser Val Phe Ser Thr Leu Ser Asp His Phe Tyr
1 5 10 15
Ser Ser Ser Leu Ser Asn Thr Ala Arg Asn Leu Tyr Ile Cys Leu Phe
20 25 30
His Ile Thr
35

<210> 1542
<211> 28
<212> PRT
<213> Homo sapiens
<400> 1542
Met Gly Arg Trp Ala Leu Asp Val Ala Phe Leu Trp Lys Ala Val Leu

1 5 10 15
Thr Leu Gly Leu Val Leu Leu Tyr Tyr Cys Phe Ser
20 25

<210> 1543
<211> 128
<212> PRT
<213> Homo sapiens
<400> 1543
Met Ala Leu His Val Pro Lys Ala Pro Gly Phe Ala Gln Met Leu Lys
1 5 10 15
Glu Gly Ala Lys His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn
20 25 30
Ile Gln Ala Cys Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly
35 40 45
Pro Asn Gly Met Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe
50 55 60
Val Thr Asn Asp Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His
65 70 75 80
Pro Ala Ala Lys Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu
85 90 95
Val Gly Asp Gly Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu
100 105 110
Glu Leu Ala Glu Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val
115 120 125

<210> 1544
<211> 33
<212> PRT
<213> Homo sapiens
<400> 1544
Met Ala Asn Arg Tyr Thr Met Asp Leu Thr Ala Ile Tyr Glu Ser Leu
1 5 10 15
Leu Ser Leu Ser Pro Asp Val Thr Leu Thr His Phe Ala His Cys Asn
20 25 30
Leu

<210> 1545
<211> 68
<212> PRT
<213> Homo sapiens
<400> 1545
Met Met Glu Glu Ser Gly Ile Glu Thr Thr Pro Pro Gly Thr Pro Pro
1 5 10 15
Pro Asn Pro Ala Gly Leu Ala Ala Thr Ala Met Ser Ser Thr Pro Val
20 25 30
Pro Leu Ala Ala Thr Ser Ser Phe Ser Ser Pro Asn Val Ser Ser Met
35 40 45
Glu Ser Phe Pro Pro Leu Ala Tyr Ser Thr Pro Gln Pro Pro Leu Pro
50 55 60
Pro Val Arg Pro
65

<210> 1546
<211> 50
<212> PRT
<213> Homo sapiens
<400> 1546
Met Leu Cys Leu Thr Glu Gly Ala Lys Asp Glu Cys Asn Val Val Glu
1 5 10 15
Val Val Ala Arg Asn His Asp His Gln Glu Ile Ala Val Pro Val Ala
20 25 30
Xaa Leu Lys Leu Ser Cys Gln Pro Met Leu Ser Leu Asp Asp Phe Gln

35 40 45
Leu Gln
50

<210> 1547
<211> 139
<212> PRT
<213> Homo sapiens
<400> 1547
Met Pro Thr Val Ser Val Lys Arg Asp Leu Leu Phe Gln Ala Leu Gly
1 5 10 15
Arg Thr Tyr Thr Asp Glu Glu Phe Asp Glu Leu Cys Phe Glu Phe Gly
20 25 30
Leu Glu Leu Asp Glu Ile Thr Ser Glu Lys Glu Ile Ile Ser Lys Glu
35 40 45
Gln Gly Asn Val Lys Ala Ala Gly Ala Ser Asp Val Val Leu Tyr Lys
50 55 60
Ile Asp Val Pro Ala Asn Arg Tyr Asp Leu Leu Cys Leu Glu Gly Leu
65 70 75 80
Val Arg Gly Leu Gln Val Phe Lys Glu Arg Ile Lys Ala Pro Val Tyr
85 90 95
Lys Arg Val Met Pro Asp Gly Lys Ile Gln Lys Leu Ile Ile Thr Glu
100 105 110
Glu Thr Ala Lys Ile Arg Pro Phe Ala Val Ala Ala Val Leu Arg Asn
115 120 125
Ile Lys Phe Thr Lys Asp Arg Tyr Asp Ser Phe
130 135

<210> 1548
<211> 71
<212> PRT
<213> Homo sapiens
<400> 1548
Met Phe Ser Glu Glu Leu Trp Leu Glu Asn Glu Lys Lys Cys Ala Val
1 5 10 15
Val Arg Lys Ser Lys Gln Gly Arg Lys Arg Gln Glu Leu Leu Ala Val
20 25 30
Ala Phe Gly Val Lys Val His Thr Phe Arg Gly Pro His Trp Cys Glu
35 40 45
Tyr Cys Ala Asn Phe Met Trp Gly Leu Ile Ala Gln Gly Val Arg Cys
50 55 60
Ser Asp Cys Gly Leu Asn Val
65 70

<210> 1549
<211> 29
<212> PRT
<213> Homo sapiens
<400> 1549
Met Val Val Phe Met Thr Tyr Val Thr Leu Pro Phe Phe Phe Ser Phe
1 5 10 15
Ile Ser Ser Leu Leu Ser Phe Phe Phe Leu Phe Leu Leu
20 25

<210> 1550
<211> 50
<212> PRT
<213> Homo sapiens
<400> 1550
Met Gln Glu Leu Phe Leu Lys Phe Val Asp Glu Asn Trp Glu Gly Ser
1 5 10 15
Leu Lys Ser Lys Tyr Val Arg Gly Ser Asp Pro Val Leu Lys Leu Leu
20 25 30

Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu Lys Trp Thr
35 40 45
Gln Thr
50

<210> 1551
<211> 68
<212> PRT
<213> Homo sapiens
<400> 1551
Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe Tyr
1 5 10 15
Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu Ser Thr
20 25 30
Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn Cys Ser Lys
35 40 45
Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr Asp Gly Tyr Leu
50 55 60
Ala Lys Asp Gly
65

<210> 1552
<211> 52
<212> PRT
<213> Homo sapiens
<400> 1552
Met Leu Glu Glu Leu Lys Ala Gly Gln Glu Leu Glu Glu Gln Thr Ile
1 5 10 15
Ser His Gly Phe Ala Arg Gly Val Arg Arg Gly Val Ala Ile Val Gly
20 25 30
Lys Gly Leu Glu Trp His Gly Cys Trp Trp Met Cys His Gly Tyr Arg
35 40 45
Ile Leu Ala Gly
50

<210> 1553
<211> 37
<212> PRT
<213> Homo sapiens
<400> 1553
Met Arg Leu Gly Ser Ser Lys Leu Lys Ser Asn Gln Leu Leu Gln Glu
1 5 10 15
Ala Leu Ser Arg Met Lys Trp Gly Gly Pro Ser Phe Gln Pro Arg Lys
20 25 30
Pro Thr Val Pro Gly
35

<210> 1554
<211> 57
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -13..-1

<400> 1554
Met Leu Leu Leu Leu Leu Leu Leu Pro Leu Ala Leu Gly Asp Lys Gly
-10 -5 1
Asp Gly Gly Arg Gln Thr Ile Trp Gly Trp Leu Leu Ala Ala Ser Ala
5 10 15
Gly Ala Gly Asp Gly Ala Gly Gly Pro Val Cys Pro Cys Ala Leu Leu
20 25 30 35

Leu Leu Leu Pro Pro Gly Trp Leu Asp
40

<210> 1555
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -18..-1

<400> 1555
Met Lys Leu Leu Met Val Leu Met Leu Ala Ala Leu Leu Leu His Cys
-15 -10 -5
Tyr Ala Asp Ser Gly Cys Lys Leu Leu Glu Asp Met Val Glu Lys Thr
1 5 10
Ile Asn Ser Asp Ile Ser Ile Pro Glu Tyr Lys Glu Leu Leu Gln Glu
15 20 25 30
Phe Ile Asp Ser Asp Ala Ala Ala Glu Ala Met Gly Lys Phe Lys Gln
35 40 45
Cys Phe Leu Asn Gln Ser His Arg Thr Leu Lys Asn Phe Gly Leu Met
50 55 60
Met His Thr Val Tyr Asp Ser Ile Trp Cys Asn Met Lys Ser Asn
65 70 75

<210> 1556
<211> 95
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -31..-1

<400> 1556
Met Val Ala Met Ala Ala Gly Pro Ser Gly Cys Leu Val Pro Ala Phe
-30 -25 -20
Gly Leu Arg Leu Leu Leu Ala Thr Val Leu Gln Ala Val Ser Ala Phe
-15 -10 -5 1
Gly Ala Glu Phe Ser Ser Glu Ala Cys Arg Glu Leu Gly Phe Ser Ser
5 10 15
Asn Leu Leu Cys Ser Ser Cys Asp Leu Leu Gly Gln Phe Asn Leu Leu
20 25 30
Gln Leu Asp Pro Asp Cys Arg Gly Cys Cys Gln Glu Glu Ala Gln Phe
35 40 45
Glu Thr Lys Lys Leu Tyr Ala Gly Ala Ile Leu Glu Val Cys Gly
50 55 60

<210> 1557
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -32..-1

<400> 1557
Met Phe Ala Pro Ala Val Met Arg Ala Phe Arg Lys Asn Lys Thr Leu
-30 -25 -20
Gly Tyr Gly Val Pro Met Leu Leu Leu Ile Val Gly Gly Ser Phe Gly
-15 -10 -5

Leu Arg Glu Phe Ser Gln Ile Arg Tyr Asp Ala Val Lys Ser Lys Met
1 5 10 15
Asp Pro Glu Leu Glu Lys Lys Leu Lys Glu Asn Lys Ile Ser Leu Glu
20 25 30
Ser Glu Tyr Glu Lys Ile Lys Asp Ser Lys Phe Asp Asp Trp Lys Asn
35 40 45
Ile Arg Gly Pro Arg Pro Trp Glu Asp Pro Asp Leu Leu Gln Gly Lys
50 55 60
Lys Ser Arg Lys Pro
65

<210> 1558
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1558
Met Gln Ala Gln Ala Pro Val Val Val Val Thr Gln Pro Gly Val Gly
-50 -45 -40
Pro Gly Pro Ala Pro Gln Asn Ser Asn Trp Gln Thr Gly Met Cys Asp
-35 -30 -25 -20
Cys Phe Ser Asp Cys Gly Val Cys Leu Cys Gly Thr Phe Cys Phe Pro
-15 -10 -5
Cys Leu Gly Cys Gln Val Ala Ala Asp Met Asn Glu Cys Cys Leu Cys
1 5 10
Gly Thr Ser Val Ala Met Arg Thr Leu Tyr Arg Thr Arg Tyr Gly Ile
15 20 25
Pro Gly Ser Ile Cys Asp Asp Tyr Met Ala Thr Leu Cys Cys Pro His
30 35 40 45
Cys Thr Leu Cys Gln Ile Lys Arg Asp Ile Asn Arg Arg Arg Ala Met
50 55 60
Arg Thr Phe

<210> 1559
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -24..-1

<400> 1559
Met Asp Lys Ser Leu Leu Leu Glu Leu Pro Ile Leu Leu Cys Cys Phe
-20 -15 -10
Arg Ala Leu Ser Gly Ser Leu Ser Met Arg Asn Asp Ala Val Asn Glu
-5 1 5
Ile Val Ala Val Lys Asn Asn Phe Pro Val Ile Glu Ile Val Arg Cys
10 15 20
Arg Met Cys His Leu Gln Phe Pro Gly Glu Lys Cys Ser Arg Gly Arg
25 30 35 40
Gly Ile Cys Thr Ala Thr Thr Glu Glu Ala Cys Met Val Gly Arg Met
45 50 55
Phe Lys Arg Asp Gly Asn Pro Trp Leu Thr Phe Met Gly Cys Leu Lys
60 65 70
Asn Cys Ala Asp Val Lys Gly Ile Arg Trp Ser Val Tyr Leu Val Asn
75 80 85
Phe Arg Cys Xaa Arg Ser His Asp Leu Cys Asn Glu Asp Leu
90 95 100

<210> 1560
<211> 102
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1560
Met Asp Leu Leu Trp Ile Leu Pro Ser Leu Trp Leu Leu Leu Leu Gly
-15 -10 -5
Gly Pro Ala Cys Leu Lys Thr Gln Glu His Pro Ser Cys Pro Gly Pro
1 5 10 15
Arg Glu Leu Glu Ala Ser Lys Val Val Leu Leu Pro Ser Cys Pro Gly
20 25 30
Ala Pro Gly Ser Pro Gly Glu Lys Gly Ala Pro Gly Pro Gln Gly Pro
35 40 45
Pro Gly Pro Pro Gly Lys Met Gly Pro Lys Gly Glu Pro Gly Asp Pro
50 55 60
Val Asn Leu Leu Arg Cys Gln Glu Gly Pro Arg Asn Cys Arg Glu Leu
65 70 75 80
Leu Ser Arg Ala Pro Pro
85

<210> 1561
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1561
Met Glu Ser Pro Ser Xaa Ser Ala Val Val Leu Pro Ser Thr Pro Gln
-15 -10 -5
Ala Ser Ala Asn Pro Ser Ser Pro Tyr Thr Asn Ser Ser Arg Lys Gln
1 5 10
Pro Met Ser Ala Thr Leu Arg Glu Arg Leu Arg Lys Thr Arg Phe Ser
15 20 25
Phe Asn Ser Ser Xaa Asn Val Val Asn Val Leu Lys
30 35 40

<210> 1562
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1562
Met Asp Phe Trp Leu Trp Pro Leu Tyr Phe Leu Pro Val Ser Gly Ala
-15 -10 -5
Leu Arg Ile Leu Pro Glu Val Lys Val Glu Gly Glu Leu Gly Gly Ser
1 5 10 15
Val Thr Ile Lys Cys Pro Leu Pro Glu Met His Val Arg Ile Tyr Leu
20 25 30
Cys Arg Glu Met Ala Gly Ser Gly Thr Cys Gly Thr Val Val Ser Thr
35 40 45

Thr Asn Phe Ile Xaa Ala Glu Tyr Lys Gly Arg Val Thr Leu Arg Ala
50 55 60
Ile Pro Thr Gln Glu Ser Val Pro Ser Gly Gly Asn Thr Ala Asp Arg
65 70 75 80
Lys

<210> 1563
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1563
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala
-30 -25 -20
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
-15 -10 -5
Tyr Ser Xaa Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
1 5 10
Leu Ser Xaa Leu Leu Ser Xaa Ala Phe Leu Leu Val Arg Xaa Leu Pro
15 20 25 30
Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Ser
35 40 45
Xaa Xaa

<210> 1564
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -17..-1

<400> 1564
Met Ala Gln Leu Trp Leu Ser Cys Phe Leu Leu Pro Ala Leu Val Val
-15 -10 -5
Ser Val Ala Ala Asn Val Ala Pro Xaa Phe Leu Ala Asn Met Thr Ser
1 5 10 15
Val Ile Leu Pro Glu Asp Cys Leu Trp Val Pro Arg Pro Ser Gly Trp
20 25 30

<210> 1565
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -34..-1

<400> 1565
Met Val Gly Glu Ala Gly Arg Asp Leu Arg Arg Arg Arg Ala Val Ala
-30 -25 -20
Val Thr Ala Glu Lys Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val
-15 -10 -5
Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu
1 5 10
Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro
15 20 25 30

Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Xaa Gly Asn Pro Cys
35 40 45
Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile
50 55 60
Val Met Met Lys Asn Arg Arg Ser Ser
65 70

<210> 1566
<211> 88
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -19..-1

<400> 1566
Met Val Ala Trp Arg Ser Ala Phe Leu Val Cys Leu Ala Phe Ser Leu
-15 -10 -5
Ala Thr Leu Val Gln Arg Gly Ser Gly Asp Phe Asp Asp Phe Asn Leu
1 5 10
Glu Asp Ala Val Lys Glu Thr Ser Ser Val Lys Gln Pro Trp Asp His
15 20 25
Thr Thr Thr Thr Thr Thr Asn Arg Pro Gly Thr Thr Arg Ala Pro Ala
30 35 40 45
Lys Pro Pro Gly Ser Gly Leu Asp Leu Ala Asp Ala Leu Asp Asp Gln
50 55 60
Asp Asp Gly Arg Arg Asn Arg Val
65

<210> 1567
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -53..-1

<400> 1567
Met Ala Asp Pro Asp Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp
-50 -45 -40
Phe Asn Tyr Gly Ser Ser Val Ala Ser Ala Thr Val His Ile Arg Met
-35 -30 -25
Ala Phe Leu Arg Lys Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu
-20 -15 -10
Thr Thr Val Thr Ser Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr
-5 1 5 10
Phe Val His Glu Ser Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser
15 20 25
Leu Gly Leu Ile Phe Ala Leu Xaa Leu Asn Arg His Lys Tyr Pro Leu
30 35 40
Asn Leu Tyr Leu Leu Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val
45 50 55
Ala Val Val Val Thr Val Leu
60 65

<210> 1568
<211> 104
<212> PRT
<213> Homo sapiens

<220>

<221> SIGNAL
<222> -55..-1

<400> 1568
Met Ser Ser Gln Lys Gly Asn Val Ala Arg Ser Arg Pro Gln Lys His
-55 -50 -45 -40
Gln Asn Thr Phe Ser Phe Lys Asn Asp Lys Phe Asp Lys Ser Val Gln
-35 -30 -25
Thr Lys Ser Met Asn Asn Leu Ser Phe Ser Glu Leu Cys Cys Leu Phe
-20 -15 -10
Cys Cys Pro Pro Cys Pro Gly Lys Ile Ala Ser Lys Leu Ala Phe Leu
-5 1 5
Pro Pro Asp Pro Thr Tyr Thr Leu Met Cys Asp Glu Ser Gly Ser Val
10 15 20 25
Gly Leu Tyr Ile Cys Leu Asn Glu Gln Thr Gly Ser Ile Leu Leu Glu
30 35 40
Lys Lys Met Leu Leu Ser Val Ser
45

<210> 1569
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -62..-1

<400> 1569
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu Thr
-60 -55 -50
Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu Ile Asn
-45 -40 -35
Val Pro Lys Pro Lys Arg Arg Asn Gly Val Asn Phe Ser Leu Ala Val
-30 -25 -20 -15
Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala Gly Leu Leu Val
-10 -5 1
Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg Val Leu Glu Met Tyr
5 10 15
Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp Ser Pro Ser Phe Ser Leu
20 25 30
Leu Gln Ser Ala His Pro Gly Glu His Leu Ala Gln Gly Ala Ser Arg
35 40 45 50
Leu Gln Ser Cys Arg Pro Asn Ser Pro Gly Ser Ala Ser Xaa
55 60

<210> 1570
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -56..-1

<400> 1570
Met Ala Pro Thr Lys Pro Ser Phe Gln Gln Asp Pro Ser Arg Arg Glu
-55 -50 -45
Arg Leu Gln Ala Leu Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser
-40 -35 -30 -25
Arg Arg Gly Lys Glu Asn Phe Glu Phe Tyr Glu Leu Ala Lys Leu Leu
-20 -15 -10
Pro Leu Pro Ala Ala Ile Thr Ser Gln Leu Asp Lys Ala Ser Ile Ile

```
            -5                      1                   5
Arg Leu Thr Ile Ser Tyr Leu Lys Met Arg Asp Phe Ala Asn Gln Gly
    10                  15                  20
Asp Pro Pro Trp Asn Leu Arg Met Glu Gly Pro Pro Pro Asn Thr Ser
25                  30                  35                  40
Val Lys Val Ile Gly Ala Gln Arg Arg Arg Ser Pro Ser Ala Leu Ala
                45                  50                  55
Ile Glu Val Phe Glu Ala His Leu Gly Ser His Ile Leu Gln Ser Trp
            60                  65                  70
Met Ala Leu Tyr Leu His
        75
```

<210> 1571
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1571

```
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20                 -15                 -10                 -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
                1                   5
```

<210> 1572
<211> 28
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -20..-1

<400> 1572

```
Met Glu Glu Leu Gln Asp Gln Ala Leu Leu Ser Val Cys Ser Thr Asp
-20                 -15                 -10                 -5
Val Thr Thr Ala His Ala Trp Leu Thr Val Leu Val
                1                   5
```

<210> 1573
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -45..-1

<400> 1573

```
Met Val Gly Arg Val Arg Val Cys Arg Lys Tyr Pro Pro Thr Thr Leu
-45                 -40                 -35                 -30
Trp Glu Gly Ala Arg Gly His Arg Gln Ile Ser Val Ser Pro Trp Asn
                -25                 -20                 -15
Ile Cys Cys Ala Ala Ala Ala Ala Ala Ala Ala Gly Ser Arg Ile
            -10                 -5                  1
```

<210> 1574
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -52..-1

<400> 1574
Met Lys Arg Leu Glu Ala Lys Tyr Ala Pro Leu His Leu Val Pro Leu
-50 -45 -40
Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg Glu Gly
-35 -30 -25
Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met Phe Glu
-20 -15 -10 -5
Val Ile Leu Thr Arg Ile Arg Ser Tyr Leu Gln Asp Pro Ile Trp Arg
1 5 10
Gly Pro Pro Pro Thr Asn Gly Val Met His Val Asp Glu Cys Val Glu
15 20 25
Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile Pro Val
30 35 40
Gly Thr Asn Glu Phe Thr Ala Glu Gln Cys Phe Gly Asp Gly Leu Asn
45 50 55 60
Trp Ala Gly Ser Pro Xaa Leu Ser Cys Xaa Ala Ser Ser Val Ala Leu
65 70 75
Thr Cys Ser Thr Ser Val Thr Thr Cys
80 85

<210> 1575
<211> 101
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -71..-1

<400> 1575
Met Ala Leu Val Pro Cys Gln Val Leu Arg Met Ala Ile Leu Leu Ser
-70 -65 -60
Tyr Cys Ser Ile Leu Cys Asn Tyr Lys Ala Ile Glu Met Pro Ser His
-55 -50 -45 -40
Gln Thr Tyr Gly Gly Ser Trp Lys Phe Leu Thr Phe Ile Asp Leu Val
-35 -30 -25
Ile Gln Ala Val Phe Phe Gly Ile Cys Val Leu Xaa Asp Leu Ser Ser
-20 -15 -10
Leu Leu Thr Arg Gly Ser Gly Asn Gln Glu Gln Glu Arg Gln Leu Lys
-5 1 5
Lys Leu Ile Ser Leu Arg Asp Trp Met Leu Ala Val Leu Ala Phe Leu
10 15 20 25
Leu Gly Phe Leu Leu
30

<210> 1576
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -69..-1

<400> 1576
Met Ala Thr His His Leu Gly Leu Pro Ala Ser Gln Pro Leu Pro Gly
-65 -60 -55
Ile Leu Ser Arg Ala Pro Ser Leu Pro Pro Arg Ser Pro Ala Thr Arg

```
            -50                        -45                       -40
Ser Arg Val Ser Ser Pro Trp Gly Glu Ser Ser Ser Ser Leu Leu Phe
        -35                     -30                     -25
Pro Asp Cys His Ile Ser Phe Pro Ala Leu Thr Gly Ser Gln Leu Leu
    -20                     -15                     -10
Gly Asp Thr Ile Pro Arg Pro His Leu Pro Pro Thr Ala Ala Cys
-5                  1                   5                   10
```

<210> 1577
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -35..-1

<400> 1577

```
Met Thr Pro Ser Arg Leu Pro Trp Leu Leu Ser Trp Val Ser Ala Thr
-35                 -30                     -25                 -20
Ala Trp Arg Ala Ala Arg Ser Pro Leu Leu Cys His Ser Leu Arg Lys
                -15                     -10                 -5
Thr Ser Ser Ser Gln Gly Gly Lys Ser Glu Leu Val Lys Gln Ser Leu
            1                   5                   10
Lys Lys Pro Lys Leu Pro Glu Gly Arg Phe Asp Ala Pro Glu Asp Ser
    15                  20                  25
His Leu Glu Lys Glu Pro Leu Glu Lys Phe Pro Asp Asp Val Xaa Pro
30                  35                  40                  45
Val Thr Lys Glu Lys Gly Gly Pro Arg Gly Pro Glu Pro Thr Arg Tyr
                50                  55                  60
Gly Asp Trp Glu Arg Lys Gly Arg Cys Ile Asp Phe
            65                  70
```

<210> 1578
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -51..-1

<400> 1578

```
Met Glu Lys Leu Arg Arg Val Leu Ser Gly Gln Asp Asp Glu Glu Gln
    -50                 -45                     -40
Gly Leu Thr Ala Gln Val Leu Asp Ala Ser Ser Leu Ser Phe Asn Thr
-35                 -30                     -25                 -20
Arg Leu Lys Trp Phe Ala Ile Cys Phe Val Cys Gly Val Phe Phe Ser
                -15                     -10                 -5
Ile Leu Gly Thr Gly Leu Leu Trp Leu Pro Gly Gly Ile Lys Leu Phe
            1                   5                   10
Ala Val Phe Tyr Thr Leu Gly Asn Leu Ala Ala Leu Xaa Val His Ala
    15                  20                  25
Xaa
30
```

<210> 1579
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL

<222> -93..-1

<400> 1579
Met Cys Glu Asn Gln Glu Glu Pro Ala Gly Ser Val Cys Cys His Arg
-90 -85 -80
Val Ser Ala Cys Arg Gly Gly Thr Pro Gly Gly Gly Arg Gly Gln Ser
-75 -70 -65
His Cys Arg Gly Pro Asp Trp Glu Asn Asn Asp Met Ala Gly Ala Ser
-60 -55 -50
Leu Gly Ala Arg Phe Tyr Arg Gln Ile Lys Arg His Pro Gly Ile Ile
-45 -40 -35 -30
Pro Met Ile Gly Leu Ile Cys Leu Gly Met Gly Ser Ala Ala Leu Tyr
-25 -20 -15
Leu Leu Arg Leu Ala Leu Arg Ser Pro Asp Val Trp Leu Gly Gln Lys
-10 -5 1
Glu Gln Pro Gly Ala Leu Glu Pro Pro Glu Pro Gln
5 10 15

<210> 1580
<211> 134
<212> PRT
<213> Homo sapiens

<220>
<221> SIGNAL
<222> -16..-1

<400> 1580
Met Ala Ala Ala Gly Leu Ala Leu Leu Xaa Arg Arg Val Ser Ser Ala
-15 -10 -5
Leu Lys Ser Ser Arg Ser Leu Ile Thr Pro Gln Val Pro Ala Cys Thr
1 5 10 15
Gly Phe Phe Leu Ser Leu Leu Pro Lys Ser Thr Pro Asn Val Thr Ser
20 25 30
Phe His Gln Tyr Arg Leu Leu His Thr Thr Leu Ser Arg Lys Gly Leu
35 40 45
Glu Glu Phe Phe Asp Asp Pro Lys Asn Trp Gly Gln Glu Lys Val Lys
50 55 60
Ser Gly Ala Ala Trp Thr Cys Gln Gln Leu Arg Asn Lys Ser Asn Glu
65 70 75 80
Asp Leu His Lys Leu Trp Tyr Val Leu Leu Lys Glu Arg Asn Met Leu
85 90 95
Leu Thr Leu Glu Gln Glu Ala Lys Arg Gln Arg Leu Pro Met Pro Ser
100 105 110
Pro Glu Arg Leu Asp Arg
115

<210> 1581
<211> 64
<212> PRT
<213> Homo sapiens
<400> 1581
Met Asn Glu Ser Lys Pro Gly Asp Ser Gln Asn Leu Ala Cys Val Phe
1 5 10 15
Cys Arg Lys His Asp Asp Cys Pro Asn Lys Tyr Gly Glu Lys Lys Thr
20 25 30
Lys Glu Lys Trp Asn Leu Thr Val His Tyr Tyr Cys Leu Leu Met Ser
35 40 45
Ser Gly Ile Trp Gln Arg Gly Lys Glu Glu Glu Gly Val Met Val Phe
50 55 60

<210> 1582
<211> 79

<212> PRT
<213> Homo sapiens
<400> 1582
Met Ala Val Ala Arg Ala Gly Val Leu Gly Val Gln Trp Leu Gln Arg
1 5 10 15
Ala Ser Arg Asn Val Met Pro Leu Gly Ala Arg Thr Ala Ser His Met
20 25 30
Thr Lys Asp Met Phe Pro Gly Pro Tyr Pro Arg Thr Pro Glu Glu Arg
35 40 45
Ala Ala Ala Ala Lys Lys Tyr Asn Met Arg Val Glu Asp Tyr Glu Pro
50 55 60
Tyr Pro Asp Asp Gly Met Gly Tyr Gly Asp Leu Phe Leu Xaa Val
65 70 75

<210> 1583
<211> 66
<212> PRT
<213> Homo sapiens
<400> 1583
Met Glu Val Asp Ala Pro Gly Val Asp Gly Arg Asp Gly Leu Arg Glu
1 5 10 15
Arg Arg Gly Phe Ser Glu Gly Gly Arg Gln Asn Phe Asp Val Arg Pro
20 25 30
Gln Ser Gly Ala Asn Gly Leu Pro Lys His Ser Tyr Trp Leu Asp Leu
35 40 45
Trp Leu Phe Ile Leu Phe Asp Val Val Val Phe Leu Phe Val Tyr Phe
50 55 60
Leu Pro
65

<210> 1584
<211> 45
<212> PRT
<213> Homo sapiens
<400> 1584
Met Tyr Val Tyr Val Cys Val Trp Val Cys Val Tyr Thr Val Glu Ser
1 5 10 15
Lys Leu Glu Asn Ser Ser Ile Tyr Pro Pro Pro Ser Pro Val Glu Xaa
20 25 30
Lys Lys Ile Phe Thr Phe Val Thr Phe Leu Phe Pro Pro
35 40 45

<210> 1585
<211> 25
<212> PRT
<213> Homo sapiens
<400> 1585
Met Gly Pro Gly Gly Ala Leu His Gly Gly Met Lys Thr Leu Leu Pro
1 5 10 15
Trp Thr Ala Arg Ala Ser Arg Ser Pro
20 25

<210> 1586
<211> 98
<212> PRT
<213> Homo sapiens
<400> 1586
Met Tyr Gly Lys Gly Lys Ser Asn Ser Ser Ala Val Pro Ser Asp Ser
1 5 10 15
Gln Ala Arg Glu Lys Leu Ala Leu Tyr Val Tyr Glu Tyr Leu Leu His
20 25 30
Val Gly Ala Gln Lys Ser Ala Gln Thr Phe Leu Ser Glu Ile Arg Trp
35 40 45

Glu Lys Asn Ile Thr Leu Gly Glu Pro Pro Gly Phe Leu His Ser Trp
50 55 60
Trp Cys Val Phe Trp Asp Leu Tyr Cys Ala Ala Pro Glu Arg Arg Glu
65 70 75 80
Thr Cys Glu His Ser Ser Glu Ala Lys Ala Phe His Asp Tyr Val Xaa
85 90 95
Asn Ile

<210> 1587
<211> 50
<212> PRT
<213> Homo sapiens
<400> 1587
Met Cys Leu Leu Glu Val Pro Gly Ala Thr Lys Leu Leu Ala Ala Arg
1 5 10 15
Arg Thr Leu Lys Arg Asn Gly Ile Ser Pro Pro Asn Gln Glu Gly Leu
20 25 30
Ala Leu Leu Leu Gly Glu Leu Thr Thr His Lys Gln Met Arg Thr Lys
35 40 45
Thr Glu
50

<210> 1588
<211> 32
<212> PRT
<213> Homo sapiens
<400> 1588
Met Asn Arg Thr Ala Met Arg Ala Ser Gln Lys Asp Phe Glu Asn Ser
1 5 10 15
Xaa Asn Gln Val Lys Leu Leu Lys Lys Asp Pro Gly Asn Glu Xaa Ser
20 25 30

<210> 1589
<211> 58
<212> PRT
<213> Homo sapiens
<400> 1589
Met Ala Ser Ser Gly Ala Gly Asp Pro Leu Asp Ser Lys Arg Gly Glu
1 5 10 15
Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
20 25 30
Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Pro Ser Gly Arg Arg
35 40 45
Ser Tyr His Gly Gly Glu Pro Gly Thr Ser
50 55

<210> 1590
<211> 98
<212> PRT
<213> Homo sapiens
<400> 1590
Met Ser Ser Asp Asp Lys Ser Lys Ser Asn Asp Pro Lys Thr Glu Pro
1 5 10 15
Lys Asn Cys Asp Pro Lys Cys Glu Gln Lys Cys Glu Ser Lys Cys Gln
20 25 30
Pro Ser Cys Leu Lys Lys Leu Leu Gln Arg Cys Phe Glu Lys Cys Pro
35 40 45
Trp Glu Lys Cys Pro Ala Pro Pro Lys Cys Leu Pro Cys Pro Ser Gln
50 55 60
Ser Pro Ser Ser Cys Pro Pro Gln Pro Cys Thr Lys Pro Cys Pro Pro
65 70 75 80
Lys Cys Pro Ser Ser Cys Pro His Ala Cys Pro Xaa Pro Cys Pro Pro
85 90 95

Pro Glu

<210> 1591
<211> 43
<212> PRT
<213> Homo sapiens
<400> 1591
Met Cys Gly Gly Trp Asp Pro Val Ala His Pro Cys Arg Ser Cys Pro
1               5                   10                  15
Ser His Ala Arg Arg Arg Val Phe Val Val Thr Pro Cys Cys His Leu
            20                  25                  30
Phe Ser Ser Leu Cys Glu Asp Leu Asp Trp Gln
        35                  40

<210> 1592
<211> 157
<212> PRT
<213> Homo sapiens
<400> 1592
Met Ala Thr Pro Pro Lys Arg Arg Ala Val Glu Ala Thr Gly Glu Lys
1               5                   10                  15
Val Leu Arg Tyr Glu Thr Phe Ile Ser Asp Val Leu Gln Arg Asp Leu
            20                  25                  30
Arg Lys Val Leu Asp His Arg Asp Lys Val Tyr Glu Gln Leu Ala Lys
        35                  40                  45
Tyr Leu Gln Leu Arg Asn Val Ile Glu Arg Leu Gln Glu Ala Lys His
    50                  55                  60
Ser Glu Leu Tyr Met Gln Val Asp Leu Gly Cys Asn Phe Phe Val Asp
65                  70                  75                  80
Thr Val Val Pro Asp Thr Ser Arg Ile Tyr Val Ala Leu Gly Tyr Gly
                85                  90                  95
Phe Phe Leu Glu Leu Thr Leu Ala Glu Ala Leu Lys Phe Ile Asp Arg
            100                 105                 110
Lys Ser Ser Leu Leu Thr Glu Leu Ser Asn Ser Leu Thr Lys Asp Ser
        115                 120                 125
Met Asn Ile Lys Ala His Ile His Met Leu Leu Glu Gly Leu Arg Glu
    130                 135                 140
Leu Gln Gly Leu Gln Asn Phe Pro Glu Lys Pro His His
145                 150                 155

<210> 1593
<211> 119
<212> PRT
<213> Homo sapiens
<400> 1593
Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys
1               5                   10                  15
Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg
            20                  25                  30
Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Val Pro Met Val Leu
        35                  40                  45
Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser Ser Ile Ala
    50                  55                  60
Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly Gly Val Ala
65                  70                  75                  80
Ser Gly Ser Leu Val Ala Thr Leu Gln Ser Leu Gly Ala Thr Gly Leu
                85                  90                  95
Ser Gly Leu Thr Lys Xaa Ile Leu Gly Ser Ile Gly Ser Ala Ile Ala
            100                 105                 110
Ala Val Ile Ala Arg Phe Tyr
        115

<210> 1594

<211> 81
<212> PRT
<213> Homo sapiens
<400> 1594
Met Tyr Ile Gln Cys Cys Glu Trp Leu Gln Ser Trp Arg Ser Lys Asp
1 5 10 15
Glu Phe Cys Leu Glu Glu Ser Gly Lys Ala Ser Trp Arg Arg Glu Gln
20 25 30
Trp His Gly Pro Xaa Xaa Val Arg Ser Phe Gln Phe Ile Pro Phe Lys
35 40 45
His Cys Ser His Val Ala Phe Lys His Ser Ile Val Leu Ala Val Thr
50 55 60
Gln Ala His Ser Ala Lys Gly Ser Thr Ser Phe Ser Ala Met Arg Thr
65 70 75 80
Tyr

<210> 1595
<211> 65
<212> PRT
<213> Homo sapiens
<400> 1595
Met Val Gly Val Ser Val Cys His His Ile Arg Val Gly Ile Lys Arg
1 5 10 15
Arg Lys Ala Ala Leu Leu Glu Leu Cys Gly Leu Leu Gln Val Arg Val
20 25 30
Ala Gly Asn Arg Thr Thr Leu Leu Leu Glu Glu Lys Arg Asn Ser Phe
35 40 45
Ser Ala Xaa Thr Arg Lys Ala Val Phe Phe Ser Gly Asp Leu His Phe
50 55 60
Ser
65

<210> 1596
<211> 111
<212> PRT
<213> Homo sapiens
<400> 1596
Met Pro Ser Arg Thr Ala Arg Tyr Ala Arg Tyr Ser Pro Arg Gln Arg
1 5 10 15
Arg Arg Arg Met Leu Ala Asp Arg Ser Val Arg Phe Pro Asn Asp Val
20 25 30
Leu Phe Leu Asp His Ile Arg Gln Gly Asp Leu Glu Gln Val Gly Arg
35 40 45
Phe Ile Arg Thr Arg Lys Val Ser Leu Ala Thr Ile His Pro Ser Gly
50 55 60
Leu Ala Ala Leu His Glu Ala Val Leu Ser Gly Asn Leu Glu Cys Val
65 70 75 80
Lys Leu Leu Val Lys Tyr Gly Ala Asp Ile His Gln Arg Asp Glu Ala
85 90 95
Gly Trp Thr Pro Leu His Ile Ala Cys Ser Asp Gly Tyr Leu Thr
100 105 110

<210> 1597
<211> 33
<212> PRT
<213> Homo sapiens
<400> 1597
Met Ala Trp Gly Gly Trp Gly Ala His Ser Ala Cys Ser Glu Glu Arg
1 5 10 15
Ala Thr Arg Pro Val Glu Gly Ala Tyr Ser Gly Arg Trp Gly Gln Ala
20 25 30
Gln

<210> 1598
<211> 113
<212> PRT
<213> Homo sapiens
<400> 1598

```
Met Asp Pro Asn Pro Arg Ala Ala Leu Glu Arg Gln Gln Leu Arg Leu
1               5                   10                  15
Arg Glu Arg Gln Lys Phe Phe Glu Asp Ile Leu Gln Pro Glu Thr Glu
            20                  25                  30
Phe Val Phe Pro Leu Ser His Leu His Leu Glu Ser Gln Arg Pro Pro
        35                  40                  45
Ile Gly Ser Ile Ser Ser Met Glu Val Asn Val Asp Thr Leu Glu Gln
    50                  55                  60
Val Glu Leu Ile Asp Leu Gly Asp Pro Asp Ala Ala Asp Val Phe Leu
65                  70                  75                  80
Pro Cys Glu Asp Pro Pro Pro Thr Pro Gln Ser Ser Gly Val Asp Asn
                85                  90                  95
His Leu Glu Glu Leu Ser Leu Pro Xaa Ala Tyr Ile Arg Gln Asp His
            100                 105                 110
Ile
```

<210> 1599
<211> 58
<212> PRT
<213> Homo sapiens
<400> 1599

```
Met Val Val Phe Gly Tyr Glu Ala Gly Thr Lys Pro Arg Asp Ser Gly
1               5                   10                  15
Val Val Pro Val Gly Thr Glu Glu Ala Pro Lys Asp Thr Lys Tyr Ile
            20                  25                  30
Ser Asn Gly Asp Ile Trp Asn Asn Ser Trp Phe Leu Trp Asn Ile Leu
        35                  40                  45
Lys Leu Pro Val Gln Thr Leu Leu Gln Gly
    50                  55
```

<210> 1600
<211> 247
<212> DNA
<213> Homo sapiens
<400> 1600

```
gaaaattact ttgacctttt gttagtgatc ccattcagct agtaccaagc tgaagattga      60
tattcgttaa tggttaatat aaatttactg ctctaggtta agcctaacat atgtaattgc     120
tactagccta ttacttttta gtccattggg aatcactaaa aaaagtagag gctttagctt     180
cattcctcgg ctgcttaaat catattgtaa tgttttaaat tgttatgtcg tcctgtataa     240
ccttagg                                                               247
```

<210> 1601
<211> 225
<212> DNA
<213> Homo sapiens
<400> 1601

```
aaaattattt tgagacaaaa catgggaaag gagggagttg gccaggagtt tatcatgaag      60
catatacagg agtcatcccc tacgttgaca ctggtaagtt gacttcagtc acatgaaaca     120
tgtcaccttt ccataaatac tccattccct tttgtgattt tgttctttgc acatgttgtt     180
ctatctctgc ctggaatgtg ttctccacct tttgattgtc tgcca                     225
```

<210> 1602
<211> 258
<212> DNA
<213> Homo sapiens
<400> 1602

```
gtgaccacag tctgcagagg ccagagagag caggaaagga aatggaaagg aacctcacct      60
tcatgcttgg ggaaaaggag aaacctgtgt taatgtgtct tcccaacatc ccactctctt     120
```

```
cagcaatcgc tggaacagcc atgggccatc cctgctgagt caggaaagaa gctgagggaa     180
gagtcgggat tgaaaagcag cagacaaggg aaatgtggac acaagcacat gaagagaaca     240
ccatgtgaac ataaagat                                                   258

<210> 1603
<211> 341
<212> DNA
<213> Homo sapiens
<400> 1603
aaggttactt gactgggagt tctcagacct ccagtttcag ccctgccctc agcctccaat      60
ccgtaagaga yacccagccc cagcaattgg attgggcagc ccgtcttgac acaccactgt     120
gctgagtgct tgaggacgtg tttcaacaga tggttggggt tagtgtgtgt catcacattc     180
gagtggggat taagagaagg aaggctgcct tgctggagct gtgtggtctt ctccaagtga     240
gagtcgcagg caatagaact actttgcttt tggaggaaaa ggaggaattc attttcagca     300
gacacaagaa aagcagtttt tttttcaggt gctgacggcc a                         341

<210> 1604
<211> 292
<212> DNA
<213> Homo sapiens
<400> 1604
cactggcgcg ggttgagttc cctgttgccc ttggtctcgg ggtcgctgtm ggcgctgagg      60
ctgcagctat catggtgaac ttacttcaga ttgtgcggga ccactgggtt catgttcttg     120
tccctatggg atttgtcatt ggatgttatt tagacagaaa gagtgatgaa cggctaactg     180
ccttccggaa caagagtatg ttatttaaaa gggaattgca acccagtgaa gaagttacct     240
ggaagtaaag actggctaga ttatcgaatg ttcacatttt aaagttctga ga             292

<210> 1605
<211> 357
<212> DNA
<213> Homo sapiens
<400> 1605
ctgctctaag ctgcagcaag agaaactgtg tgtgagggga agaggcctgt ttcgctgtcg      60
ggtctctagt tcttgcacgc tctttaagag tctgcactgg aggaactcct gccattacca     120
gctcccttct tgcagaaggg agggggaaac atacatttat tcatgccagt ctgttgcatg     180
caggcttttt ggcttcctac cttgcaacaa aataattgca ccaactcctt agtgccgatt     240
ccgcccacag agagtcctgg arccacagtc tttttgcttt tgcattgtag gagagggact     300
aagtgctaga gactatgtcg ctttcctgag ctaccgagag cgctcgtgaa ctggaat        357

<210> 1606
<211> 293
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 13
<223> n=a, g, c or t

<400> 1606
attccctacc cancagccct cgcgcggtcc ggcacagcgg acaccaggac tccaaaatgg      60
cgtcagttgg tgagtgtccg gccccagtac cagtgaagga caagaaactt ctggaggtca     120
aactggggga gctgccaagc tggatcttga tgcggractt cagtcctagt ggcattttcg     180
gagcgtttca aaraggttac accggtacta caacaagtac atcaatgtga agaaggggag     240
catctcgggg attaccatgg tgctacccta ccacacattc gaagaacccg tat            293

<210> 1607
<211> 361
<212> DNA
<213> Homo sapiens

<220>
```

<221> misc_feature
<222> 323
<223> n=a, g, c or t

<400> 1607
tgttgtcttt atcagactta cattgcctct gtgaatatca gccttggtct actccaagtg 60
caggacaaac acaaagaact ctctgcacag ttcattactc cattaggtgg ttcagatgca 120
attccagccc ttagtcaggt tctttccagt gtcctcaaac acagtaagga gagtgctcta 180
agtgactctt tgtgtctcac acaatctctt gggttcccag gtcactggtg tagtagccag 240
ctgcatccaa gaagccaggt gagcctgtgc caccaatcac agatactcct taccaaccat 300
ctgccaaccc atgccagccc tgntgcccat ggatgtgcgg ctgtccatgt gccacgccca 360
c 361

<210> 1608
<211> 305
<212> DNA
<213> Homo sapiens
<400> 1608
aagacggaag ctcggttgat gtttctgcag aagttttccc ccttggtcgg tggcggastg 60
ctgagcgcga tagtagcagc tccggcggca gcaacattga ctacgaggaa tggcggcggc 120
tgccgcagga cctgcagcat cccagaggtg cagattttaa tttcagtgac tgaattaaaa 180
ggtgtcaaga agctcgaatg gtatgtaggt ctcccatggt atttcaattt aaaaagaagt 240
aagcacttga aattttttgg tttaagcaaa tttgttttta cctttataat ttattttaaa 300
taata 305

<210> 1609
<211> 242
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 152
<223> n=a, g, c or t

<400> 1609
aatctggtct ttctgtagac ccaagtcaga aggaaccatt tgtggagtta aatagaatat 60
tagaggcatt aaaggtcaga gttctgagac ctgctctgga gtgggcagtg tcaaaccggg 120
aaatgcttat agctcaaaca gctccttgga anttaagcta cacagactgt attttattag 180
cttgttaatg ggtggaacca caaatcagcg agaggcatta caatatgcta aaaattttca 240
gc 242

<210> 1610
<211> 196
<212> DNA
<213> Homo sapiens
<400> 1610
ggaagcgatt tcatagccac ggtttttggc tttcatcgct ttttctacat gtttttagcc 60
tcaccagaag tctttcatct cggtggtcca actcaggatc tcagcctcat tattttctta 120
cccttctgga gtgcatatgt gcctttacag ttctgtttgc aaacgctgtc tagcatacta 180
agaggatgtt agcaaa 196

<210> 1611
<211> 228
<212> DNA
<213> Homo sapiens
<400> 1611
atattgaata agcgacccgg cctcctaggg ggtcgtcgtg gtgcagacag tttagcagaa 60
cagcctccgc ggctccgggg agaaggtgag gtcttgtatg gatgggaagg gtgaggtgcg 120
tcggccagag gcttatttat tgacgggact gtttcctttg gcccacgcga cgtagcttct 180
gttgtccttg actgggcgcc gcctcccgcc ccgccgcctc ggaagccc 228

<210> 1612
<211> 221
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 108
<223> n=a, g, c or t

<400> 1612
tatttagag atggaacaaa gagaacacat agatattcaa taatttactc aaaagtctgt 60
gaggagccct agaaagaaat tcaggtctcc tatgtactga tcacagcnca gaaccccagg 120
aagccagagg tgttccaccc caatccttca ccctcacccc acatcatggt ggcccctggg 180
acctggatgg aaaacctctg gcwtcctggg gttctgggct g 221

<210> 1613
<211> 360
<212> DNA
<213> Homo sapiens
<400> 1613
agttgcctgc agagcctgag gtcagggaag gtctcagatg gttcatacct tggtgtatac 60
atgagttcat aggcctggga ttaaggatta tccctgcaat cttgcctgcc ttgcagataa 120
gctactttct gaatcctaaa gcgctcttcc agctttcaca tttgattccg tggcagaagg 180
ctcacagcct cacaaagtgg agacaggcag acagtcccac ctcatttcaa ctccagagtt 240
ggggaacgtg ctgggggtgc tcagccagag cctctcagcc aggccttgtg aggcagaggg 300
atccttacca ggcagatggt ctggaggaga ggcagaccgg gagaaagcat agtgtgccag 360

<210> 1614
<211> 171
<212> DNA
<213> Homo sapiens
<400> 1614
cagtaaggta gcaggattca aattattttt tccagtattg acatttagaa tgtcatgttg 60
gacatttaaa atttttctgg ttgtagcctc attactgtat agaaatcaac taccagatga 120
gtagttgaca gacacagcta gcttggttgc ttgcttgctg ttcttgccgc c 171

<210> 1615
<211> 193
<212> DNA
<213> Homo sapiens
<400> 1615
acatctttag tagagacggg caatccaccc gcctcggctc ccagagtact gggatgacag 60
gcgtgagcac cacgtccggc cacaaaagag ctttgatgca cacggtgaca gccacatggt 120
gcacccggaa gaacaagggg cctgaagtta gttagaccct ccttgctggt tctaccacag 180
tcgcacgccc cac 193

<210> 1616
<211> 349
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 99
<223> n=a, g, c or t

<400> 1616
atggttggaa tcatattcag caggagtaag ctgactaact tacaaaaaca ggtgtgtgct 60
catattgtcc aagctattcg catggaagct accagagtnc gtgaagaatg ggaacatgct 120

atatcaagca aagaaaatgc caattctcag ccaaatgatg aagatgcctc ctctgatgcc 180
tactgctttg agctgctctc tatggtttta gcactgagtg gctctaacgt tggccggcaa 240
tatctggctc aacagctaac cctgcttcag gatctcttcc gctgcttcac acagcctctc 300
ctagagtcca gagacaggta cctctttact agaagagttt gctgaagta 349

<210> 1617
<211> 155
<212> DNA
<213> Homo sapiens
<400> 1617
atacacatat ccatggtttg tgagaggctc ctcactaccc gtcctgtctc agaatgtcag 60
aatgccctgt ttccttccct tttgtggaca agtcaactct atacaatatt tgaagggatt 120
attctgaacc catctgaatg accaaggcct gaggc 155

<210> 1618
<211> 185
<212> DNA
<213> Homo sapiens
<400> 1618
cttgaaatgg gctgagtccc tcttgctcac ccttgacttg gaaaaaccag tttctctttt 60
attgtctgtt actaatctct attctaaaaa ttcagctcaa ttctcaacca tactccaaac 120
tctctctttt ccagctacct ttactccctc tccttcaatt ccactttcct ctgcttactt 180
ttttt 185

<210> 1619
<211> 169
<212> DNA
<213> Homo sapiens
<400> 1619
gggcgcaatg gcggatacgc tggagtcctc gctggaggac ccactgcgga gtttgtgcga 60
gttttggaga agcgggatgg tacagtgcta cgactacagc agtatagctc cggtggcgtg 120
ggtgcgttgt gtgggacgct gccattgtcc tttctaaata cctggaaac 169

<210> 1620
<211> 246
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 122
<223> n=a, g, c or t

<400> 1620
cagaggtttt gttttcttca taatttttat cactatctga attattttga ttctttgttt 60
atttgtgcat ttcacgttgt ttcctatatt ccgttcaatg taagctctat gagaccaaga 120
anstgggcag ttttattcac cataagtatt ccaagcccta gtggttcctg gcacattttg 180
tattcacaat aaatatttgt taagtcaatg accagatgaa tggcttttaa actcaagata 240
gttttt 246

<210> 1621
<211> 280
<212> DNA
<213> Homo sapiens
<400> 1621
agtctaggga aagtcattca gtggatgtga tcttggctca caggggacga tgtcaagctc 60
ttcctggctc cttctcagcc ttgttgctgt aactgctgct cagtccacca ttgaggaaca 120
ggccaaagac atttttggac aagtttaacc acgaagccga agacctgttc tatcaaagtt 180
cacttgcttc ttggaattat aacaccaata ttactgaaga gaatgtccaa aacatgaata 240
atgctgggga caaatggtct gcctttttaa aggaacagtc 280

<210> 1622

<211> 400
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 43
<223> n=a, g, c or t

<400> 1622
agggagggac agagagcgaa ctgtcagatc ggagcgagag cgngcgcccg agagagggag 60
agagagagag ggagggagag gaaaagtgag agagggaaag agagcgcgaa cgagggcgca 120
gagcgagctc ctgctgcaac tctgctccag cacggccagc gccagcgccc gccgtcggtg 180
cactctacga gccgtgcagc gtgcccactg gagttgttgt gtatcaagga tcgatcccct 240
atatgcacac acacacctcc acctccacca atgcactctt cttcctcctc cttctccaga 300
caactgctgg gaaaaaaata aaacaccaac cccaaccgtc agcaacaagg taasmgagcg 360
attcgacatc attttttttc ctgttcaatt ttttccttgt 400

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 :
C12N 15/11, 15/10, C07K 14/47, C12P 21/00, C12Q 1/68, C07K 16/18, G06F 17/30, 17/50

A3

(11) International Publication Number: WO 99/53051

(43) International Publication Date: 21 October 1999 (21.10.99)

(21) International Application Number: PCT/IB99/00712

(22) International Filing Date: 9 April 1999 (09.04.99)

(30) Priority Data:

| | | |
|---|---|---|
| 09/057,719 | 9 April 1998 (09.04.98) | US |
| 09/069,047 | 28 April 1998 (28.04.98) | US |

(71) Applicant (*for all designated States except US*): GENSET [FR/FR]; 24, rue Royale, F-75008 Paris (FR).

(72) Inventors; and
(75) Inventors/Applicants (*for US only*): DUMAS MILNE EDWARDS, Jean-Baptiste [FR/FR]; 8, rue Grégoire-de-Tours, F-75006 Paris (FR). DUCLERT, Aymeric [FR/FR]; 6 ter, rue Victorine, F-94100 Saint-Maur (FR). GIORDANO, Jean-Yves [FR/FR]; 12, rue Duhesme, F-75018 Paris (FR).

(74) Agents: MARTIN, Jean-Jacques et al.; Cabinet Regimbeau, 26, avenue Kléber, F-75116 Paris (FR).

(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).

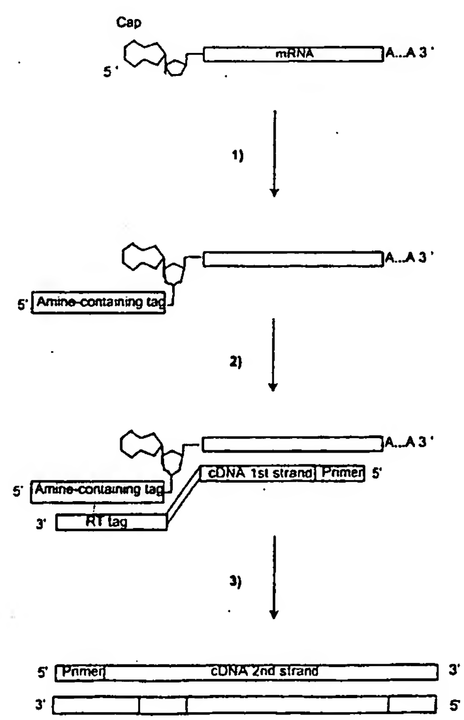
**Published**
*With international search report.*

(88) Date of publication of the international search report: 6 April 2000 (06.04.00)

(54) Title: 5' ESTS AND ENCODED HUMAN PROTEINS

(57) Abstract

The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be otained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.



*FOR THE PURPOSES OF INFORMATION ONLY*

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| AL | Albania | ES | Spain | LS | Lesotho | SI | Slovenia |
| AM | Armenia | FI | Finland | LT | Lithuania | SK | Slovakia |
| AT | Austria | FR | France | LU | Luxembourg | SN | Senegal |
| AU | Australia | GA | Gabon | LV | Latvia | SZ | Swaziland |
| AZ | Azerbaijan | GB | United Kingdom | MC | Monaco | TD | Chad |
| BA | Bosnia and Herzegovina | GE | Georgia | MD | Republic of Moldova | TG | Togo |
| BB | Barbados | GH | Ghana | MG | Madagascar | TJ | Tajikistan |
| BE | Belgium | GN | Guinea | MK | The former Yugoslav Republic of Macedonia | TM | Turkmenistan |
| BF | Burkina Faso | GR | Greece | | | TR | Turkey |
| BG | Bulgaria | HU | Hungary | ML | Mali | TT | Trinidad and Tobago |
| BJ | Benin | IE | Ireland | MN | Mongolia | UA | Ukraine |
| BR | Brazil | IL | Israel | MR | Mauritania | UG | Uganda |
| BY | Belarus | IS | Iceland | MW | Malawi | US | United States of America |
| CA | Canada | IT | Italy | MX | Mexico | UZ | Uzbekistan |
| CF | Central African Republic | JP | Japan | NE | Niger | VN | Viet Nam |
| CG | Congo | KE | Kenya | NL | Netherlands | YU | Yugoslavia |
| CH | Switzerland | KG | Kyrgyzstan | NO | Norway | ZW | Zimbabwe |
| CI | Côte d'Ivoire | KP | Democratic People's Republic of Korea | NZ | New Zealand | | |
| CM | Cameroon | | | PL | Poland | | |
| CN | China | KR | Republic of Korea | PT | Portugal | | |
| CU | Cuba | KZ | Kazakstan | RO | Romania | | |
| CZ | Czech Republic | LC | Saint Lucia | RU | Russian Federation | | |
| DE | Germany | LI | Liechtenstein | SD | Sudan | | |
| DK | Denmark | LK | Sri Lanka | SE | Sweden | | |
| EE | Estonia | LR | Liberia | SG | Singapore | | |

# INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 99/00712

**A. CLASSIFICATION OF SUBJECT MATTER**
IPC 6 C12N15/11 C12N15/10 C07K14/47 C12P21/00 C12Q1/68
C07K16/18 G06F17/30 G06F17/50

According to International Patent Classification (IPC) or to both national classification and IPC

**B. FIELDS SEARCHED**

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | BRENNER ET AL.: "Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus ...." EMBL SEQUENCE DATABASE, 9 May 1996 (1996-05-09), XP002121588 HEIDELBERG DE | 1,2 |
| Y | Ac U52112 the whole document & BRENNER ET AL.: "Genomic organization of two novel genes on human Xq28: compact head to head arrangement of IDH gamma and TRAP delta is conserved in rat and mouse" GENOMICS, vol. 44, no. 1, 1997, pages 8-14, --- | 4-21 |

-/--

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 4 November 1999 | 28. JAN. 2000 |

| Name and mailing address of the ISA | Authorized officer |
|---|---|
| European Patent Office, P.B. 5818 Patentlaan 2<br>NL - 2280 HV Rijswijk<br>Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,<br>Fax: (+31-70) 340-3016 | CEDER O. |

2

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| X | SAKAI ET AL.: "Protein kinase C substrate, 80 kD protein, heavy chain (PKCSH)" SWISSPROT SEQUENCE DATA BASE, 1 January 1990 (1990-01-01), XP002121589 HEIDELBERG DE Ac P14314 the whole document -& SAKAI ET AL.: "Human 80K-H protein (kinase C substrate) mRNA, complete compound" EMBL SEQUENCE DATABASE, 1 February 1990 (1990-02-01), XP002121590 HEIDELBERG DE Ac J03075 the whole document & SAKAI ET AL.: "Isolation of cDNAs encoding a substrate for protein kinase C: nucleotide sequence and chromosomal mapping of the gene for a human 80K protein" GENOMICS, vol. 5, 1989, pages 309-315, --- | 3 |
| Y | WO 96 34981 A (GENSET ;MERENKOVA IRENA NICOLAEVNA (FR); DUMAS MILNE EDWARDS JEAN) 7 November 1996 (1996-11-07) cited in the application page 13, line 24 -page 14, line 14; claim 26 --- | 4 |
| Y | GREENWOOD M T ET AL: "Cloning of the gene encoding human somatostatin receptor 2: sequence analysis of the 5@?-flanking promoter region" GENE, vol. 159, no. 2, 4 July 1995 (1995-07-04), page 291-292 XP004042228 ISSN: 0378-1119 abstract --- | 5 |
| Y | KATO S ET AL: "Construction of a human full-length cDNA bank" GENE, vol. 150, 1 January 1994 (1994-01-01), pages 243-250, XP002081364 ISSN: 0378-1119 cited in the application abstract page 245, left-hand column --- | 6,10 |

-/--

2

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| Y<br><br><br>A | WO 97 38003 A (HUMAN GENOME SCIENCES INC ;LI HAODONG (US); WEI YING FEI (US)) 16 October 1997 (1997-10-16)<br>seq Id No 2<br>claims 10-12 | 7,11,20, 21<br><br>3 |
| Y | LOCKHART D J ET AL: "EXPRESSION MONITORING BY HYBRIDIZATION TO HIGH-DENSITY OLIGONUCLEOTIDE ARRAYS" BIO/TECHNOLOGY, vol. 14, no. 13, 1 December 1996 (1996-12-01), pages 1675-1680, XP002022521 ISSN: 0733-222X<br>abstract | 8,9 |
| Y | WO 98 07830 A (INST GENOMIC RESEARCH ;UNIV PENNSYLVANIA (US); UNIV JOHNS HOPKINS) 26 February 1998 (1998-02-26)<br>page 3, line 4 - line 28<br>page 31, line 6 -page 35, line 16 | 7,11-21 |
| X | MUZNY ET AL.: "Homo sapiens, working draft sequence, 97 unordered pieces" EMBL SEQUENCE DATABASE, 3 February 1998 (1998-02-03), XP002121591 HEIDELBERG DE Ac AC004085<br>the whole document | 1,2 |
| X | ADAMS ET AL.: "EST177394 Jurkat T-cells VI homo sapiens cDNA 5' end similar to protein kinase C substrate 80K-H" EMBL SEQUENCE DATABASE, 18 April 1997 (1997-04-18), XP002121592 HEIDELBERG DE Ac AA306438<br>the whole document<br>-& ADAMS ET AL.: "Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequences" NATURE, vol. 377, 1995, pages 3-174, XP002069461 | 3 |
| A | "zr94d07.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:683341 5' EST" EMBL SEQUENCE DATABASE, 5 February 1997 (1997-02-05), XP002121593 HEIDELBERG DE Ac AA215334<br>the whole document | 1,2 |

-/--



Form PCT/ISA/210 (continuation of second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| A | ADAMS M D ET AL: "RAPID CDNA SEQUENCING (EXPRESSED SEQUENCE TAGS) FROM A DIRECTIONALLY CLONED HUMAN INFANT BRAIN CDNA LIBRARY" NATURE GENETICS, vol. 4, no. 4, 1 August 1993 (1993-08-01), pages 373-380, STANDARD, XP002064427 ISSN: 1061-4036 | |
| A | ADAMS M D ET AL: "3,400 NEW EXPRESSED SEQUENCE TAGS IDENTIFY DIVERSITY OF TRANSCRIPTS IN HUMAN BRAIN" NATURE GENETICS, vol. 4, no. 3, 1 July 1993 (1993-07-01), pages 256-267, XP000645060 ISSN: 1061-4036 | |
| A | TASHIRO K ET AL: "SIGNAL SEQUENCE TRAP: A CLONING STRATEGY FOR SECRETED PROTEINS AND TYPE I MEMBRANE PROTEINS" SCIENCE, vol. 261, 30 July 1993 (1993-07-30), pages 600-603, XP000673204 ISSN: 0036-8075 | |
| A | CARNINCI P ET AL: "High-efficiency full-length cDNA cloning by biotinylated CAP trapper" GENOMICS, vol. 37, no. 3, 1 November 1996 (1996-11-01), pages 327-336, XP002081729 ISSN: 0888-7543 | |

2

**INTERNATIONAL SEARCH REPORT**

International application No.
PCT/IB 99/00712

**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.: -
because they relate to subject matter not required to be searched by this Authority, namely:

Rule 39.1(v) PCT - Presentation of information
Although claim 12 could be considered as a mere presentation of information, Rule 39.1(v) PCT, the search has been carried out as far as possible in our systematic documentation.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

**Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Invention 1: 1-21 partially

**Remark on Protest**

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.1

Although claim 12 could be considered as a mere presentation of information, Rule 39.1(v) PCT, the search has been carried out as far as possible in our systematic documentation.

--------------------

Continuation of Box I.1

Rule 39.1(v) PCT - Presentation of information

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Invention 1: 1-21 all partially

   Nucleic acid comprising a sequence as in Seq.ID.No. 24, complementary sequence and fragments thereof. Polypeptide, Seq.Id.No. 812, encoded by said nucleotide sequence. Vector comprising Seq.Id.No. 24 and host cell comprising the vector. Methods of making cDNA and polypeptide utilising Seq.Id.No. 24. Array of ESTs comprising Seq.Id.No. 24, or a fragment thereof. An antibody binding to an epitop of the polypeptide of Seq.Id.No. 812. A computer readable medium and a computer system storing and/or utilising the sequence of Seq.Id.No. 24 or 812.

2. Claims: Invention 2-811 : 1-21 all partially

   Idem as subject 1 but limited to each of the DNA sequences as in Seq.Id.No. 25-811 and 1600-1622, and corresponding polypeptides when applicible, where invention 2 is limited to Seq.Id.No. 25 and 813, invention 3 is limited to Seq.Id.No. 26 and 814, .........., invention 788 is limited to Seq.Id.No. 811 and 1599, invention 789 is limited to Seq.Id.No. 1600, invention 790 is limited to Seq.Id.No. 1601, .........., invention 811 is limited to Seq.Id.No. 1622.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/IB 99/00712

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
|---|---|---|---|
| WO 9634981 A | 07-11-1996 | FR 2733765 A | 08-11-1996 |
| | | FR 2733762 A | 08-11-1996 |
| | | AU 5982996 A | 21-11-1996 |
| | | CA 2220045 A | 07-11-1996 |
| | | EP 0824598 A | 25-02-1996 |
| | | JP 11510364 T | 14-09-1999 |
| WO 9738003 A | 16-10-1997 | AU 5389096 A | 29-10-1997 |
| | | US 5945303 A | 31-08-1999 |
| WO 9807830 A | 26-02-1998 | NONE | |